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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, polypeptide sequences encoded by these nucleic acids and uses thereof.

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NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, circulating soluble factors, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize

one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-93. The polypeptides sequences are designated SEQ ID NO: 94-186. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is unknown or any of the four bases.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1-93 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1-93. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1-93 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-93. The sequence information can be a segment of any one of SEQ ID NO: 1-93 that uniquely identifies or represents the sequence information of SEQ ID NO: 1-93.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information are provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

10 In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-93 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-93 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and
15 exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-93; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1-93;
20 and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-93. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-93; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence
25 Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

30 The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in SEQ ID NO: 94-186; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a

nucleotide sequence set forth in SEQ ID NO: 1-93; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%,
5 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention.
10 Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention
15 comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of
20 techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides
25 of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for
30 physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the

polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

- Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

- The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions.
- The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

- The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

- The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other

substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound binds to a polypeptide of the invention is identified.

The methods of the invention also provide methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2); for which they have a signature region (as set forth in Table 3); or for which they have homology to a gene family (as set forth in Table 4). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the

natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or

synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures, or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NO: 1-93.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation, and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular

Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-93. The sequence information can be a segment of any one of SEQ ID NO: 1-93 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO: 1-93. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1+4^{25}$) times the increased probability for mismatch at each nucleotide position (3×25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 500 amino acids, more preferably less than 200 amino acids more preferably less than 150 amino acids, and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include an initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e.g., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by

comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may
5 be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the
10 properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis
15 of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine,
20 and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting
25 recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions, or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may
30 change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells

chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include

an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the

- 5 recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers.
- 10 Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

- The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence
- 15 when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1
- 20 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2): 134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

- Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell.. Such a
- 25 sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

- The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1
- 30 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

- 5 As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more
- 10 than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the
- 15 invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially
- 20 equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower
- 25 percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least
- 30 about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence

(e.g., via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J. (1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

- 5 The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

 The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the
10 introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

 As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based
15 systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

- 20 Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

 Nucleotide sequences of the invention are set forth in the Sequence Listing.

- 25 The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 1-93; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO: 94-186; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO: 94-186. The polynucleotides of the present invention also include, but are not limited to, a
30 polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1-93; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing as SEQ ID NO: 94-186; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a

polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 94-186. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1-93 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-93 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-93 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpr, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least

about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-93, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically hybridize to) any one of the polynucleotides of the invention are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1-93, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-93 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO: 1-93, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altschul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

5 The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids
10 encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative
15 choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions
20 ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine
25 sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of
30 the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith,

Nucleic Acids Res. 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., *supra*, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-93, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et

al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a

- 5 polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic
10 cell and can be a unicellular organism or part of a multicellular organism.

- The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-93 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a
15 nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-93 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available
20 for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

- 25 The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the
30 isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced

or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

- 5 Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid
10 sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE NUCLEIC ACIDS

- Another aspect of the invention pertains to isolated antisense nucleic acid molecules
15 that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1-93, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific
20 aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID NO: 94-186 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1-93 are additionally provided.
- 25 In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence
30 of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO: 1-93), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of an mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of an mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxoacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxoacetic acid methylester, uracil-5-oxoacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or

genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific
5 interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed
10 on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III
15 promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641).
20 The antisense nucleic acid molecule can also comprise a 2'-*o*-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

25 In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a
30 mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO: 1-93). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is

complementary to the nucleotide sequence to be cleaved in an mRNA of SEQ ID NO: 1-93 (see, e.g., Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742). Alternatively, polynucleotides of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel *et al.*, (1993)

5 *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (e.g., promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; 10 and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med* 15 *Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed 20 using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting 25 replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

30 In another embodiment, PNAs of the invention can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaire *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

25

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells

5 express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the

10 multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

15 The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one

20 of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1

25 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to

30 produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition,

Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the

control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (*gpt*) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No.

PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

5 4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 94-186 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-93 or the corresponding full length or mature protein. Polypeptides of the invention also
10 include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-93 or (b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 94-186 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention
15 also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 94-186 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least
20 about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 94-186.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein
25 may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding
30 sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide

sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins
5 are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

10 The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical
15 polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The
20 synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may
25 be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used
30 herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic

sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 94-186.

The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

- 5 The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.
- 10 Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.
- 15 The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBaf™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."
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- 25
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The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography.

- 5 The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

- 10 Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and
15 Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

- Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl
20 or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

- 25 The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic
30 agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes,

- dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

- Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., *Nucleic Acids Research* 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., *J. Molec. Biol.* 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., *Nucleic Acids Res.* vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., *J. Comp. Biol.*, Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, *ISMB-97*, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., *Nucleic Acids Res.*, Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference), the GeneAtlas software (Molecular Simulations Inc. (MSI), San Diego, CA) (Sanchez and Sali (1998) *Proc. Natl. Acad. Sci.*, 95, 13597-13602; Kitson DH et al, (2000) "Remote homology detection using structural modeling - an evaluation" Submitted; Fischer and Eisenberg (1996) *Protein Sci.* 5, 947-955), Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark), and the Kyte-Doolittle hydrophobicity prediction algorithm (*J. Mol Biol*, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

- The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a

fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein. In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprise one or more domains fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, e.g., cancer as well as modulating (e.g., promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, e.g., by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs

between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a
5 GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

10 Mutations in the polynucleotides of the invention may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly
15 viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of
20 any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for
25 therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense
30 molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell. These methods can be used to increase or decrease the expression of
5 the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous
10 promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g.,
15 ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

20 In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a
25 different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by
30 targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element.

- 5 Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (*gpt*) gene.
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- The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultschi et al., each of which is incorporated by reference herein in its entirety.
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4.9 TRANSGENIC ANIMALS

- In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals,
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can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecci, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the

polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant

protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map
5 related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other
10 support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that
15 described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the
20 labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to
25 screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A
30 Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate.

- 5 In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

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4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

- A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or
15 inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of therapeutic compositions of the
20 present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

- 25 Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986;
30 Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

- Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- γ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

- Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

- Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

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4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent

stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues,

5 transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors.

The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage,
10 tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the
15 desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors
20 and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance
25 the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder layer for the stem cell populations in culture or *in vivo*. Stromal support cells for feeder layers may include embryonic bone marrow
30 fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for

generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin. Invest.*, 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell sources (including hematopoietic stem cells and embryonic stem cells) and

cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci., U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders.

Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation,

those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of

bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the

5 composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or
10 ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention
15 contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth
20 of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of
25 neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies,
30 and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as

stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with
5 vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such
10 tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and
15 conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

20 Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in:
25 Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

30 A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and

disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animal models such as the cumulative contact enhancement test (Lastbom et al., *Toxicology* 125: 59-66, 1998), skin prick test (Hoffmann et al., *Allergy* 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., *Arch. Toxicol.* 73: 501-9), and murine local lymph node assay (Kimber et al., *J. Toxicol. Environ. Health* 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of

an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing
5 non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without
10 limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by
15 T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the
20 necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in
25 humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed.,
30 Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of

- 5 autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of
- 10 blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed.,
- 15 Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in

20 cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form

25 of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected

30 cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In

addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation,

- those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986;
- 5 Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

- Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of
- 10 Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of
- 15 Experimental Medicine 172:631-640, 1990.

- Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer
- 20 Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

- Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et
- 25 al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad. Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

- A polypeptide of the present invention may also exhibit activin- or inhibin-related
- 30 activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present

invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of

cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

- 5 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

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4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

- A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

- 25 Therapeutic compositions of the invention can be used in the following:
Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

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4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the

invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without

necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a

- 5 pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include:
- Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl
- 10 (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX),
- 15 Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguanzone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

- In addition, therapeutic compositions of the invention may be used for prophylactic
- 20 treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

- 25 *In vitro* models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanela et al., J. Natl. Can. Inst.,
- 30 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-

97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

5 A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved
10 in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present
15 invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described
20 in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenberg et
25 al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

30 Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide

to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules.

- 5 Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

- This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays.
- 10 Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

- Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.
- 20

- Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.
- 25

- The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).
- 30

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis

methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.*, 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population

expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this

invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- 5 (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of
10 the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not
15 limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
- (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or
20 injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.
- Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or
25 differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:
- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*,
30 e.g., choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.
- Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set

forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motor sensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of

- the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity
- 5 which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

- The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for
- 10 diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to
- 15 inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

- Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of
- 20 the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that
- 25 hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The
- 30 array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

5 4.10.20 **ARTHRITIS AND INFLAMMATION**

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

15 The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would
20 reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies
25 or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

30 One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An

exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of

5 polypeptide administered per dose will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1 µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution,

10 dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

15 4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be

20 administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic

25 material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2,

30 G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming

growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use
5 in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-
10 inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hyl, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical
15 compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that
20 therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or
25 amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in
30 combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the

present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated

from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

5 Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of
10 conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or
15 elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water,
20 petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90%
25 by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a
30 pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or

other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene

glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable

polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with

inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of
5 the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins
10 including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T
15 cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution.
20 Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

25 The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient.
30 Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not

increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μg to about 100 mg (preferably about 0.1 μg to about 10 mg, more preferably about 0.1 μg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For

5 compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a

10 viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the

15 methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted

20 medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate,

25 tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised

30 of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole

weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

- 5 A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,
- 10 poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby
- 15 providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors
- 20 (TGF- α and TGF- β), and insulin-like growth factor (IGF).

- The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue
- 25 regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used
- 30 in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by

periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate *in vitro* assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD_{50} and ED_{50} . Compounds which exhibit high therapeutic

indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 $\mu\text{g/kg}$ to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 $\mu\text{g/kg}$ to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be

prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

- 5 Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab}' and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule
10 obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a
15 reference to all such classes, subclasses and types of human antibody species.

- An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively,
20 the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as the amino acid sequences shown in SEQ ID NO: 94-186, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that
25 contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

- In certain embodiments of the invention, at least one epitope encompassed by the
30 antigenic peptide is a region of -related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for

targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; 5 Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

10 A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: 15 A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

4.13.1 POLYCLONAL ANTIBODIES

20 For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a 25 recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response 30 include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents.

Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

- The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

4.13.2 MONOCLONAL ANTIBODIES

- The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

- Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

- The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly

myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine
5 phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a
10 medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984);
15 Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by
20 immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target
25 antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.
30 The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

4.13.3 HUMANIZED ANTIBODIES

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the

imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

4.13.4 HUMAN ANTIBODIES

10 Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 *Immunol Today* 4: 72) and the EBV
15 hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp.
20 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by
25 introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806;
30 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al. (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature

Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in

culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

- 5 In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

4.13.5 F_{ab} FRAGMENTS AND SINGLE CHAIN ANTIBODIES

- 10 According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or
- 15 derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F_{(ab)₂} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab)₂} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing
- 20 agent and (iv) F_v fragments.

4.13.6 BISPECIFIC ANTIBODIES

- Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the
- 25 binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

- Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two
- 30 immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the

correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab' -TNB derivatives is then reconverted to the Fab' -thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab' -TNB

derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992)

5 describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

10 Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced
15 at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a
20 light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (scFv) dimers has also been reported. See, Gruber et
25 al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an
30 immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific

antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

4.13.7 HETEROCONJUGATE ANTIBODIES

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptopbutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

4.13.8 EFFECTOR FUNCTION ENGINEERING

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

4.13.9 IMMUNOCONJUGATES

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

5 Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, 10 PAPII, and PAP-S), momordica charantia inhibitor, curcun, croton, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of 15 bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimide HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates 20 (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyl-diethylene triamine-pentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionuclide to the antibody. See WO94/11026.

25 In another embodiment, the antibody can be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

30

4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media"

refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as

5 magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for

10 recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means

15 chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application,

20 such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO: 1-93 or a representative

25 fragment thereof, or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO: 1-93 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which

30 implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important

proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with

nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

- 5 In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

- 10 In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

- Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, 15 amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 20 (1985); Tijssen, P., *Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay 25 format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

- 30 In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the

following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO: 1-93, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

(a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and

(b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein

encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the

ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

5 Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO: 1-93. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide
10 sequences SEQ ID NO: 1-93 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used
15 in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the
20 cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective
25 genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The
30 technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound

to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, (1991). In this technology, a phosphoramidate bond is employed (Chu *et al.*, (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ μ l) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. The single-stranded DNA solution is then dispensed into CovaLink NH strips (75 μ l/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 μ l added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may

also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

- 5 To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

- 10 One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

15 4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

- The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from
20 mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

- 25 The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

- Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are
30 passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The

results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *CviJI*, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and
5 fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *CviJI* normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*CviJI***), yield a quasi-random distribution of DNA fragments from
10 the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *CviJI*** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *CviJI*** restricts
15 pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 µg instead of
20 2-5 µg); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are
25 contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which
30 correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type

of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one
5 example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm
10 space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to
15 flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following
20 examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently,
25 the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5. EXAMPLES

5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences

5.2 EXAMPLE 2

Assemblage of Novel Nucleic Acids

The nucleic acids of the present invention, designated as SEQ ID NO: 1-93 were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST, gb pri, UniGene, and exons from public domain genomic sequences predicated by GenScan) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Further, inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), full-length gene sequences and their corresponding protein sequences were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTXY algorithm against Genbank (i.e., dbEST, gb pri, UniGene, and Genpept). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and go-zip-2 (Hyseq,

Inc.). The full-length nucleotide sequences are shown in the Sequence Listing as SEQ ID NO: 1-93. The corresponding polypeptide sequences are SEQ ID NO: 94-186.

Table 1 shows the various tissue sources of SEQ ID NO: 1-93.

The nearest neighbor results for polypeptides encoded by SEQ ID NO: 1-93 (i.e. SEQ ID NO: 94-186) were obtained by a BLASTP (version 2.0a1 19MP-WashU) search against Genpept, Geneseq and SwissProt databases using BLAST algorithm. The nearest neighbor result showed the closest homologue with functional annotation for SEQ ID NO: 1-93. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1-93 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), polypeptides encoded by SEQ ID NO: 1-93 (i.e. SEQ ID NO: 94-186) were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the Pfam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) polypeptides encoded by SEQ ID NO: 1-93 (i.e. SEQ ID NO: 94-186) were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the product of all the e-value of similar domains found, the pFam score for the identified domain within the sequence, number of similar domains found, and the position of the domain in the SEQ ID NO: being interrogated..

The GeneAtlas™ software package (Molecular Simulations Inc. (MSI), San Diego, CA) was used to predict the three-dimensional structure models for the polypeptides encoded by SEQ ID NO: 1-93 (i.e. SEQ ID NO: 94-186). Models were generated by (1) PSI-BLAST which is a multiple alignment sequence profile-based searching developed by Altschul et al, (Nucl. Acids. Res. 25, 3389-3408 (1997)), (2) High Throughput Modeling (HTM) (Molecular Simulations Inc. (MSI) San Diego, CA,) which is an automated sequence and structure searching procedure (<http://www.msi.com/>), and (3) SeqFold™ which is a fold recognition method described by Fischer and Eisenberg (J. Mol. Biol. 209, 779-791 (1998)). This analysis was carried out, in part, by comparing the polypeptides of the invention with the known NMR (nuclear magnetic resonance) and x-ray crystal three-dimensional structures as

templates. Table 5 shows, "PDB ID", the Protein DataBase (PDB) identifier given to template structure; "Chain ID", identifier of the subcomponent of the PDB template structure; "Compound Information", information of the PDB template structure and/or its subcomponents; "PDB Function Annotation" gives function of the PDB template as annotated by the PDB files (<http://www.rcsb.org/PDB/>); start and end amino acid position of the protein sequence aligned; PSI-BLAST score, the verify score, the SeqFold score, and the Potential(s) of Mean Force (PMF). The verify score is produced by GeneAtlas™ software (MSI), is based on Dr. Eisenberg's Profile-3D threading program developed in Dr. David Eisenberg's laboratory (US patent no. 5,436,850 and Luthy, Bowie, and Eisenberg, Nature, 356:83-85 (1992)) and a publication by R. Sanchez and A. Sali, Proc. Natl. Acad. Sci. USA, 95:13597-12502. The verify score produced by GeneAtlas normalizes the verify score for proteins with different lengths so that a unified cutoff can be used to select good models as follows:

$$\text{Verify score (normalized)} = (\text{raw score} - 1/2 \text{ high score}) / (1/2 \text{ high score})$$

The PFM score, produced by GeneAtlas™ software (MSI), is a composite scoring function that depends in part on the compactness of the model, sequence identity in the alignment used to build the model, pairwise and surface mean force potentials (MFP). As given in Table 5, a verify score between 0 to 1.0, with 1 being the best, represents a good model. Similarly, a PMF score between 0 to 1.0, with 1 being the best, represents a good model. A SeqFold™ score of more than 50 is considered significant. A good model may also be determined by one of skill in the art based all the information in Table 5 taken in totality.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determined from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et al, as reference, were obtained for the polypeptide sequences. Table 6 shows the position of the last

amino acid of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

Table 7 correlates each of SEQ ID NO: 1-93 to a specific chromosomal location.

- Table 8 is a correlation table of the novel polynucleotide sequences SEQ ID NO: 1-93, novel polypeptide sequences SEQ ID NO: 94-186, and their corresponding priority nucleotide sequences in the priority application USSN 09/728,952, herein incorporated by reference in its entirety.

TABLE 1

Tissue Origin	RNA/Tissue Source	Library Name	SEQ ID NO:
adult brain	GIBCO	AB3001	26 40 43
adult brain	GIBCO	ABD003	2-5 40 47 54-55 57
adult brain	Clontech	ABR001	2 39 85
adult brain	Clontech	ABR006	3-4 40 47 69 80
adult brain	Clontech	ABR008	1 3-6 10 12 15-16 30-31 40 42 47 50 54-55 57 67-68 72-74 86
adult brain	Invitrogen	ABR013	1
adult brain	Invitrogen	ABR015	47
brain	Invitrogen	ABR016	57
adult brain	Invitrogen	ABT004	10 15 42 47
cultured preadipocytes	Stratagene	ADP001	43
adrenal gland	Clontech	ADR002	2 24 39-40 43 46 50 56 68 73
adult heart	GIBCO	AHR001	2-5 14 40 43 49 60 64-65 71
adult kidney	GIBCO	AKD001	2 7 15 19 40 43-44 49-51 53 71 77
adult kidney	Invitrogen	AKT002	2-5 39-40 43 49-50 53 57 83 85
adult lung	GIBCO	ALG001	39-40 43-44 85
lymph node	Clontech	ALN001	38 44
young liver	GIBCO	ALV001	7
adult liver	Invitrogen	ALV002	7 9 38 43 47 52 82
adult liver	Clontech	ALV003	56
adult ovary	Invitrogen	AOV001	2-5 7 15-18 38-40 43-44 49 52 56-57 77 85
placenta	Invitrogen	APL002	44
adult spleen	GIBCO	ASP001	10 38 43 50 61-62
testis	GIBCO	ATS001	24 44 53 56
adult bladder	Invitrogen	BLD001	15 56
bone marrow	Clontech	BMD001	40-41 48 50 57-58
bone marrow	Clontech	BMD002	2-5 17-18 24 30-31 38 41 43 48 53-55 58-60 68 73 86
Mixture of 16 tissues- mRNAs	Various Vendors*	CTL016	24
adult cervix	BioChain	CVX001	11 15 39-40 54-55 63 66 71 77 82 85
endothelial cells	Stratagene	EDT001	2-4 15-16 40 43-44 47 50 57
fetal brain	Clontech	FBR006	2-6 10 13 16 31 42 46 49 66-68 73 78 86
fetal brain	Invitrogen	FBT002	24 44 47 61-62
fetal heart	Invitrogen	FHR001	43 68 73 77 86
fetal kidney	Clontech	FKD001	44 72
fetal kidney	Clontech	FKD002	49 66 77 88

Tissue Origin	RNA/Tissue Source	Library Name	SEQ ID NO:
fetal lung	Clontech	FLG001	64-65
fetal lung	Invitrogen	FLG003	15 39 63-65 71-72 85
fetal liver-spleen	Columbia University	FLS001	2-5 7 9 22-24 26 35 38-41 44-46 49 51-52 54-55 59-62 68 73 77 85 87
fetal liver-spleen	Columbia University	FLS002	7 22-24 35 39-41 43-46 54-55 59-62 67 73 76 83-85
fetal liver-spleen	Columbia University	FLS003	26
fetal liver	Invitrogen	FLV001	22-24 44 49-50 52 61-62
fetal liver	Clontech	FLV004	41 68 73
fetal muscle	Invitrogen	FMS001	3-5 15 24 50 52
fetal muscle	Invitrogen	FMS002	56
fetal skin	Invitrogen	FSK001	3-5 15 22-24 39-40 44 51-53 57 61-62 79-82 85
fetal skin	Invitrogen	FSK002	3-5 31 49 72
fetal spleen	BioChain	FSP001	43
umbilical cord	BioChain	FUC001	3-5 10 15 39-40 44 72
fetal brain	GIBCO	HFB001	2 10 40 47 50 63 77 86
macrophage	Invitrogen	HMP001	43
infant brain	Columbia University	IB2002	1 6 12 31 40 42 44 47 52 56 61-62 66 72 82 86
infant brain	Columbia University	IB2003	50 56 86
infant brain	Columbia University	IBS001	72
fibroblast	Stratagene	LFB001	39-40 49 57
lung tumor	Invitrogen	LGT002	3-5 38-40 43 49 54-57 85
lymphocytes	ATCC	LPC001	58
leukocyte	GIBCO	LUC001	3-5 15 17-19 26 31 38 43-44 50 54-55 58
leukocyte	Clontech	LUC003	41 43
melanoma from cell line ATCC #CRL 1424	Clontech	MBL004	2 57
mammary gland	Invitrogen	MMG001	3-5 15 30 38 43-44 47 50 54-57 71
induced neuron cells	Stratagene	NTD001	42
neuronal cells	Stratagene	NTU001	1 24 42 72
pituitary gland	Clontech	PIT004	47
placenta	Clontech	PLA003	14 19 43 63-65
rectum	Invitrogen	REC001	10 22-24 61-62 68 73
salivary gland	Clontech	SAL001	40
small intestine	Clontech	SIN001	2 22-24 30 66 68-69 73 84
skeletal muscle	Clontech	SKM001	3-5 40 51
spinal cord	Clontech	SPC001	40 45 50 70
adult spleen	Clontech	SPLc01	8 15-16 40 43 68 73 86
stomach	Clontech	STO001	57-58 75
thalamus	Clontech	THA002	30 51 57 82
thymus	Clontech	THM001	2-5 24 43 86
thymus	Clontech	THMc02	2 15 33 38 44 46 48-49 66 73 86
thyroid gland	Clontech	THR001	2 7 15 39-40 54-55 58 69 71 86-87
trachea	Clontech	TRC001	44 54-55
uterus	Clontech	UTR001	8

- The 16 tissue/mRNAs and their vendor sources are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) Normal adult kidney mRNA (Invitrogen), 3) Normal fetal brain mRNA (Invitrogen), 4) Normal adult liver mRNA (Invitrogen), 5) Normal fetal kidney mRNA (Invitrogen), 6) Normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) Human bone marrow mRNA (Clontech), 10) Human leukemia lymphoblastic mRNA (Clontech), 11) Human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human so/spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

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TABLE 2

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
94	gi15080005	Homo sapiens	nogo receptor, clone MGC:19831 IMAGE:4040540, mRNA, complete cds.	1305	100
94	gi12407653	Homo sapiens	Nogo receptor mRNA, complete cds.	1305	100
94	gi15385806	Homo sapiens	Predicted human Nogo receptor gene	1305	100
95	AAB53348	Homo sapiens	Human colon cancer antigen protein sequence SEQ ID NO:888.	1864	99
95	AAG73782	Homo sapiens	Human colon cancer antigen protein SEQ ID NO:4546.	1864	99
95	gi15928738	Mus musculus	RIKEN cDNA 1110064N10 gene	1407	94
96	gi5531827	Homo sapiens	p47	1694	98
96	gi12803909	Homo sapiens	p47, clone MGC:3347 IMAGE:3635947, mRNA, complete cds.	1689	98
96	gi8979825	Homo sapiens	Human DNA sequence from clone RP4-776F14 on chromosome 20p12.2-13. Contains the 5' end of the FKBP1A gene for FK506-binding protein 1A (12kD), the gene for P47 protein, part of a novel member of the PTPNS (protein tyrosine phosphatase, non-receptor type substrate 1) gene family, ESTs, STSs, GSSs and two CpG islands, complete sequence.	1689	98
97	gi7022811	Homo sapiens	cDNA FLJ10649 fis, clone NT2RP2005835, weakly similar to SHP1 PROTEIN.	1541	99
97	AAB93031	Homo sapiens	Human protein sequence SEQ ID NO:11803.	1541	99

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
97	gi6563210	Homo sapiens	p47 protein mRNA, complete cds.	813	90
98	AAB42552	Homo sapiens	Human ORFX ORF2316 polypeptide sequence SEQ ID NO:4632.	826	90
98	AAB12868	Homo sapiens	Human P47 amino acid sequence.	815	89
98	gi12803909	Homo sapiens	p47, clone MGC:3347 IMAGE:3635947, mRNA, complete cds.	806	89
99	gi12836289	Mus musculus	putative	347	68
99	gi1006665	Homo sapiens	H.sapiens mRNA for transcript associated with monocyte to macrophage differentiation.	346	68
99	gi7290797	Drosophila melanogaster	CG4615 gene product	159	37
100	gi7020785	Homo sapiens	cDNA FLJ20581 fis, clone REC00491.	2996	99
100	gi2988399	Homo sapiens	Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.	1874	60
100	gi666014	Homo sapiens	Human SA mRNA for SA gene product, complete cds.	1873	60
101	gi5915662	Homo sapiens	integrin alpha 11 subunit precursor (ITGA11) mRNA, complete cds.	497	98
101	AAB30929	Homo sapiens	Amino acid sequence of a human alpha11 integrin chain.	497	98
101	AAB50085	Homo sapiens	Human A259.	497	98
102	gi431608	Oncorhynchus mykiss	complement component C3	223	30
102	gi213373	Naja naja	complement component C3	209	29
102	gi755815	Gallus gallus	complement C3 precursor	206	31
103	gi7020791	Homo sapiens	cDNA FLJ20584 fis, clone KAT09532.	1052	100
103	gi14250646	Homo sapiens	Similar to hypothetical protein FLJ20584, clone MGC:3446 IMAGE:3627081, mRNA, complete cds.	810	89
103	gi13278391	Mus musculus	Similar to hypothetical protein FLJ20584	729	70
104	gi10799397	Homo sapiens	chromosome 19, BAC BC349142 (CTC-518B2), complete sequence.	1404	99
104	gi6249632	Homo sapiens	kallikrein-like protein 5 gene, alternative splice products, complete cds.	1404	99
104	gi11244770	Homo sapiens	serine protease gene cluster, complete sequence.	1301	100
105	gi12310959	Homo sapiens	unnamed protein product	2095	100
105	AAV33741	Homo sapiens	Beta-secretase.	1694	99
105	AAB61142	Homo sapiens	Human NOV12 protein.	2088	99
106	gi14017771	Homo sapiens	mRNA for KIAA1776 protein (fibrillin3), complete cds.	2940	55
106	gi762831	Mus musculus	fibrillin 2	2153	50
106	gi3688648	Mus musculus	mutant fibrillin-1	2102	46

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
107	AAB24199	Homo sapiens	Human GTP-binding protein-coupled receptor BG3 protein sequence.	925	100
107	gi7328047	Homo sapiens	mRNA; cDNA DKFZp434B1272 (from clone DKFZp434B1272); partial cds.	760	100
107	AAB01249	Homo sapiens	Human EMR1 hormone receptor.	254	41
108	AAV93948	Homo sapiens	Amino acid sequence of a lectin ss3939 polypeptide.	1979	98
108	AAE03651	Homo sapiens	Human extracellular matrix and cell adhesion molecule-15 (XMAD-15).	1979	98
108	AAV91490	Homo sapiens	Human secreted protein sequence encoded by gene 40 SEQ ID NO:163.	1969	98
109	gi6979311	Homo sapiens	cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds.	2875	99
109	AAV82776	Homo sapiens	Human chordin related protein (Clone dj167_19).	2875	99
109	AAV53034	Homo sapiens	Human secreted protein clone dj167_19 protein sequence SEQ ID NO:74.	2875	99
110	AAW99070	Homo sapiens	Human PIGR-1.	678	100
110	gi12405479	Homo sapiens	unnamed protein product	672	99
110	AAB31568	Homo sapiens	Amino acid sequence of human leukocyte surface receptor (LSR).	672	99
111	AAW99070	Homo sapiens	Human PIGR-1.	612	100
111	gi12405479	Homo sapiens	unnamed protein product	606	99
111	AAB31568	Homo sapiens	Amino acid sequence of human leukocyte surface receptor (LSR).	606	99
112	gi9663958	Homo sapiens	mRNA for cysteinyl leukotriene CysLT2 receptor, complete cds; cDNA: PSEC0146 from clone PLACE1006979.	1788	100
112	gi10442008	Homo sapiens	cysteinyl leukotriene receptor CYSLT2 gene, complete cds.	1788	100
112	gi14582394	Homo sapiens	cysteinyl leukotriene receptor type 2 (CYSLT2) gene, complete cds.	1788	100
113	gi4580013	Homo sapiens	TRAF4-associated factor 2 mRNA, partial cds.	1432	70
113	gi4689252	Homo sapiens	sorting nexin 6 (SNX6) mRNA, complete cds.	1432	70
113	AAB58368	Homo sapiens	Lung cancer associated polypeptide sequence SEQ ID 706.	1432	70
114	gi14042571	Homo sapiens	cDNA FLJ14791 fis, clone NT2RP4001064, weakly similar to SYNAPTONEMAL COMPLEX PROTEIN SC65.	3090	92
114	gi14272600	Homo sapiens	unnamed protein product	3090	92
114	AAB93215	Homo sapiens	Human protein sequence SEQ	3090	92

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
115	gi12053261	Homo sapiens	ID NO:12194. mRNA; cDNA DKFZp434A196 (from clone DKFZp434A196); complete cds.	1502	76
115	gi9754902	Mus musculus	espin	1462	78
115	gi5327035	Homo sapiens	Human DNA sequence from clone 20208 on chromosome 1p36.11-36.31. Contains the 5' part of a gene for a novel rat Espin LIKE protein containing Ank repeats, the gene for the ortholog of rodent HES2 (Hairy and Enhancer of Split 2) and the 5' end of the gene for HBACH (Brain Acyl-CoA Hydrolase (Acyl Coenzyme A Thioester Hydrolase, EC 3.1.2.2). Contains ESTs, GSSs and putative CpG islands, complete sequence.	2451	69
116	gi5327035	Homo sapiens	Human DNA sequence from clone 20208 on chromosome 1p36.11-36.31. Contains the 5' part of a gene for a novel rat Espin LIKE protein containing Ank repeats, the gene for the ortholog of rodent HES2 (Hairy and Enhancer of Split 2) and the 5' end of the gene for HBACH (Brain Acyl-CoA Hydrolase (Acyl Coenzyme A Thioester Hydrolase, EC 3.1.2.2). Contains ESTs, GSSs and putative CpG islands, complete sequence.	3530	91
116	gi4375916	Homo sapiens	H.sapiens gene from PAC 163M9, similar to rat Espin gene, partial cds.	3333	93
116	gi3320122	Rattus norvegicus	espin	3269	75
117	AAE01020	Homo sapiens	Human pif-1 type helicase protein.	1875	78
117	gi5523990	Homo sapiens	DNA helicase homolog (PIF1) mRNA, partial cds.	1842	97
117	gi7295800	Drosophila melanogaster	CG3238 gene product	1196	46
118	AAE01020	Homo sapiens	Human pif-1 type helicase protein.	911	99
118	gi5523990	Homo sapiens	DNA helicase homolog (PIF1) mRNA, partial cds.	834	85
118	gi7295800	Drosophila melanogaster	CG3238 gene product	620	46
119	gi10434929	Homo sapiens	cDNA FLJ13080 fis, clone NT2RP3002007, weakly similar to SAP1 PROTEIN.	3490	99
119	AAB94461	Homo sapiens	Human protein sequence SEQ ID NO:15114.	3490	99
119	AAB95164	Homo sapiens	Human protein sequence SEQ	3483	99

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			ID NO:17211.		
120	gi29715	Homo sapiens	Human mRNA for pro-cathepsin L (major excreted protein MEP).	1597	87
120	gi190418	Homo sapiens	Human cathepsin L gene, complete cds.	1597	87
120	AAW47031	Homo sapiens	Human procathepsin L.	1597	87
121	AAG63220	Homo sapiens	Amino acid sequence of a human lipid metabolism enzyme.	4116	99
121	gi15862521	Homo sapiens	unnamed protein product	3834	99
121	gi14715017	Homo sapiens	Similar to phospholipase C, delta, clone MGC:9744 IMAGE:3854215, mRNA, complete cds.	3195	99
122	gi13676465	Macaca fascicularis	hypothetical protein	495	41
122	gi2253280	Bos taurus	butyrophilin	490	44
122	gi162773	Bos taurus	butyrophilin precursor	487	44
123	AAB25682	Homo sapiens	Human secreted protein sequence encoded by gene 18 SEQ ID NO:71.	1616	96
123	gi2982501	Homo sapiens	mRNA for neuropathy target esterase.	952	65
123	AAV70474	Homo sapiens	Human cyclic nucleotide-associated protein-2 (CNAP-2).	952	65
124	AAB24084	Homo sapiens	Human PRO1317 protein sequence SEQ ID NO:71.	1739	100
124	AAB37984	Homo sapiens	Human secreted protein encoded by gene 1 clone HTDAA93.	1739	100
124	AAV99418	Homo sapiens	Human PRO1317 (UNQ783) amino acid sequence SEQ ID NO:277.	1739	100
126	gi292057	Homo sapiens	Human EBV induced G-protein coupled receptor (EBI2) mRNA, complete cds.	196	40
126	AAR54080	Homo sapiens	Epstein Barr virus induced (EBI-2) polypeptide.	196	40
126	AAW53623	Homo sapiens	Epstein Barr virus induced gene 2 (EBI-2).	196	40
127	gi63426	Gallus gallus	lysozyme	428	43
127	gi12843551	Mus musculus	putative	367	41
127	gi12578467	Homo sapiens	unnamed protein product	366	40
128	gi13195239	Homo sapiens	complement factor H-related protein 5 mRNA, complete cds.	1492	100
128	gi180498	Homo sapiens	Human complement H factor mRNA, complete cds.	585	51
128	gi309166	Mus musculus	complement factor H-related protein	583	44
129	gi11275568	Homo sapiens	mucin 5B (MUC5B) gene, partial cds.	7389	99
129	gi3789927	Homo sapiens	mucin (MUC5B) mRNA, partial cds.	7176	97
129	gi4038587	Homo sapiens	partial MUC5B gene, exon 1-29.	7151	98
130	gi2853301	Homo sapiens	mucin (MUC3) mRNA, partial cds.	3473	77
130	gi6466801	Homo sapiens	intestinal mucin 3 (MUC3) gene,	3218	76

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
130	gi9929920	Homo sapiens	partial cds. MUC3A mRNA for intestinal mucin, partial cds.	2904	100
131	gi1235725	Homo sapiens	mRNA for macrophage lectin 2, complete cds.	1014	79
131	gi204303	Rattus norvegicus	Gal/GalNAc-specific lectin precursor	879	55
131	gi15928688	Mus musculus	Similar to macrophage galactose N-acetyl-galactosamine specific lectin	806	51
132	AAB43122	Homo sapiens	Human ORFX ORF2886 polypeptide sequence SEQ ID NO:5772.	3123	94
132	gi1177164	Mus musculus	polydom protein	2668	77
132	gi14198157	Mus musculus	polydomain protein	2668	77
133	gi7110160	Homo sapiens	guanine nucleotide exchange factor (LARG) mRNA, complete cds.	7932	99
133	AAW64468	Homo sapiens	Human secreted protein from clone CW420.2.	6937	99
133	AAB90743	Homo sapiens	Human CW420.2 protein sequence SEQ ID 186.	6937	99
134	AAM00758	Homo sapiens	Human bone marrow protein, SEQ ID NO: 121.	1804	100
134	gi13937956	Homo sapiens	clone MGC:14710 IMAGE:4250452, mRNA, complete cds.	1677	67
134	gi32645	Homo sapiens	Human mRNA for 56-KDa protein induced by interferon.	1671	67
135	gi4580013	Homo sapiens	TRAF4-associated factor 2 mRNA, partial cds.	1432	70
135	gi4689252	Homo sapiens	sorting nexin 6 (SNX6) mRNA, complete cds.	1432	70
135	AAB58368	Homo sapiens	Lung cancer associated polypeptide sequence SEQ ID 706.	1432	70
136	gi6165618	Homo sapiens	gamma-interferon inducible lysosomal thiol reductase (GILT) mRNA, complete cds.	1149	100
136	AAB58455	Homo sapiens	Lung cancer associated polypeptide sequence SEQ ID 793.	1149	100
136	AAAY71214	Homo sapiens	Human irritable bowel disease related polypeptide IMX44.	1142	99
137	gi14042571	Homo sapiens	cDNA FLJ14791 fis, clone NT2RP4001064, weakly similar to SYNAPTONEMAL COMPLEX PROTEIN SC65.	3090	92
137	gi14272600	Homo sapiens	unnamed protein product	3090	92
137	AAB93215	Homo sapiens	Human protein sequence SEQ ID NO:12194.	3090	92
138	gi35330	Homo sapiens	H.sapiens mRNA for procarboxypeptidase A1.	1198	97
138	gi2299431	unidentified	unnamed protein product	1198	97
138	AAW01504	Homo sapiens	Wild-type human pancreatic carboxypeptidase 1.	1198	97

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
139	gi12053081	Homo sapiens	mRNA; cDNA DKFZp434L0718 (from clone DKFZp434L0718); complete cds.	2766	100
139	AAAY10853	Homo sapiens	Amino acid sequence of a human secreted protein.	417	87
139	AAB42173	Homo sapiens	Human ORFX ORF1937 polypeptide sequence SEQ ID NO:3874.	202	39
141	AAB93455	Homo sapiens	Human protein sequence SEQ ID NO:12712.	546	100
141	gi599683	Bos taurus	Cleavage and Polyadenylation specificity factor (CPSF) 100kD subunit	546	100
141	gi2331036	Mus musculus	cleavage and polyadenylation specificity factor	538	98
142	gi29715	Homo sapiens	Human mRNA for pro-cathepsin L (major excreted protein MEP).	1597	87
142	gi190418	Homo sapiens	Human cathepsin L gene, complete cds.	1597	87
142	AAW47031	Homo sapiens	Human procathepsin L.	1597	87
143	gi1103582	Homo sapiens	H.sapiens mRNA for ARP1 protein.	1055	100
143	gi9843764	Homo sapiens	Human DNA sequence from clone RP4-583P15 on chromosome 20 Contains ESTs, STSs, GSSs and ten CpG islands. Contains the TNFRSF6B gene for tumor necrosis factor receptor 6b (decoy), the 3' part of the KIAA1088 gene, the ARFRP1 gene for ADP-ribosylation factor related protein 1, two genes for novel proteins, the gene for a GLUT4 enhancer factor and the gene for a novel zinc finger protein similar to rat RIN ZF and the gene for a novel BTB/POZ domain containing zinc finger protein, complete sequence.	1055	100
143	gi7012932	Homo sapiens	SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds.	1055	100
144	gi13623501	Homo sapiens	clone MGC:12837 IMAGE:4124286, mRNA, complete cds.	1008	100
144	gi571466	Rattus norvegicus	phospholipase C delta-4	741	73
144	gi1304189	Rattus norvegicus	phospholipase C delta4	734	72
145	gi12053129	Homo sapiens	mRNA; cDNA DKFZp434C2322 (from clone DKFZp434C2322); complete	1185	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			cds.		
145	gi16117338	Homo sapiens	vWF-CP(ADAMTS13) mRNA for von Willebrand factor-cleaving protease, complete cds.	1185	100
145	gi15963593	Homo sapiens	ADAMTS13 (ADAMTS13) mRNA, complete cds, alternatively spliced.	1185	100
146	gi6624133	Homo sapiens	PAC clone RP4-539M6 from 22, complete sequence.	322	98
146	gi4164418	Rattus norvegicus	45 kDa secretory protein	247	75
146	gi13543184	Mus musculus	Unknown (protein for MGC:6302)	245	75
147	AAB98640	Homo sapiens	Human autoimmune disease associated protein 16.	766	99
147	gi7768747	Homo sapiens	genomic DNA, chromosome 21q, section 92/105.	292	68
147	gi12654677	Homo sapiens	U2(RNU2) small nuclear RNA auxiliary factor 1 (non-standard symbol), clone MGC:2223 IMAGE:3534272, mRNA, complete cds.	292	68
148	AAB98640	Homo sapiens	Human autoimmune disease associated protein 16.	757	98
148	gi7768747	Homo sapiens	genomic DNA, chromosome 21q, section 92/105.	691	79
148	gi12654677	Homo sapiens	U2(RNU2) small nuclear RNA auxiliary factor 1 (non-standard symbol), clone MGC:2223 IMAGE:3534272, mRNA, complete cds.	691	79
149	AAG63220	Homo sapiens	Amino acid sequence of a human lipid metabolism enzyme.	4116	99
149	gi15862521	Homo sapiens	unnamed protein product	3834	99
149	gi14715017	Homo sapiens	Similar to phospholipase C, delta, clone MGC:9744 IMAGE:3854215, mRNA, complete cds.	3195	99
150	gi11493982	Homo sapiens	TLH29 protein precursor (TLH29) mRNA, complete cds.	538	95
150	AAV12410	Homo sapiens	Human 5' EST secreted protein SEQ ID NO:441.	527	94
150	AAG89188	Homo sapiens	Human secreted protein, SEQ ID NO: 308.	505	98
151	gi11863671	Homo sapiens	mRNA for putative tumor stroma and activated macrophage protein DLM-1 (DLM-1 gene).	1362	99
151	gi13160377	Homo sapiens	Human DNA sequence from clone RP4-718J7 on chromosome 20q13.31-13.33 Contains the PCK1 gene for soluble phosphoenolpyruvate carboxykinase 1, part of a novel gene similar to mouse DLM-1	1246	94

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			(tumour stroma and activated macrophage protein), the 3' end of the TMEPA1 gene encoding an androgen induced 1b transmembrane protein (PMEPA1), two putative novel genes, a CpG island, ESTs, STSs and GSSs, complete sequence.		
151	gi6563280	Mus musculus	tumor stroma and activated macrophage protein DLM-1	565	51
152	gi13592175	Leishmania major	ppg3	220	26
152	gi601930	Oryctolagus cuniculus	neurofilament-H	184	25
152	gi5420387	Leishmania major	proteophosphoglycan	186	26
153	AAB42658	Homo sapiens	Human ORFX ORF2422 polypeptide sequence SEQ ID NO:4844.	8542	99
153	gi15077826	Homo sapiens	rap guanine nucleotide exchange factor mRNA, complete cds.	7521	98
153	gi6650766	Homo sapiens	PDZ domain-containing guanine nucleotide exchange factor 1 mRNA, complete cds.	6208	100
154	gi1657312	Homo sapiens	H.sapiens mRNA for FAA protein.	7165	98
154	AAW48663	Homo sapiens	Fanconi anaemia of complementation group A protein.	7165	98
154	gi2230888	Homo sapiens	H.sapiens Fanconi anaemia group A gene, exon 1 and joined CDS.	7162	98
155	gi1657312	Homo sapiens	H.sapiens mRNA for FAA protein.	4876	100
155	AAW48663	Homo sapiens	Fanconi anaemia of complementation group A protein.	4876	100
155	gi2230888	Homo sapiens	H.sapiens Fanconi anaemia group A gene, exon 1 and joined CDS.	4873	99
156	AAB60469	Homo sapiens	Human cell cycle and proliferation protein CCYPR-17, SEQ ID NO:17.	846	100
156	AAV76403	Homo sapiens	Fragment of human secreted protein encoded by gene 85.	600	100
156	gi12861086	Mus musculus	putative	512	66
157	gi16041826	Homo sapiens	interferon regulatory factor 2, clone MGC:9260 IMAGE:3920890, mRNA, complete cds.	1626	100
157	gi33967	Homo sapiens	Human mRNA for interferon regulatory factor-2 (IRF-2).	1612	99
157	AAB70698	Homo sapiens	Human IRF-2 protein sequence SEQ ID NO:7.	1612	99
158	gi16041826	Homo sapiens	interferon regulatory factor 2, clone MGC:9260	892	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			IMAGE:3920890, mRNA, complete cds.		
158	gi33967	Homo sapiens	Human mRNA for interferon regulatory factor-2 (IRF-2).	892	100
158	AAB70698	Homo sapiens	Human IRF-2 protein sequence SEQ ID NO:7.	892	100
159	gi7637906	Homo sapiens	Ral guanine nucleotide exchange factor RalGPS1A mRNA, complete cds.	2768	100
159	gi2224643	Homo sapiens	Human mRNA for KIAA0351 gene, complete cds.	1758	100
159	gi11321424	Mus musculus	Ral-A exchange factor RalGPS2	1228	70
160	gi7716046	Mus musculus	regulator factor X 5	606	38
160	gi840789	Homo sapiens	H.sapiens mRNA for DNA binding regulatory factor.	580	35
160	AAB40374	Homo sapiens	Human ORFX ORF138 polypeptide sequence SEQ ID NO:276.	565	98
161	gi13436464	Homo sapiens	Similar to cleavage and polyadenylation specific factor 6, 68kD subunit, clone MGC:4425 IMAGE:2958189, mRNA, complete cds.	364	48
161	gi12653847	Homo sapiens	Similar to cleavage and polyadenylation specific factor 6, 68kD subunit, clone MGC:1242 IMAGE:3506481, mRNA, complete cds.	364	48
161	gi871299	Homo sapiens	H.sapiens HPBRII-4 mRNA.	359	47
162	gi4699969	Homo sapiens	PAC clone RP4-568B10 from 7q31.1-q31.2, complete sequence.	1379	99
162	gi13876344	Mus musculus	protocadherin gamma A9	265	28
162	gi14625441	Homo sapiens	mRNA for KIAA1773 protein (dachous homologue), complete cds.	246	29
163	gi7959299	Homo sapiens	mRNA for KIAA1516 protein, partial cds.	8192	99
163	gi11065786	Homo sapiens	phospholipase C epsilon mRNA, partial cds.	8186	99
163	gi10518469	Homo sapiens	phosphoinositide-specific phospholipase C PLC-epsilon mRNA, complete cds.	8127	99
164	gi386827	Homo sapiens	Human inhibin beta-B-subunit gene, exon 2, and complete cds.	2197	99
164	AAV92017	Homo sapiens	Human inhibin B beta subunit.	2197	99
164	AAV92019	Homo sapiens	Human activin B subunit.	2197	99
165	gi16040975	Homo sapiens	HIF-3A mRNA for hypoxia-inducible factor-3 alpha, complete cds.	1480	99
165	gi4558637	Homo sapiens	chromosome 19, BAC 82621 (CIT-B-139a18), complete sequence.	1480	99
165	gi14042618	Homo sapiens	cDNA FLJ14819 fis, clone OVARC1000241, moderately similar to HYPOXIA-	1476	98

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			INDUCIBLE FACTOR 1 ALPHA.		
166	gi10434070	Homo sapiens	cDNA FLJ12529 fis, clone NT2RM4000156, weakly similar to H.sapiens HPBRII-7 gene.	975	98
166	AAB94099	Homo sapiens	Human protein sequence SEQ ID NO:14318.	975	98
166	gi13436464	Homo sapiens	Similar to cleavage and polyadenylation specific factor 6, 68kD subunit, clone MGC:4425 IMAGE:2958189, mRNA, complete cds.	883	48
167	gi7533125	Homo sapiens	fibroblast growth factor receptor 3 (FGFR3) mRNA, complete cds, alternatively spliced.	3664	100
167	gi211443	Gallus gallus	cek2 protein	1842	92
167	gi186782	Homo sapiens	Human secreted fibroblast growth factor receptor (K-sam-III) mRNA, complete cds.	2482	73
169	gi13543469	Homo sapiens	Similar to Natriuretic peptide precursor A, (pronatriodilatin, also Anf, Pnd), clone MGC:14467 IMAGE:4273949, mRNA, complete cds.	181	97
169	gi3171893	Homo sapiens	DNA sequence from PAC 934G17 on chromosome 1p36.21. Contains the alternatively spliced CLCN6 gene for chloride channel proteins CLC-6A (KIAA0046) -B, -C and -D, the alternatively spliced NPPA gene coding for Atrial Natriuretic Factor ANF precursor (Atrial Natriuretic peptide ANP, Prepronatriodilatin), the NPPB gene for Brain Natriuretic Protein BNP, and a pseudogene similar to SBF1 (and other Myotubularin-related protein genes). Contains ESTs, STSs and the genomic marker D1S2740, complete sequence.	181	97
169	gi825625	Homo sapiens	Human gene fragment for pronatriodilatin precursor (exons 1 and 2).	181	97
170	gi13274524	Homo sapiens	complement-c1q tumor necrosis factor-related protein (CTRP7) mRNA, complete cds.	1576	100
170	gi12228258	Homo sapiens	unnamed protein product	1576	100
170	AAB50371	Homo sapiens	Human ZACRP7.	1576	100
171	AAB08783	Homo sapiens	Amino acid sequence of a human serpin polypeptide.	742	87
171	gi2077914	Bos taurus	thrombin inhibitor	516	67
171	gi12655087	Homo sapiens	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin),	511	66

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			member 6, clone MGC:2180 IMAGE:3051381, mRNA, complete cds.		
172	gi63426	Gallus gallus	lysosome	428	43
172	gi12843551	Mus musculus	putative	367	41
172	gi12578467	Homo sapiens	unnamed protein product	366	40
173	gi2443367	Homo sapiens	mRNA for Nck, Ash and phospholipase C gamma-binding protein NAP4, partial cds.	2432	100
173	AAW93275	Homo sapiens	Human SOCS19 protein.	2432	100
173	AAW62623	Homo sapiens	Homo sapiens SOCS11 protein.	953	100
174	gi12834584	Mus musculus	putative	414	97
174	gi7582391	Mus musculus	p53 apoptosis-associated target	414	97
174	AAB70474	Homo sapiens	PERP (p53 apoptosis effector related to PMP-22) protein sequence.	414	97
175	gi12834584	Mus musculus	putative	1054	99
175	gi7582391	Mus musculus	p53 apoptosis-associated target	1054	99
175	AAV33261	Homo sapiens	Human p99 protein.	1054	99
176	AAB95035	Homo sapiens	Human protein sequence SEQ ID NO:16788.	221	62
177	gi6650766	Homo sapiens	PDZ domain-containing guanine nucleotide exchange factor 1 mRNA, complete cds.	243	87
177	gi15077826	Homo sapiens	rap guanine nucleotide exchange factor mRNA, complete cds.	243	87
177	AAB42658	Homo sapiens	Human ORFX ORF2422 polypeptide sequence SEQ ID NO:4844.	243	87
178	AAB43122	Homo sapiens	Human ORFX ORF2886 polypeptide sequence SEQ ID NO:5772.	3099	94
178	gi11177164	Mus musculus	polydom protein	3095	79
178	gi14198157	Mus musculus	polydomain protein	3095	79
179	gi6572379	Homo sapiens	Human DNA sequence from clone 579N16 on chromosome 22. Contains the 3' part of the gene for KIAA0685, the SBF1 gene for SET binding factor 1, a novel gene, ESTs, an STS, GSSs and three putative CpG islands, complete sequence.	8482	99
179	gi3015538	Homo sapiens	nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds.	8315	98
179	gi12698077	Homo sapiens	mRNA for KIAA1766 protein, partial cds.	3621	62
180	gi1234787	Xenopus laevis	up-regulated by thyroid hormone in tadpoles; expressed specifically in the tail and only at metamorphosis; membrane bound or extracellular protein; C-terminal basic region	1563	69
180	gi10435980	Homo sapiens	cDNA FL113840 fis, clone THYRO1000783, moderately similar to Xenopus laevis tail-	1562	94

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			specific thyroid hormone up-regulated (gene 5) mRNA.		
180	AAB94773	Homo sapiens	Human protein sequence SEQ ID NO:15860.	1562	94
181	gi12848947	Mus musculus	putative	582	60
181	gi5453324	Mus musculus	syntaxin4-interacting protein synip	576	59
181	AAB57636	Homo sapiens	AF-6 protein PDZ domain.	143	35
182	gi14041850	Homo sapiens	cDNA FLJ14369 fis, clone HEMBA1001174, highly similar to ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.	940	100
182	gi12855057	Mus musculus	putative	940	100
182	AAB92480	Homo sapiens	Human protein sequence SEQ ID NO:10563.	940	100
183	gi11275568	Homo sapiens	mucin 5B (MUC5B) gene, partial cds.	7389	99
183	gi3789927	Homo sapiens	mucin (MUC5B) mRNA, partial cds.	7176	97
183	gi4038587	Homo sapiens	partial MUC5B gene, exon 1-29.	7151	98
184	gi2853301	Homo sapiens	mucin (MUC3) mRNA, partial cds.	3473	77
184	gi6466801	Homo sapiens	intestinal mucin 3 (MUC3) gene, partial cds.	3218	76
184	gi9929920	Homo sapiens	MUC3A mRNA for intestinal mucin, partial cds.	2904	100
185	gi6492116	Homo sapiens	carboxylesterase-related protein mRNA, complete cds.	210	61
185	gi550147	Rattus norvegicus	carboxylesterase BS-3 (egasyn)	215	62
185	gi15929734	Mus musculus	Similar to carboxylesterase 2 (intestine, liver)	207	59
186	gi854065	Human herpesvirus 6	U88	540	54
186	gi10434098	Homo sapiens	cDNA FLJ12547 fis, clone NT2RM4000634.	417	44
186	AAB95124	Homo sapiens	Human protein sequence SEQ ID NO:17122.	417	44

TABLE 3

SEQ ID NO:	Accession No.	Description	Results*
102	BL00477	Alpha-2-macroglobulin family thiolester region proteins.	BL00477J 19.04 6.604e-19 15-46
104	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134B 15.99 5.154e-25 194-218 BL00134A 11.96 7.158e-19 47-64
104	BL00021	Kringle domain proteins.	BL00021B 13.33 1.000e-16 47-65
104		CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE	PR00722A 12.27 3.348e-16 48-64 PR00722C 10.87 4.000e-16 193-206
104	PR00722	Type I fibronectin domain proteins.	BL01253G 11.34 9.234e-18 193-207 BL01253D 4.84 4.877e-11 47-61
104	BL00495	Apple domain proteins.	BL00495K 12.58 5.631e-09 49-82 BL00495N 11.04 6.919e-09 186-221
105	PD02327	GLYCOPROTEIN ANTIGEN PRECURSOR IMMUNOGLO.	PD02327B 19.84 4.098e-10 154-176
105	PR00442	G-PROTEIN ALPHA SUBUNIT GROUP Q SIGNATURE	PR00442E 7.23 1.740e-09 292-301
105	PR00440	G-PROTEIN ALPHA SUBUNIT GROUP 12 SIGNATURE	PR00440E 11.16 3.192e-09 292-301
105	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 6.478e-09 106-116 DM00179 13.97 9.609e-09 298-308
106	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243H 17.53 4.391e-11 162-188
106	DM00864	EGF-LIKE DOMAIN.	DM00864B 11.34 5.836e-10 878-897
106	PR00907	THROMBOMODULIN SIGNATURE	PR00907G 11.63 5.366e-11 955-982 PR00907G 11.63 5.366e-11 1092-1119 PR00907G 11.63 9.066e-10 1356-1383 PR00907G 11.63 3.351e-09 1314-1341
106	PR00010	TYPE II EGF-LIKE SIGNATURE	PR00010C 11.16 3.250e-12 920-931 PR00010A 11.79 7.923e-11 490-502 PR00010C 11.16 5.071e-09 1404-1415 PR00010C 11.16 6.571e-09 1361-1372
106	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 7.520e-09 1388-1434
106	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 1.000e-15 915-931 BL01187B 12.04 8.412e-15 1482-1498 BL01187B 12.04 7.750e-14 546-562 BL01187B 12.04 7.750e-14 1356-1372 BL01187A 9.98 4.214e-13 939-951 BL01187B 12.04 4.913e-13 873-889 BL01187B 12.04 4.913e-13 1399-1415 BL01187A 9.98 1.000e-12 488-500 BL01187B 12.04 8.000e-12 465-481 BL01187B 12.04 1.900e-11 1314-1330 BL01187B 12.04 3.100e-11 1441-1457 BL01187B 12.04 4.600e-11 504-520

SEQ ID NO:	Accession No.	Description	Results*
			BL01187B 12.04 8.500e-11 955-971 BL01187B 12.04 8.500e-11 1092-1108 BL01187B 12.04 9.400e-11 1197-1213 BL01187B 12.04 2.286e-10 302-318 BL01187B 12.04 8.200e-10 1524-1540 BL01187A 9.98 9.143e-10 1338-1350 BL01187A 9.98 9.571e-10 1423-1435 BL01187A 9.98 9.571e-10 1506-1518 BL01187B 12.04 2.125e-09 762-778 BL01187A 9.98 7.000e-09 284-296 BL01187A 9.98 7.000e-09 897-909 BL01187A 9.98 7.000e-09 1179-1191 BL01187A 9.98 8.125e- 09 1381-1393
106	BL00022	EGF-like domain proteins.	BL00022B 7.54 1.000e-09 924-931 BL00022A 7.48 9.000e-09 194-201
107	BL00649	G-protein coupled receptors family 2 proteins.	BL00649G 13.52 4.194e-13 102-128
107	PR00249	SECRETIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00249E 14.90 6.958e-09 20-46
107	BL00890	ABC-2 type transport system integral membrane proteins signal.	BL00890A 12.19 1.000e-08 17-28
108	BL00615	C-type lectin domain proteins.	BL00615B 12.25 9.400e-12 163-177
108	PD02205	POLYPROTEIN GLYCOPROTEIN M PRECURSOR CONTAINS.	PD02205O 15.72 7.140e-09 163-195
109	BL01208	VWFC domain proteins.	BL01208B 15.83 1.000e-13 443-458 BL01208B 15.83 1.000e-12 377-392
109	BL00222	Insulin-like growth factor binding proteins.	BL00222B 11.09 1.333e-09 58-74
110	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 8.372e-10 84-116
111	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 8.372e-10 81-113
112	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 6.211e-23 104-144 BL00237C 13.19 4.115e-13 240-267 BL00237D 11.23 5.286e-13 297-314
112	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237G 19.63 5.680e-15 287-314 PR00237A 11.48 4.706e-14 40-65 PR00237B 13.50 9.550e-14 73-95 PR00237F 13.57 9.609e-14 245-270 PR00237C 15.69 7.300e-11 118-141 PR00237E 13.03 1.000e-10 202-226
112	PR00425	BRADYKININ RECEPTOR SIGNATURE	PR00425C 13.23 5.759e-09 104-124
115	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 1.209e-09 845-880
115	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 4.717e-13 510-543 DM00215 19.43 5.941e-11 494-527 DM00215 19.43 1.000e-10 501-534 DM00215 19.43 4.857e-10

SEQ ID NO:	Accession No.	Description	Results*
			511-544 DM00215 19.43 9.357e-10 627-660 DM00215 19.43 9.518e-10 506-539 DM00215 19.43 1.610e-09 508-541 DM00215 19.43 1.610e-09 515-548 DM00215 19.43 2.831e-09 499-532 DM00215 19.43 4.356e-09 640-673
115	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 6.417e-09 513-534
115	PR00546	THYROID HORMONE RECEPTOR SIGNATURE	PR00546D 9.44 6.444e-09 848-867
115	PD02059	CORE POLYPROTEIN PROTEIN GAG CONTAINS: P.	PD02059B 24.48 6.958e-09 636-671
115	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.639e-11 511-526 PR00049D 0.00 8.714e-11 508-523 PR00049D 0.00 1.643e-10 512-527 PR00049D 0.00 8.857e-10 643-658 PR00049D 0.00 2.678e-09 644-659 PR00049D 0.00 5.271e-09 510-525 PR00049D 0.00 6.949e-09 645-660 PR00049D 0.00 7.254e-09 646-661
115	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 8.435e-09 293-306
115	PF00023	Ank repeat proteins.	PF00023A 16.03 3.625e-10 132-148 PF00023A 16.03 6.786e-09 300-316 PF00023A 16.03 8.393e-09 200-216 PF00023A 16.03 9.357e-09 40-56 PF00023A 16.03 1.000e-08 166-182
116	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 1.209e-09 787-822
116	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 4.717e-13 452-485 DM00215 19.43 5.941e-11 436-469 DM00215 19.43 1.000e-10 443-476 DM00215 19.43 4.857e-10 453-486 DM00215 19.43 9.357e-10 569-602 DM00215 19.43 9.518e-10 448-481 DM00215 19.43 1.610e-09 450-483 DM00215 19.43 1.610e-09 457-490 DM00215 19.43 2.831e-09 441-474 DM00215 19.43 4.356e-09 582-615
116	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 6.417e-09 455-476
116	PR00546	THYROID HORMONE RECEPTOR SIGNATURE	PR00546D 9.44 6.444e-09 790-809
116	PD02059	CORE POLYPROTEIN PROTEIN GAG CONTAINS: P.	PD02059B 24.48 6.958e-09 578-613
116	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.639e-11 453-468 PR00049D 0.00 8.714e-11 450-465 PR00049D 0.00 1.643e-10 454-469 PR00049D 0.00 8.857e-10 585-600 PR00049D 0.00 2.678e-09 586-601 PR00049D 0.00 5.271e-09 452-467 PR00049D 0.00 6.949e-09 587-602 PR00049D 0.00 7.254e-09 588-603

SEQ ID NO:	Accession No.	Description	Results*
116	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 8.435e-09 293-306
116	PF00023	Ank repeat proteins.	PF00023A 16.03 3.625e-10 132-148 PF00023A 16.03 6.786e-09 300-316 PF00023A 16.03 8.393e-09 200-216 PF00023A 16.03 9.357e-09 40-56 PF00023A 16.03 1.000e-08 166-182
119	PR00830	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16) SIGNATURE	PR00830A 8.41 6.286e-11 441-461
119	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE	PR00300A 9.56 8.859e-10 437-456
119	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 8.875e-10 436-452
119	BL00113	Adenylate kinase proteins.	BL00113A 12.74 6.262e-09 438-455
119	PR00918	CALICIVIRUS NON-STRUCTURAL POLYPROTEIN FAMILY SIGNATURE	PR00918A 13.76 7.341e-09 431-452
119	BL00674	AAA-protein family proteins.	BL00674C 22.60 5.696e-24 467-510 BL00674D 23.41 8.740e-18 525-572 BL00674B 4.46 1.000e-17 434-456 BL00674E 15.24 3.571e-10 602-622 BL00674A 16.91 8.826e-09 400-421
119	BL01128	Shikimate kinase proteins.	BL01128A 18.84 8.953e-09 437-471
120	PR00705	PAPAIN CYSTEINE PROTEASE (C1) FAMILY SIGNATURE	PR00705A 10.55 4.000e-21 132-148 PR00705B 10.22 2.385e-10 276-287
120	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.	BL00139D 9.24 1.818e-18 295-312 BL00139A 10.29 1.000e-14 132-142 BL00139C 9.23 2.800e-10 275-285
120	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE	PR00704C 11.88 6.162e-09 132-149
121	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 8.636e-11 715-729
121	PR00390	PHOSPHOLIPASE C SIGNATURE	PR00390A 15.09 5.390e-20 342-361 PR00390E 14.63 9.357e-20 608-627 PR00390D 15.76 3.250e-17 587-609 PR00390C 12.52 5.714e-14 471-489 PR00390B 12.57 1.269e-11 373-394 PR00390F 12.03 5.333e-10 758-769
121	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 8.535e-09 498-533
121	BL50007	Phosphatidylinositol-specific phospholipase X-box domain proteins	BL50007D 19.54 7.698e-35 582-624 BL50007B 20.90 6.571e-30 407-445 BL50007A 19.61 4.671e-21 343-389

SEQ ID NO:	Accession No.	Description	Results*
		prof.	BL50007E 25.63 7.585e-20 744-781 BL50007C 8.97 4.522e-14 472-489 BL50007A 19.61 8.946e-09 348-394
123	PR00336	LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN SIGNATURE	PR00336D 9.96 2.393e-09 29-52
126	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237E 13.03 6.400e-12 76-100 PR00237D 8.94 1.450e-11 26-48
126	BL00237	G-protein coupled receptors proteins.	BL00237B 5.28 9.182e-09 84-96
127	PR00749	LYSOZYME G SIGNATURE	PR00749C 7.26 4.600e-16 84-103 PR00749F 13.63 2.364e-13 157-174 PR00749D 13.61 1.222e-12 103-124 PR00749E 18.92 5.061e-10 124-143 PR00749B 16.54 6.589e-09 60-82 PR00749H 8.22 7.368e-09 191-212
129	PF00094	von Willebrand factor type D domain proteins.	PF00094B 10.43 3.935e-18 596-614 PF00094B 10.43 8.286e-14 1060-1078
129	PD02576	PRECURSOR GLYCOPROTEIN SIGNAL CELL.	PD02576A 27.60 6.118e-34 894-943 PD02576A 27.60 9.182e-25 424-473 PD02576A 27.60 8.147e-10 791-840
129	BL01253	Type I fibronectin domain proteins.	BL01253G 11.34 8.989e-09 1151-1165
130	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243H 17.53 4.375e-10 1190-1216
130	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.508e-11 1195-1214 PR00011B 13.08 4.522e-10 1195-1214 PR00011A 14.06 2.479e-09 1195-1214
130	DM00191	w SPAC8A4.04C RESISTANCE SPAC8A4.05C DAUNORUBICIN.	DM00191D 13.94 6.009e-09 438-477
130	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 7.485e-09 232-281
130	PF00624	Flocculin repeat proteins.	PF00624J 6.21 9.782e-10 256-311 PF00624F 11.04 1.218e-09 726-762 PF00624G 10.91 3.032e-09 69-124 PF00624J 6.21 4.488e-09 257-312 PF00624J 6.21 6.512e-09 633-688 PF00624J 6.21 7.279e-09 270-325 PF00624G 10.91 8.476e-09 643-698 PF00624J 6.21 8.744e-09 161-216 PF00624J 6.21 9.233e-09 74-129
130	PF00997	Kappa casein.	PF00997D 9.95 9.894e-09 136-171
131	BL00615	C-type lectin domain proteins.	BL00615A 16.68 7.231e-16 195-213 BL00615B 12.25 7.750e-13 294-308
131	PR00356	TYPE II ANTIFREEZE PROTEIN SIGNATURE	PR00356B 14.85 2.648e-09 195-213
132	PR00343	SELECTIN	PR00343C 16.85 4.906e-12 10-29 PR00343C

SEQ ID NO:	Accession No.	Description	Results*
		SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	16.85 4.098e-10 125-144 PR00343C 16.85 5.636e-09 68-87 PR00343C 16.85 7.818e-09 418-437
132	PF00084	Sushi domain proteins (SCR repeat proteins.	PF00084B 9.45 7.188e-10 351-363 PF00084B 9.45 5.950e-09 59-71 PF00084C 11.25 7.353e-09 199-209 PF00084B 9.45 7.750e-09 174-186 PF00084C 11.25 9.471e-09 434-444
134	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 8.615e-10 456-477
138	BL00132	Zinc carboxypeptidases, zinc-binding region 1 proteins.	BL00132C 21.35 2.552e-35 25-66 BL00132E 17.72 8.333e-27 95-122 BL00132F 13.26 2.500e-24 123-145 BL00132D 12.70 7.000e-18 69-84 BL00132G 10.94 8.594e-17 180-198
138	PR00765	CARBOXYPEPTIDASE A METALLOPROTEASE (M14) FAMILY SIGNATURE	PR00765D 14.16 1.857e-14 128-142 PR00765C 12.55 1.667e-11 75-84
139	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 2.800e-12 493-506 PD00078B 13.14 6.400e-10 460-473
139	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 6.417e-10 467-522
139	PF00023	Ank repeat proteins.	PF00023B 14.20 1.818e-09 496-506 PF00023B 14.20 9.182e-09 463-473 PF00023A 16.03 9.679e-09 467-483
142	PR00705	PAPAIN CYSTEINE PROTEASE (C1) FAMILY SIGNATURE	PR00705A 10.55 4.000e-21 132-148 PR00705B 10.22 2.385e-10 276-287
142	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.	BL00139D 9.24 1.818e-18 295-312 BL00139A 10.29 1.000e-14 132-142 BL00139C 9.23 2.800e-10 275-285
142	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE	PR00704C 11.88 6.162e-09 132-149
143	BL01019	ADP-ribosylation factors family proteins.	BL01019B 19.49 9.757e-34 106-161 BL01019A 13.20 6.351e-31 62-102 BL01019C 12.52 8.091e-19 165-191
143	BL01020	SAR1 family proteins.	BL01020C 15.35 3.494e-18 90-141
143	PR00328	GTP-BINDING SAR1 PROTEIN SIGNATURE	PR00328A 10.62 4.638e-11 26-50 PR00328C 13.16 4.170e-10 89-115
144	BL50007	Phosphatidylinositol-specific phospholipase X-box domain proteins prof.	BL50007E 25.63 2.761e-18 173-210
144	PR00390	PHOSPHOLIPASE C SIGNATURE	PR00390F 12.03 4.176e-11 187-198
144	PR00399	SYNAPTOTAGMIN SIGNATURE	PR00399D 14.48 4.490e-09 177-188
144	PR00360	C2 DOMAIN	PR00360B 13.61 5.909e-11 144-158

SEQ ID NO:	Accession No.	Description	Results*
		SIGNATURE	PR00360C 8.77 1.321e-09 166-175 PR00360A 14.59 5.500e-09 114-127
149	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 8.636e-11 715-729
149	PR00390	PHOSPHOLIPASE C SIGNATURE	PR00390A 15.09 5.390e-20 342-361 PR00390E 14.63 9.357e-20 608-627 PR00390D 15.76 3.250e-17 587-609 PR00390C 12.52 5.714e-14 471-489 PR00390B 12.57 1.269e-11 373-394 PR00390F 12.03 5.333e-10 758-769
149	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 8.535e-09 498-533
149	BL50007	Phosphatidylinositol-specific phospholipase X-box domain proteins prof.	BL50007D 19.54 7.698e-35 582-624 BL50007B 20.90 6.571e-30 407-445 BL50007A 19.61 4.671e-21 343-389 BL50007E 25.63 7.585e-20 744-781 BL50007C 8.97 4.522e-14 472-489 BL50007A 19.61 8.946e-09 348-394
153	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00720B 16.57 6.595e-15 996-1020
153	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791C 20.98 6.011e-12 606-645
153	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYN.	PD00289 9.97 5.050e-11 625-639
153	PR00834	HTRA/DEGQ PROTEASE FAMILY SIGNATURE	PR00834F 10.91 2.946e-09 621-634
153	BL00888	Cyclic nucleotide-binding domain proteins.	BL00888B 14.79 4.682e-09 355-379
154	PR00826	FANCONI ANAEMIA GROUP A PROTEIN SIGNATURE	PR00826G 13.17 1.143e-30 1346-1370 PR00826B 11.56 1.150e-29 1123-1146 PR00826A 10.40 1.161e-27 1105-1124 PR00826E 14.92 1.141e-24 1294-1313 PR00826D 6.81 1.132e-23 1253-1272 PR00826F 9.90 1.136e-23 1323-1341 PR00826C 7.00 1.110e-13 1238-1248
154	PR00723	SUBTILISIN SERINE PROTEASE FAMILY (S8) SIGNATURE	PR00723C 10.64 3.340e-09 772-789
155	PR00826	FANCONI ANAEMIA GROUP A PROTEIN SIGNATURE	PR00826G 13.17 1.143e-30 1303-1327 PR00826B 11.56 1.150e-29 1080-1103 PR00826A 10.40 1.161e-27 1062-1081 PR00826E 14.92 1.141e-24 1251-1270 PR00826D 6.81 1.132e-23 1210-1229 PR00826F 9.90 1.136e-23 1280-1298 PR00826C 7.00 1.110e-13 1195-1205
155	PR00723	SUBTILISIN SERINE PROTEASE FAMILY (S8) SIGNATURE	PR00723C 10.64 3.340e-09 772-789
157	PR00267	INTERFERON REGULATORY FACTOR	PR00267D 13.82 3.118e-29 36-59 PR00267C 14.28 4.857e-21 13-31

SEQ ID NO:	Accession No.	Description	Results*
		SIGNATURE	
157	BL00601	Tryptophan pentad repeat proteins (IRF family) proteins.	BL00601B 20.92 4.500e-31 32-61 BL00601C 19.42 7.429e-09 72-85
159	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00720B 16.57 7.677e-17 137-161
160	PR00209	ALPHA/BETA GLIADIN FAMILY SIGNATURE	PR00209B 4.88 7.457e-10 1-20
160	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699A 8.91 4.143e-21 144-173 PD02699B 18.28 5.655e-09 173-197
162	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 6.671e-15 219-267
163	BL50007	Phosphatidylinositol-specific phospholipase X-box domain proteins prof.	BL50007A 19.61 1.000e-40 675-721 BL50007B 20.90 3.872e-27 734-772 BL50007D 19.54 5.105e-27 1056-1098 BL50007C 8.97 3.935e-14 802-819 BL50007E 25.63 5.661e-14 1217-1254
163	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 4.545e-11 1191-1205
163	PR00390	PHOSPHOLIPASE C SIGNATURE	PR00390B 12.57 5.974e-20 700-721 PR00390A 15.09 6.049e-20 674-693 PR00390E 14.63 7.070e-16 1082-1101 PR00390D 15.76 7.107e-16 1061-1083 PR00390C 12.52 1.000e-13 801-819 PR00390F 12.03 5.500e-09 1231-1242
164	BL00250	TGF-beta family proteins.	BL00250A 21.24 1.500e-31 303-339 BL00250B 27.37 8.200e-30 371-407
164	PR00671	INHIBIN BETA B CHAIN SIGNATURE	PR00671G 5.35 3.250e-27 184-206 PR00671C 4.18 1.173e-26 40-60 PR00671H 13.45 1.000e-25 231-252 PR00671B 4.29 1.474e-25 20-40 PR00671E 8.84 1.115e-23 124-142 PR00671A 8.36 1.429e-22 2-21 PR00671F 13.86 1.105e-21 149-166 PR00671D 3.47 1.100e-20 61-77
164	PR00672	INHIBIN BETA C CHAIN SIGNATURE	PR00672E 10.40 1.419e-10 142-165
164	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 3.874e-11 28-43 PR00049D 0.00 9.319e-11 30-45 PR00049D 0.00 2.983e-09 34-49 PR00049D 0.00 2.983e-09 34-49
164	PR00669	INHIBIN ALPHA CHAIN SIGNATURE	PR00669F 5.57 8.483e-09 320-338
164	PR00438	GROWTH FACTOR CYSTINE KNOT SUPERFAMILY SIGNATURE	PR00438A 13.54 1.000e-08 328-338
165	PR00785	NUCLEAR TRANSLOCATOR SIGNATURE	PR00785I 13.44 5.957e-10 284-302
165	BL00038	Myc-type, 'helix-loop-helix' dimerization domain proteins.	BL00038B 16.97 3.930e-09 92-113
166	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 5.408e-11 268-289 PR00211B 0.86 9.048e-10 274-295 PR00211B 0.86

SEQ ID NO:	Accession No.	Description	Results*
			2.167e-09 280-301
166	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.407e-09 235-250
166	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.186e-09 212-245 DM00215 19.43 6.949e-09 243-276 DM00215 19.43 7.559e-09 227-260 DM00215 19.43 9.085e-09 217-250
167	BL00240	Receptor tyrosine kinase class III proteins.	BL00240F 17.74 2.105e-36 533-581 BL00240E 11.56 5.875e-33 481-519 BL00240D 23.07 9.882e-22 403-458 BL00240C 22.58 8.962e-20 352-401 BL00240G 28.45 4.770e-19 580-633
167	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 4.938e-21 495-526 BL00107B 13.31 6.400e-15 562-578
167	BL00239	Receptor tyrosine kinase class II proteins.	BL00239E 17.14 9.400e-39 534-584 BL00239F 28.15 2.765e-22 588-633 BL00239B 25.15 6.958e-15 414-462 BL00239C 18.75 3.211e-13 482-505 BL00239D 16.81 9.118e-13 507-533
167	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109D 17.04 5.091e-27 563-586 PR00109B 12.27 5.846e-21 495-514 PR00109E 14.41 8.500e-21 607-630 PR00109C 12.85 1.000e-13 544-555 PR00109A 15.00 8.364e-12 443-457
167	BL00790	Receptor tyrosine kinase class V proteins.	BL00790Q 7.68 1.889e-17 541-574 BL00790Q 15.61 4.529e-12 599-648 BL00790M 8.74 7.831e-11 486-508 BL00790N 13.25 4.411e-10 508-535
167	BL50001	Src homology 2 (SH2) domain proteins profile.	BL50001B 17.40 2.714e-11 492-513 BL50001D 11.00 5.500e-10 562-573
167	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 6.211e-10 221-231
167	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870D 15.74 9.617e-09 213-248
169	PR00711	ATRIAL NATRIURETIC PEPTIDE SIGNATURE	PR00711A 12.00 9.769e-20 11-30
170	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007A 19.33 1.000e-16 158-185 PR00007C 15.60 8.200e-15 229-251 PR00007B 14.16 5.846e-14 185-205 PR00007D 9.64 5.250e-10 264-275
170	BL01113	C1q domain proteins.	BL01113B 18.26 1.581e-29 164-200 BL01113C 13.18 3.077e-15 229-249 BL01113A 17.99 1.243e-13 50-77 BL01113A 17.99 6.108e-13 35-62 BL01113A 17.99 3.077e-12 41-68 BL01113A 17.99 1.574e-10 38-65 BL01113A 17.99 9.617e-10 44-71 BL01113A 17.99 7.577e-09 59-86 BL01113A 17.99 7.577e-09 110-137
170	BL00420	Speract receptor repeat proteins domain proteins.	BL00420A 20.42 5.154e-12 44-73 BL00420A 20.42 1.655e-11 86-115 BL00420A 20.42 2.328e-10 101-130 BL00420A 20.42 4.185e-09 47-76 BL00420A 20.42 9.031e-09 50-79
171	BL00284	Serpins proteins.	BL00284A 15.64 5.500e-21 26-50
172	PR00749	LYSOZYME Q	PR00749C 7.26 4.600e-16 84-103 PR00749F

SEQ ID NO:	Accession No.	Description	Results*
		SIGNATURE	13.63 2.364e-13 157-174 PR00749D 13.61 1.222e-12 103-124 PR00749E 18.92 5.061e-10 124-143 PR00749B 16.54 6.589e-09 60-82 PR00749H 8.22 7.368e-09 191-212
173	PR00678	PI3 KINASE P85 REGULATORY SUBUNIT SIGNATURE	PR00678H 9.13 4.960e-14 406-429
173	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 6.748e-11 78-93
173	PR00401	SH2 DOMAIN SIGNATURE	PR00401A 14.00 8.800e-11 400-415
173	PR00239	MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE	PR00239E 1.58 2.518e-10 86-98
173	PR00021	SMALL PROLINE-RICH PROTEIN SIGNATURE	PR00021A 4.31 4.214e-11 181-194 PR00021A 4.31 2.823e-09 180-193 PR00021A 4.31 3.848e-09 182-195 PR00021A 4.31 6.582e-09 183-196 PR00021A 4.31 9.430e-09 178-191 PR00021A 4.31 9.886e-09 179-192
178	PR00343	SELECTIN SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	PR00343C 16.85 4.906e-12 10-29 PR00343C 16.85 4.098e-10 125-144 PR00343C 16.85 5.636e-09 68-87 PR00343C 16.85 7.818e-09 418-437
178	PF00084	Sushi domain proteins (SCR repeat proteins).	PF00084B 9.45 7.188e-10 351-363 PF00084B 9.45 5.950e-09 59-71 PF00084C 11.25 7.353e-09 199-209 PF00084B 9.45 7.750e-09 174-186 PF00084C 11.25 9.471e-09 434-444
182	BL01019	ADP-ribosylation factors family proteins.	BL01019B 19.49 5.200e-39 90-145 BL01019A 13.20 1.973e-31 46-86 BL01019C 12.52 1.857e-25 147-173
182	BL01020	SAR1 family proteins.	BL01020C 15.35 7.798e-14 74-125
182	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 6.365e-10 17-39
182	PR00440	G-PROTEIN ALPHA SUBUNIT GROUP 12 SIGNATURE	PR00440C 9.54 3.143e-09 62-80
182	PR00328	GTP-BINDING SAR1 PROTEIN SIGNATURE	PR00328A 10.62 5.883e-11 18-42 PR00328C 13.16 5.065e-09 73-99
183	PF00094	von Willebrand factor type D domain proteins.	PF00094B 10.43 3.935e-18 596-614 PF00094B 10.43 8.286e-14 1060-1078
183	PD02576	PRECURSOR GLYCOPROTEIN SIGNAL CELL.	PD02576A 27.60 6.118e-34 894-943 PD02576A 27.60 9.182e-25 424-473 PD02576A 27.60 8.147e-10 791-840
183	BL01253	Type I fibronectin domain proteins.	BL01253G 11.34 8.989e-09 1151-1165
184	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243H 17.53 4.375e-10 1190-1216
184	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.508e-11 1195-1214 PR00011B 13.08 4.522e-10 1195-1214

SEQ ID NO:	Accession No.	Description	Results*
			PR00011A 14.06 2.479e-09 1195-1214 DM00191D 13.94 6.009e-09 438-477
184	DM00191	w SPAC8A4.04C RESISTANCE SPAC8A4.05C DAUNORUBICIN.	
184	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 7.485e-09 232-281
184	PF00624	Flocculin repeat proteins.	PF00624J 6.21 9.782e-10 256-311 PF00624F 11.04 1.218e-09 726-762 PF00624G 10.91 3.032e-09 69-124 PF00624J 6.21 4.488e-09 257-312 PF00624J 6.21 6.512e-09 633-688 PF00624J 6.21 7.279e-09 270-325 PF00624G 10.91 8.476e-09 643-698 PF00624J 6.21 8.744e-09 161-216 PF00624J 6.21 9.233e-09 74-129
184	PF00997	Kappa casein.	PF00997D 9.95 9.894e-09 136-171
185	BL00122	Carboxylesterases type- B serine proteins.	BL00122E 22.02 2.862e-20 25-66 BL00122D 12.53 4.000e-11 1-17
186	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 8.181e-10 151-197
186	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243I 31.77 2.141e-09 8-51
186	PR00451	CHITIN-BINDING DOMAIN SIGNATURE	PR00451A 6.49 5.355e-09 44-53
186	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 5.592e-09 35-75
186	BL01185	C-terminal cystine knot proteins.	BL01185D 23.45 9.258e-09 50-103
186	BL00246	Wnt-1 family proteins.	BL00246E 20.32 5.553e-09 55-101 BL00246E 20.32 9.788e-09 11-57

* Results include in order: Accession No., subtype, e-value, and amino acid position of the signature in the corresponding polypeptide

TABLE 4

SEQ ID NO:	Pfam Model	Description	E-value	Score	No. of Pfam Domains	Position of the Domain
94	LRR	Leucine Rich Repeat	7.5e-36	132.5	8	58-81;82-105;106-130;131-154;155-178;179-202;203-226;227-250
96	UBX	UBX domain	7e-25	96.1	1	330-409
97	UBX	UBX domain	9.8e-25	95.6	1	299-378
100	AMP-binding	AMP-binding enzyme	2.1e-86	300.5	2	91-230;236-503
101	FG-GAP	FG-GAP repeat	2.2e-07	37.9	1	38-94
102	A2M	Alpha-2-macroglobulin family	1.1e-21	73.0	1	15-152
104	trypsin	Trypsin	3.5e-74	236.2	1	22-240
105	ig	Immunoglobulin	6.3e-24	82.1	3	46-115;148-214;250-

SEQ ID NO:	Pfam Model	Description	E-value	Score	No: of Pfam Domains	Position of the Domain
106	EGF	domain EGF-like domain	3.7e-89	309.6	19	307 124-151:159- 185:190-217:290- 326:453-488:494- 528:534-570:758- 786:861-897:903- 939:945-979:1082- 1116:1185- 1221:1302- 1338:1344- 1381:1387- 1423:1429- 1465:1471- 1506:1512-1548
106	TB	TB domain	3.5e-65	230.0	6	233-275:341- 372:802-844:994- 1031:1131- 1174:1236-1277
107	7tm_2	7 transmembrane receptor (Secretin family)	0.00044	-68.4	1	2-119
108	lectin_c	Lectin C-type domain	9e-24	92.4	1	52-178
108	Xlink	Extracellular link domain	2.2e-05	13.8	1	47-70
109	vwc	von Willebrand factor type C domain	3.6e-18	73.8	2	337-391:404-457
110	ig	Immunoglobulin domain	2.2e-05	22.4	1	29-106
111	ig	Immunoglobulin domain	2.2e-05	22.4	1	26-103
112	7tm_1	7 transmembrane receptor (rhodopsin family)	5.2e-59	189.6	1	55-305
113	PX	PX domain	1.6e-15	65.0	1	23-164
115	ank	Ank repeat	2e-54	194.2	8	35-67:69-102:127- 160:161-194:195- 228-229-262:263- 295:296-327
115	WH2	WH2 motif	0.0015	25.2	1	703-720
116	ank	Ank repeat	2e-54	194.2	8	35-67:69-102:127- 160:161-194:195- 228-229-262:263- 295:296-327
116	WH2	WH2 motif	0.0015	25.2	1	645-662
119	AAA	ATPase family associated with various cellul	2.8e-71	250.2	1	436-621
120	Peptidase C1	Papain family cysteine protease	2.3e-123	412.6	1	114-332
121	PI-PLC-X	Phosphatidylinositol-specific phospholipase	9.8e-71	248.4	1	338-488
121	PI-PLC-Y	Phosphatidylinos	2.4e-53	190.6	1	532-649

SEQ ID NO:	Pfam Model	Description	E-value	Score	No. of Pfam Domains	Position of the Domain
		itol-specific phospholipase				
121	C2	C2 domain	6.7e-23	89.5	1	667-757
121	PH	PH domain	0.00021	20.7	1	64-172
122	ig	Immunoglobulin domain	0.00088	17.2	1	52-135
123	cNMP_binding	Cyclic nucleotide-binding domain	7.9e-15	62.7	1	180-280
124	Sema	Sema domain	3.6e-118	406.0	1	64-328
126	7tm_1	7 transmembrane receptor (rhodopsin family)	4e-07	24.8	1	1-103
127	SLT	Transglycosylase SLT domain	0.0029	17.5	1	82-202
128	sushi	Sushi domain (SCR repeat)	1.3e-34	128.4	3	29-79:87-140:147-201
129	vwd	von Willebrand factor type D domain	7.9e-114	391.6	3	112-260:465-619:935-1083
129	TIL	Trypsin Inhibitor like cysteine rich domain	7.5e-14	59.5	4	369-425:735-792:834-895:1204-1258
131	lectin_c	Lectin C-type domain	2e-46	167.7	1	201-309
132	sushi	Sushi domain (SCR repeat)	1.3e-106	367.6	10	1-35:40-93:98-146:155-208:213-267:272-327:332-385:390-443:448-502:507-559
133	RhoGEF	RhoGEF domain	1.7e-18	74.9	1	791-976
133	PDZ	PDZ domain (Also known as DHR or GLGF)	1.5e-09	45.1	1	72-147
133	PH	PH domain	0.00089	18.5	1	1020-1132
134	TPR	TPR Domain	1.2e-16	68.8	6	64-97:107-140:153-186:263-296:352-385:449-482
135	PX	PX domain	1.6e-15	65.0	1	23-164
138	Zn_carboxypeptidase	Zinc carboxypeptidase	2.3e-118	406.6	1	19-227
139	ank	Ank repeat	3.9e-18	73.7	2	462-494:495-527
139	VPS9	Vacuolar sorting protein 9 (VPS9) domain	1.9e-12	54.8	1	264-369
142	Peptidase_C1	Papain family cysteine protease	2.3e-123	412.6	1	114-332
143	arf	ADP-ribosylation factor family	1.5e-43	158.1	1	8-197
143	ras	Ras family	0.00027	-88.1	1	27-208
144	C2	C2 domain	2.3e-30	114.3	1	96-186
144	PI-PLC-Y	Phosphatidylinositol-specific	7.6e-14	53.7	1	42-76

SEQ ID NO:	Pfam Model	Description	E-value	Score	No. of Pfam Domains	Position of the Domain
147	zf-CCCH	phospholipase Zinc finger C-x8-C-x5-C-x3-H type	4.5e-06	33.6	1	13-39
147	rrm	RNA recognition motif	0.014	22.0	1	32-103
148	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	3.4e-06	34.0	1	13-39
148	rrm	RNA recognition motif	0.00011	29.0	1	67-142
149	PI-PLC-X	Phosphatidylinositol-specific phospholipase	9.8e-71	248.4	1	338-488
149	PI-PLC-Y	Phosphatidylinositol-specific phospholipase	2.4e-53	190.6	1	532-649
149	C2	C2 domain	6.7e-23	89.5	1	667-757
149	PH	PH domain	0.00021	20.7	1	64-172
153	RasGEF	RasGEF domain	1e-47	172.0	1	907-1092
153	PDZ	PDZ domain (Also known as DHR or GLGF)	5.4e-17	69.9	1	580-661
153	cNMP_binding	Cyclic nucleotide-binding domain	3.6e-13	57.2	1	345-435
153	RA	Ras association (RalGDS/AF-6) domain	1.3e-05	32.1	1	799-885
157	IRF	Interferon regulatory factor transcription f	7.6e-43	155.8	1	1-76
159	RasGEF	RasGEF domain	7e-50	179.1	1	47-238
159	PH	PH domain	1.9e-15	59.9	1	390-493
160	RFX_DNA_binding	RFX DNA-binding domain	3.5e-30	113.7	1	95-173
161	rrm	RNA recognition motif	0.0041	23.8	1	84-157
162	cadherin	Cadherin domain	5.3e-27	103.1	3	27-124;140-227;241-336
163	PI-PLC-X	Phosphatidylinositol-specific phospholipase	3.5e-69	243.2	1	670-818
163	PI-PLC-Y	Phosphatidylinositol-specific phospholipase	9.6e-43	155.4	2	941-954;1031-1123
163	C2	C2 domain	1.8e-08	41.6	1	1148-1230
163	RA	Ras association (RalGDS/AF-6) domain	0.085	3.0	1	1410-1515
164	TGF-beta	Transforming growth factor beta like	1.8e-58	207.7	1	300-407
164	TGFb_propeptide	TGF-beta propeptide	1.1e-40	148.5	1	62-280
165	PAS	PAS domain	1.3e-07	33.3	2	140-192;294-337

SEQ ID NO:	Pfam Model	Description	E-value	Score	No: of Pfam Domains	Position of the Domain
166	rrm	RNA recognition motif	9.4e-08	39.2	1	84-157
167	pkinase	Protein kinase domain	3.1e-89	309.9	1	360-636
167	ig	Immunoglobulin domain	3.7e-20	70.0	3	54-111:169-230:268-289
170	C1q	C1q domain	1.3e-40	148.4	1	149-273
170	Collagen	Collagen triple helix repeat (20 copies)	6.9e-08	39.6	2	20-79:80-139
171	serpin	Serpin (serine protease inhibitor)	2.4e-50	172.8	1	1-145
172	SLT	Transglycosylase SLT domain	0.0029	17.5	1	82-202
173	SH2	SH2 domain	2.4e-16	50.8	1	400-453
178	sushi	Sushi domain (SCR repeat)	1.3e-106	367.6	10	1-35:40-93:98-146:155-208:213-267:272-327:332-385:390-443:448-502:507-559
178	EGF	EGF-like domain	7.8e-15	62.7	3	559-590:595-622:627-654
185	COesterase	Carboxylesterase	6e-27	94.9	1	3-56

TABLE 5

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
94	1a4y	A	60	249	6.3e-22	0.29	-0.02		RIBONUCLEASE INHIBITOR; CHAIN: A, D, ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
94	1a9n	A	126	242	1.3e-20	0.51	0.15		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
94	1a9n	A	161	249	1e-10	0.25	0.19		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
94	1a9n	A	60	207	1.3e-18	0.43	0.96		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
94	1a9n	A	88	231	3.9e-22	0.72	0.86		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
94	1a9n	C	126	242	1.3e-20	0.60	0.40		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
94	1a9n	C	60	207	2.6e-18	0.39	0.72		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
94	1a9n	C	88	231	1.3e-22	0.74	0.77		U2 RNA HAIRPIN IV;	COMPLEX (NUCLEAR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	PROTEIN/RNA COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONUCLEOPROTEIN
94	1fvv	A	64	249	3.9e-12	0.17	-0.11		SKP2; CHAIN: A, C; E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2; ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE- RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
94	1fs2	A	60	239	3.9e-19	0.29	0.10		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
96	1a2y	B	40	74	0.0065	-0.84	0.10		MONOCLONAL ANTIBODY D1.3; CHAIN: A, B; LYSOZYME; CHAIN: C;	COMPLEX (IMMUNOGLOBULIN/HYDROLASE) COMPLEX (IMMUNOGLOBULIN/HYDROLASE), (IMMUNOGLOBULIN V 2 REGION, SIGNAL, HYDROLASE, GLYCOSIDASE, BACTERIOLYTIC 3 ENZYME, EGG WHITE
97	1a2y	B	40	74	0.0065	-0.84	0.10		MONOCLONAL ANTIBODY D1.3; CHAIN: A, B; LYSOZYME; CHAIN: C;	COMPLEX (IMMUNOGLOBULIN/HYDROLASE) COMPLEX (IMMUNOGLOBULIN/HYDROLASE), (IMMUNOGLOBULIN V 2 REGION, SIGNAL, HYDROLASE, GLYCOSIDASE, BACTERIOLYTIC 3 ENZYME, EGG WHITE

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
100	1amu	A	37	579	0			154.59	GRAMICIDIN SYNTHETASE I; CHAIN: A, B; PHENYLALANINE; CHAIN: C, D;	PEPTIDE SYNTHETASE GRSA; PEPTIDE SYNTHETASE, GRSA, ADENYLATE FORMING
100	1amu	A	50	578	0	0.51	1.00		GRAMICIDIN SYNTHETASE I; CHAIN: A, B; PHENYLALANINE; CHAIN: C, D;	PEPTIDE SYNTHETASE GRSA; PEPTIDE SYNTHETASE, GRSA, ADENYLATE FORMING
100	1lci		41	577	0			186.29	LUCIFERASE; CHAIN: NULL;	OXIDOREDUCTASE OXIDOREDUCTASE, MONOOXYGENASE, PHOTOPROTEIN, LUMINESCENCE
100	1lci		50	576	0	0.78	1.00		LUCIFERASE; CHAIN: NULL;	OXIDOREDUCTASE OXIDOREDUCTASE, MONOOXYGENASE, PHOTOPROTEIN, LUMINESCENCE
102	1c3d		1	50	5.1e-20	-0.41	0.31		C3D; CHAIN: NULL;	COMPLEMENT COMPLEMENT, C3, C3D, ALPHA-ALPHA BARREL
102	1qtf	A	1	49	5.1e-19	-0.06	0.23		COMPLEMENT C3DG; CHAIN: A;	IMMUNE SYSTEM ALPHA-ALPHA BARREL, COMPLEMENT
104	1a0j	A	22	247	1.7e-98			210.73	TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
104	1a0j	A	22	248	1.7e-98	0.83	1.00		TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
104	1a0l	A	22	253	1.7e-76			137.52	BETA-TRYPTASE; CHAIN: A, B, C, D;	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA
104	1aht	H	22	254	1e-69			137.36	ALPHA-THROMBIN;	COMPLEX (SERINE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									1AHT 4 CHAIN: L, H; 1AHT 5 HIRUGEN; 1AHT 8 CHAIN: I; 1AHT 9	PROTEINASE/INHIBITOR
104	1aks	B	154	236	3.9e-33	0.16	1.00		ALPHA TRYPSIN; CHAIN: A, B; GLANDULAR KALLIKREIN-13; CHAIN: A, B;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE SERINE PROTEASE SERINE PROTEASE CONVERTING ENZYME (PRECE), EPIDERMAL GLANDULAR KALLIKREIN, SERINE PROTEASE, PROTEIN MATURATION COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA, HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
104	1ao5	A	22	253	1.7e-82			193.53		
104	1aut	C	22	252	1e-69			146.28	ACTIVATED PROTEIN C; CHAIN: C, L, D-PHE-PRO- MAI; CHAIN: P;	
104	1bio		22	236	1.3e-76			161.35	COMPLEMENT FACTOR D; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, HYDROLASE, COMPLEMENT, FACTOR D, CATALYTIC 2 TRIAD, SELF- REGULATION
104	1byy	A	22	253	8.5e-83			190.92	PLASMINOGEN ACTIVATOR; CHAIN: A, B, GLU- GLY-ARG- CHLOROMETHYLKE TONE INHIBITOR; CHAIN: E, F;	BLOOD CLOTTING TSV-P4; FIBRINOLYSIS, PLASMINOGEN ACTIVATOR, SERINE PROTEINASE, 2 SNAKE VENOM, COMPLEX (HYDROLASE/INHIBITOR), BLOOD CLOTTING
104	1bru	P	22	249	3.4e-85			148.11	ELASTASE; CHAIN: P;	SERINE PROTEASE PPE, SERINE PROTEASE, HYDROLASE
104	1dpo		22	253	3.4e-95			208.46	TRYPSIN; CHAIN:	SERINE PROTEASE HYDROLASE,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									NULL;	SERINE PROTEASE, DIGESTION, PANCREAS, ZYMOGEN, 2 SIGNAL, MULTIGENE FAMILY
104	1fxy	A	22	249	5.1e-87	0.94	1.00		COAGULATION FACTOR XA-TRYPSIN CHIMERA; CHAIN: A; D-PHE-PRO-ARG-CHLOROMETHYLKETONE (PPACK) WITH CHAIN: F;	COMPLEX (PROTEASE/INHIBITOR) TRYPSIN, COAGULATION FACTOR XA, CHIMERA, PROTEASE, PPACK, 2 CHLOROMETHYLKETONE, COMPLEX (PROTEASE/INHIBITOR)
104	1fxy	A	22	250	5.1e-87			189.85	COAGULATION FACTOR XA-TRYPSIN CHIMERA; CHAIN: A; D-PHE-PRO-ARG-CHLOROMETHYLKETONE (PPACK) WITH CHAIN: F;	COMPLEX (PROTEASE/INHIBITOR) TRYPSIN, COAGULATION FACTOR XA, CHIMERA, PROTEASE, PPACK, 2 CHLOROMETHYLKETONE, COMPLEX (PROTEASE/INHIBITOR)
104	1gst	A	12	249	6.8e-76			142.82	HYDROLASE (SERINE PROTEINASE) GAMMA-CHYMOTRYPSIN *A (E.C.3.4.21.1) (SP*H 7.0) 10CT 3	
104	1mct	A	22	247	5.1e-100			217.46	COMPLEX (PROTEASE/INHIBITOR) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER 1MCT 3	
104	1mct	A	22	248	5.1e-100	0.95	1.00		GOUD 1MCT 4 COMPLEX (PROTEIN)	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									ASE(INHIBITOR) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER IMCT 3 GOURD IMCT 4	
104	1nrm	A	22	245	3.4e-87	0.99	1.00		NEUROPSIN; CHAIN: A, B;	SERINE PROTEINASE SERINE PROTEINASE, GLYCOPROTEIN
104	1nrm	A	22	252	3.4e-87			233.14	NEUROPSIN; CHAIN: A, B;	SERINE PROTEINASE SERINE PROTEINASE, GLYCOPROTEIN
104	1pfx	C	22	247	1e-77			136.25	FACTOR IXA; CHAIN: C, L; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR, COMPLEX, INHIBITOR, HEMOPHILIA/VEF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
104	1sgf	A	31	253	3.4e-68			147.35	NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)
104	1sgf	G	22	248	3.4e-91	0.87	1.00		NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)
104	1sgf	G	22	253	3.4e-91			204.41	NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
104	1slw	B	22	248	6.8e-95	0.97	1.00		ECOTIN; CHAIN: A; ANIONIC TRYPSIN; CHAIN: B;	COMPLEX (SERINE PROTEASE/INHIBITOR) TRYPSIN INHIBITOR; SERINE PROTEASE, INHIBITOR, COMPLEX, METAL BINDING SITES, 2 PROTEIN ENGINEERING, PROTEASE- SUBSTRATE INTERACTIONS, 3 METALLOPROTEINS
104	1slw	B	22	253	6.8e-95			198.58	ECOTIN; CHAIN: A; ANIONIC TRYPSIN; CHAIN: B;	COMPLEX (SERINE PROTEASE/INHIBITOR) TRYPSIN INHIBITOR; SERINE PROTEASE, INHIBITOR, COMPLEX, METAL BINDING SITES, 2 PROTEIN ENGINEERING, PROTEASE- SUBSTRATE INTERACTIONS, 3 METALLOPROTEINS
104	1ton		22	253	6.8e-83			183.92	HYDROLASE (SERINE PROTEINASE) TONIN (E.C. NUMBER NOT ASSIGNED) ITRN 4	
104	1trn	A	22	249	3.4e-98	0.86	1.00		HYDROLASE (SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR ITRN 3 DIISOPROPYL- FLUOROPHOSPHO- FLUORIDATE (DFP) ITRN 4 HUMAN TRYPSIN, DFP INHIBITED ITRN 6	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
104	1tm	A	22	250	3.4e-98			200.17	HYDROLASE (SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR ITRN 3 DIISOPROPYL-FLUOROPHOSPHORIDATE (DFP) ITRN 4 HUMAN TRYPSIN, DFP INHIBITED ITRN 6	
104	1luu	H	22	242	3.4e-63			142.38	THROMBIN; CHAIN: L, H;	SERINE PROTEASE FACTOR II, SERINE PROTEASE, HYDROLASE, THROMBIN, BLOOD COAGULATION
104	2bbs		22	246	5.1e-94	0.85	1.00		HYDROLASE(SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH BENZAMIDINE INHIBITOR 2TBS 3	
104	2bbs		22	254	5.1e-94			205.95	HYDROLASE(SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH BENZAMIDINE INHIBITOR 2TBS 3	
104	5ptp		22	247	8.5e-95			212.27	BETA TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL
104	5ptp		22	248	8.5e-95	0.90	1.00		BETA TRYPSIN;	SERINE PROTEASE HYDROLASE,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: NULL;	SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL
105	1ad0	A	135	319	5.1e-20	-0.09	0.49		FAB FRAGMENT; ANTIBODY A5B7; CHAIN: A, B, C, D, IGG4 REA; CHAIN: A; RF-AN	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB COMPLEX
105	1adq	L	35	231	5.1e-24			70.41	IGM/LAMBDA; CHAIN: H, L;	(IMMUNOGLOBULIN/AUTOANTIGEN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
105	1axt	H	37	226	1.5e-29	-0.26	0.11		IMMUNOGLOBULIN IGG2A; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY REACTION
105	1b2w	L	31	232	3.4e-19			70.24	ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRUCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM
105	1b6d	A	31	228	1e-18			66.53	IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
105	1bbj	L	31	228	1.7e-19			70.26	IMMUNOGLOBULIN FAB' FRAGMENT OF MONOCLONAL ANTIBODY B7/23 1BB13 (MURINE/HUMAN	

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMP Score	SeqFold Score	Compound	PDB annotation
105	1bth	A	32	402	1.5e-40	-0.19	0.15		CHIMERA 1BBI 4 HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
105	1bth	A	34	403	1.5e-40			105.99	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
105	1bth	A	4	312	1e-33	-0.32	0.01		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
105	1bog	A	31	232	1.7e-19			69.73	ANTIBODY (CB 4-1); CHAIN: A, B; PEPTIDE; CHAIN: C;	COMPLEX (ANTIBODY/PEPTIDE) POLYSPECIFICITY, CROSS REACTIVITY, FAB-FRAGMENT, PEPTIDE, 2 HIV-1, COMPLEX (ANTIBODY/PEPTIDE)
105	1ce1	L	31	228	6.8e-19			66.53	CAMPATH-1H; LIGHT CHAIN; CHAIN: L; CAMPATH-1H; HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P; AXONIN-1; CHAIN: A;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
105	1cs6	A	32	403	1.7e-48	-0.09	0.07			CELL ADHESION NEURAL CELL ADHESION
105	1ct8	B	36	232	3.4e-31	0.06	0.28		7C8 FAB FRAGMENT; SHORT CHAIN; CHAIN: A, C; 7C8 FAB FRAGMENT; LONG CHAIN; CHAIN: B, D	IMMUNE SYSTEM ABZYM TRANSITION STATE ANALOG, IMMUNE SYSTEM
105	1evs	C	138	322	3.4e-37	-0.19	0.09		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
105	1evs	D	138	322	8.5e-39	-0.07	0.09		GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR
105	1evs	D	243	402	3.4e-25	0.14	0.27		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
105	1dfb	L	137	319	5.1e-20	-0.19	0.28		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
105	1dfb	L	31	232	1.7e-18			67.12	IMMUNOGLOBULIN 3D6 FAB 1DFB 3	
105	1dgi	R	33	322	6.8e-32	-0.38	0.19		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
105	1dm2	A	133	312	3.4e-25	0.08	0.13		IMMUNOGLOBULIN LAMBDA HEAVY CHAIN; CHAIN: A, B; ENGINEERED PEPTIDE; CHAIN: E, F;	IMMUNE SYSTEM FC IGG PHAGE DISPLAY PEPTIDE
105	1dm2	A	235	404	1.7e-30	0.03	-0.11		IMMUNOGLOBULIN	IMMUNE SYSTEM FC IGG PHAGE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									LAMBDA HEAVY CHAIN: A, B; ENGINEERED PEPTIDE: CHAIN: E, F;	DISPLAY PEPTIDE
105	1ek4	A	133	312	1e-24	0.11	0.06		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR CHAIN: C; FC FRAGMENT OF HUMAN IGG1; CHAIN: A, B;	COMPLEX CD16; IGG1-FC COMPLEX, FC FRAGMENT, IGG, FC, RECEPTOR, CD16, GAMMA
105	1ek4	A	235	404	5.1e-50	0.16	-0.07		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR CHAIN: C; FC FRAGMENT OF HUMAN IGG1; CHAIN: A, B;	COMPLEX CD16; IGG1-FC COMPLEX, FC FRAGMENT, IGG, FC, RECEPTOR, CD16, GAMMA
105	1epf	A	145	312	2.6e-23	0.04	0.99		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
105	1ev2	E	130	322	1.5e-34	-0.07	0.06		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
105	1ev2	G	138	326	1.4e-37	0.16	0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SelfFold Score	Compound	PDB annotation
									RECEPTOR 2; CHAIN: E, F, G, H; IMMUNOGLOBULIN FC AND FRAGMENT B OF PROTEIN A COMPLEX 1FC2 4	DOMAINS, B-TREFOIL FOLD
105	1fc2	D	128	322	1e-24			66.62		
105	1fc2	D	133	312	1e-24	0.04	0.07		IMMUNOGLOBULIN FC AND FRAGMENT B OF PROTEIN A COMPLEX 1FC2 4	
105	1fcg	A	133	322	1.3e-22	0.19	0.42		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
105	1fsk	C	33	232	8.5e-33	-0.14	0.12		MAJOR POLLEN ALLERGEN BET V 1- A; CHAIN: A, D, G, J; IMMUNOGLOBULIN KAPPA LIGHT CHAIN; CHAIN: B, E, H, K; ANTIBODY HEAVY CHAIN FAB; CHAIN: C, F, I, L;	IMMUNE SYSTEM BET V 1-A, BETVI ALLERGEN; BV16 FAB-FRAGMENT, KAPPA MOPC21 CODING SEQUENCE: HEAVY CHAIN OF THE MONOCLONAL ANTIBODY MST2; BET V 1, BV16 FAB FRAGMENT, ANTIBODY ALLERGEN COMPLEX
105	1fvd	A	31	232	1.2e-19			69.02	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5; VERSION 4 1FVD 3	
105	1gc1	L	34	228	3.4e-18			70.37	ENVELOPE PROTEIN GP120; CHAIN: G; CD4; CHAIN: C; ANTIBODY 17B;	COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB) COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB), HIV-1 EXTERIOR 2 ENVELOPE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqField Score	Compound	PDB annotation
									CHAIN: L, H;	GP120, T-CELL SURFACE GLYCOPROTEIN CD4, 3 ANTIGEN-BINDING FRAGMENT OF HUMAN IMMUNOGLOBULIN 17B, 4 GLYCOSYLATED PROTEIN
105	1gpo	H	36	231	3.4e-30	-0.06	0.00		ANTIBODY M41; CHAIN: L, H, M, I;	IMMUNOGLOBULIN PROTEIN ENGINEERING, ANTIBODY DESIGN, IMMUNOGLOBULIN 2 STRUCTURE, ANTIGEN-BINDING SITE, CANONICAL CONFORMATION, 3 COMPLEMENTARITY- DETERMINING REGION
105	1hyx	H	36	232	1.7e-29	0.02	-0.06		IMMUNOGLOBULIN 6D9; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY 6D9 CATALYTIC ANTIBODY, ESTER HYDROLYSIS, ESTEROLYTIC, FAB, 2 IMMUNOGLOBULIN
105	1lge	L	31	232	3.4e-16			66.36	COMPLEX (ANTIBODY/BINDIN G PROTEIN) IGG1 FAB FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III) IIGC 5 PROTEIN G, STREPTOCOCCUS IIGC 15	
105	1lgy	B	19	403	3.4e-76			72.79	IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION
105	1lgy	B	36	404	3.4e-76	-0.25	0.05		IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
105	1ltb	B	41	326	2.6e-27			68.50	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
105	1lii	A	34	231	3.4e-23			69.16	LAMBDA III BENCE JONES PROTEIN CLE; CHAIN: A, B	IMMUNOGLOBULIN
105	1lma _m	H	36	227	6.8e-30	-0.23	0.03		IMMUNOGLOBULIN ANTIGEN-BINDING FRAGMENT (FAB) (IGG2B, KAPPA) IMAM 3	IMMUNOGLOBULIN, BENCE JONES PROTEIN
105	1lmc0	H	18	404	1.5e-82			76.87	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
105	1lmc0	H	32	404	1.5e-82	-0.27	0.40		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
105	1lmc0	H	5	312	1.4e-49	-0.11	0.07		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
105	1lmb	L	243	404	6.8e-15	0.15	-0.19		IMMUNOGLOBULIN FAB FRAGMENT (MURINE SE155-4) COMPLEX WITH	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									HEPTASACCHARIDE IMFB 3 B; GAL(1-2)MAN(1-4)RAM(1-3)GAL(1-2)[ABE(1-3)]MAN(1-4)RAM IMFB 4	
105	1mmu	H	36	226	5.1e-29	0.03	0.16		IGG2A-KAPPA ANTIBODY MN12H2 (LIGHT CHAIN); CHAIN: L; IGG2A-KAPPA ANTIBODY MN12H2 (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM MURINE IMMUNOGLOBULIN IGG2A KAPPA, BACTERICIDAL ANTIBODY, 2 EPTOPE P1.16 OF FORA FROM NEISSERIA MENINGITIDIS, 3 UNLIGANDED, IMMUNE SYSTEM
105	1am3	H	33	229	1.7e-31	-0.01	0.09		SW3 ANTIBODY; CHAIN: L, H; PEPTIDE EPTOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPTOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPTOPE)
105	2f6b	A	133	325	2.6e-25	0.08	0.16		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32, RECEPTOR, FC, CD32, IMMUNE SYSTEM
105	2h1p	H	36	229	8.5e-29	-0.01	0.03		2H1; CHAIN: L, H; PA1; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE) ANTIBODY STRUCTURE, CRYPTOCOCUS, PEPTIDE, PHAGE LIBRARY, 2 POLYSACCHARIDE, COMPLEX (ANTIBODY/PEPTIDE)
105	2hmi	D	37	226	1e-28	0.06	0.06		HIV-1 REVERSE TRANSCRIPTASE; CHAIN: A, B; MONOCLONAL ANTIBODY 28; CHAIN: C, D; DNA; CHAIN: E, F;	COMPLEX (RT/DNA/FAB) HIV-1 RT; FAB 28; AIDS, HIV-1, RT, POLYMERASE
105	32e2	B	33	226	3.4e-31	-0.22	0.06		IGG1 ANTIBODY 32c2; CHAIN: A;	IMMUNE SYSTEM FAB, ANTIBODY, AROMATASE, P450

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
105	3fct	A	34	231	1.4e-18			67.63	IGG1 ANTIBODY 32C2; CHAIN: B; METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: A, C; METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: B, D;	IMMUNE SYSTEM METAL CHELATASE, CATALYTIC ANTIBODY; FAB FRAGMENT, IMMUNE 2 SYSTEM
105	6fab	L	31	232	1.7e-16			70.37	IMMUNOGLOBULIN ANTIGEN-BINDING FRAGMENT OF THE MURINE ANTI-PHENYLARSONATE 6FAB 3 ANTIBODY 36-71, FAB 36-71 6FAB 4	
105	8fab	A	34	226	1.2e-23			70.63	IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HIL) 8FAB 3	
106	1apj		1221	1284	2.6e-14	0.49	0.98		FIBRILLIN; CHAIN: NULL;	EXTRACELLULAR MATRIX FIBRILLIN FRAGMENT, MICROFIBRIL, TB MODULE, MARFAN SYNDROME 2 CONNECTIVE TISSUE, NOVEL FOLD, EXTRACELLULAR MATRIX
106	1apj		786	857	3.9e-16	0.71	0.99		FIBRILLIN; CHAIN: NULL;	EXTRACELLULAR MATRIX FIBRILLIN FRAGMENT, MICROFIBRIL, TB MODULE,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1apj		979	1043	1.2e-10	0.31	0.55		FIBRILLIN; CHAIN: NULL;	MARFAN SYNDROME, 2 CONNECTIVE TISSUE, NOVEL FOLD, EXTRACELLULAR MATRIX
106	1apq		1508	1548	1e-10	-0.15	0.12		COMPLEMENT PROTEASE CIR; CHAIN: NULL;	EXTRACELLULAR MATRIX FIBRILLIN FRAGMENT, MICROFIBRIL, TB MODULE, MARFAN SYNDROME, 2 CONNECTIVE TISSUE, NOVEL FOLD, EXTRACELLULAR MATRIX
106	1aut	L	1133	1229	5.2e-13	-0.17	0.23		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEMENT COMPLEMENT, EGF, CALCIUM BINDING, SERINE PROTEASE
106	1aut	L	115	200	5.2e-10	0.05	-0.01		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD) COAGULATION/INHIBITOR
106	1aut	L	1338	1441	1e-20	0.48	0.71		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD) COAGULATION/INHIBITOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1aut	L	1423	1522	2.6e-23	0.18	0.68		ACTIVATED PROTEIN C; CHAIN: C; L; D-PHE-PRO-MAI; CHAIN: P;	COAGULATION/INHIBITOR) COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
106	1aut	L	1449	1555	1.2e-15	-0.06	0.05		ACTIVATED PROTEIN C; CHAIN: C; L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
106	1aut	L	174	290	2.6e-10	0.01	0.10		ACTIVATED PROTEIN C; CHAIN: C; L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
106	1aut	L	487	575	2.6e-23	0.14	0.74		ACTIVATED PROTEIN C; CHAIN: C; L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
106	1aut	L	816	914	2.6e-14	0.17	0.11		ACTIVATED PROTEIN C; CHAIN:	COMPLEX (BLOOD COAGULATION/INHIBITOR)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									C, L; D-PHE-PRO-MAI; CHAIN: P;	AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
106	1aut	L	859	950	6.5e-19	0.16	0.27		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
106	1aut	L	897	987	9.1e-18	0.26	0.22		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
106	1dan	L	1039	1124	6.8e-12	0.01	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG-CHLOROMETHYLKETOINE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
106	1dan	L	1137	1230	3.4e-12	-0.05	0.07		BLOOD COAGULATION FACTOR VIIA;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG- CHLOROMETHYLKE TONE (DFFRCMK) WITH CHAIN: C;	GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
106	1dan	L	941	1032	3.4e-10	-0.17	0.04		BLOOD COAGULATION FACTOR VITA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG- CHLOROMETHYLKE TONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
106	1dqb	A	1423	1511	1e-19	0.30	-0.07		THROMBOMODULI N; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSTYLATION
106	1dqb	A	488	570	9.1e-19	0.12	0.10		THROMBOMODULI N; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSTYLATION
106	1dqb	A	897	981	5.2e-15	0.28	0.10		THROMBOMODULI N; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSTYLATION
106	1dva	L	1039	1124	6.8e-12	0.16	-0.18		DES-GLA FACTOR VITA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VITA (LIGHT CHAIN); CHAIN: L, M; (DFN)-	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1dva	L	286	379	1e-13	0.25	-0.05		PHE-ARG; CHAIN: C; D; PEPTIDE E-76; CHAIN: X, Y; DES-GLA FACTOR CHAIN; CHAIN: H, I; DES-GLA FACTOR VIA (LIGHT CHAIN); CHAIN: L, M; (DPN)- PHE-ARG; CHAIN: C; D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
106	1dva	L	941	1032	3.4e-10	-0.29	0.16		DES-GLA FACTOR CHAIN; CHAIN: H, I; DES-GLA FACTOR VIA (LIGHT CHAIN); CHAIN: L, M; (DPN)- PHE-ARG; CHAIN: C; D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
106	1dk5	I	1181	1338	3.9e-14	0.05	0.19		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULI N; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L- GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
106	1dk5	I	124	217	3.9e-12	0.23	0.11		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; N; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L- GLY-L-ARM; CHAIN: E, F, G, H;	FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	1266	1381	7.8e-16	-0.18	0.12		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; N; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L- GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	1340	1465	1.3e-22	-0.33	0.40		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; N; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L- GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	1383	1506	9.1e-27	0.19	0.21		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE

SFQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	1424	1548	1e-23	0.32	0.88		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	1466	1598	8.5e-12	0.10	0.00		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	185	320	1.3e-15	0.13	0.05		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	448	570	1.3e-23	0.07	0.53		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	489	612	1.7e-16	0.19	-0.13		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	857	979	1e-23	-0.02	0.64		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1enn		1145	1212	1.7e-12	0.05	0.29		GLY-L-ARM; CHAIN: E, F, G, H; FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1enn		1178	1224	6.5e-13	0.11	0.98		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1enn		1181	1265	1e-12	-0.33	0.78		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1enn		1337	1402	3.9e-19	0.08	0.88		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1enn		1465	1527	3.9e-19	0.18	0.72		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									NULL;	EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1emm		1506	1551	1.3e-11	0.28	0.78		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1emm		410	489	3.4e-13	0.05	-0.19		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1emm		488	549	6.5e-20	-0.58	0.62		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1emm		530	615	1e-15	0.12	0.19		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1emm		711	777	6.8e-13	-0.64	0.12		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1f5y	A	76	148	1.7e-10	0.09	-0.18		LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: A ₁	LIPID BINDING PROTEIN LDL RECEPTOR; BETA HAIRPIN, 3-10 HELIX, CALCIUM BINDING
106	1fak	L	1039	1124	6.8e-12	0.07	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: F ₂	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
106	1fak	L	1137	1230	3.4e-12	-0.18	0.03		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1fak	L	1336	1443	2.6e-23	0.25	0.28		CHAIN: I; BLOOD COAGULATION FACTOR VIL; CHAIN: L; BLOOD COAGULATION FACTOR VIL; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
106	1fak	L	1423	1526	2.6e-23	-0.10	0.23		CHAIN: I; BLOOD COAGULATION FACTOR VIL; CHAIN: L; BLOOD COAGULATION FACTOR VIL; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
106	1fak	L	163	271	1.3e-08	0.05	-0.15		CHAIN: I; BLOOD COAGULATION FACTOR VIL; CHAIN: L; BLOOD COAGULATION FACTOR VIL; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
106	1fak	L	286	379	1e-13	-0.28	0.07		CHAIN: I; BLOOD COAGULATION FACTOR VIL; CHAIN: L; BLOOD	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE

SFO ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4) PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
106	1fak	L	481	575	2.6e-22	0.02	0.99		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4) PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
106	1fak	L	857	957	1.3e-20	0.09	0.55		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4) PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
106	1fak	L	897	987	7.8e-19	-0.07	0.07		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4) PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1fak	L	941	1032	3.4e-10	-0.08	0.06		CHAIN: I; BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I; PHOSPHOLIPASE A2; CHAIN: A;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
106	1god	A	158	290	1.3e-09	0.21	-0.19		INSULIN-LIKE GROWTH FACTOR RECEPTOR I; CHAIN: A;	HYDROLASE GODMT-II; LYS49-PHOSPHOLIPASE A2, SNAKE VENOM, BOTHROPS
106	1hae		157	201	5.2e-10	0.80	-0.05		HERGULIN-ALPHA; CHAIN: NULL;	GROWTH FACTOR NEU DIFFERENTIATION FACTOR (RAT), ACETYLCHOLINE GROWTH FACTOR
106	1igr	A	122	291	3.9e-10	-0.17	0.04		INSULIN-LIKE GROWTH FACTOR RECEPTOR I; CHAIN: A;	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY
106	1jia	A	1309	1429	1.2e-22	0.10	-0.20		PHOSPHOLIPASE A2; CHAIN: A, B;	PHOSPHOLIPASE PHOSPHOLIPASE A2, AGKISTRODON HALYS PALLAS CRYSTAL 2 STRUCTURE
106	1kio		129	246	1.3e-13	0.06	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
106	1kio		1352	1533	6.5e-21	0.01	-0.13		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
106	1kio		163	327	2.6e-18	0.27	0.78		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
106	1kio		294	447	1.7e-08	0.30	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
106	1kio		735	898	3.4e-11	0.12	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1kdo		771	930	5.2e-14	0.14	0.05		NULL; LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
106	1kdo		868	1027	2.6e-12	-0.03	0.03		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
106	1pfx	L	1084	1229	2.6e-18	0.08	-0.03		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3
106	1pfx	L	1296	1408	1.3e-22	-0.05	0.30		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3
106	1pfx	L	129	249	3.9e-16	0.17	-0.15		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3
106	1pfx	L	1352	1491	2.6e-32	-0.02	0.03		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1pfx	L	1391	1535	6.5e-30	-0.03	0.16		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
106	1pfx	L	1436	1550	6.5e-24	-0.03	0.12		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
106	1pfx	L	159	312	2.6e-21	0.02	-0.18		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
106	1pfx	L	286	379	1.5e-11	0.08	-0.07		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1pfx	L	455	575	2.6e-31	-0.44	0.40		FACTOR IXA; CHAIN: C, L; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
106	1pfx	L	868	987	1.2e-24	0.13	-0.03		FACTOR IXA; CHAIN: C, L; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
106	1pp2	R	1252	1387	7.8e-19	0.08	-0.19		HYDROLASE CALCIUM-FREE PHOSPHOLIPASE A=2= (E.C.3.1.1.4) 1PP2 4	
106	1qdk	L	1471	1550	8.5e-13	0.18	0.65		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPETIDYL INHIBITOR; CHAIN: G;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
106	1tpg		119	190	3.9e-10	0.02	0.19		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN;	PLASMINOGEN ACTIVATION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1tpg		1320	1430	1e-23	0.28	-0.18		NULL; ITPG 8 T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN; NULL; ITPG 8	PLASMINOGEN ACTIVATION
106	1tpg		1405	1512	5.2e-20	0.04	-0.05		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN; NULL; ITPG 8	PLASMINOGEN ACTIVATION
106	1tpg		140	220	7.8e-16	0.60	0.40		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN; NULL; ITPG 8	PLASMINOGEN ACTIVATION
106	1tpg		471	570	3.9e-22	-0.20	0.34		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN; NULL; ITPG 8	PLASMINOGEN ACTIVATION
106	1tpg		879	969	2.6e-19	0.03	-0.13		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN; NULL; ITPG 8	PLASMINOGEN ACTIVATION
106	1whe		148	222	2.6e-12	0.14	-0.07		COAGULATION FACTOR X; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN, HYDROLASE, SERINE PROTEASE, PLASMA, BLOOD 2 COAGULATION FACTOR
106	1whe		906	984	6.5e-15	-0.07	0.17		COAGULATION FACTOR X; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN, HYDROLASE, SERINE PROTEASE, PLASMA, BLOOD 2 COAGULATION FACTOR
106	Swga	A	1081	1250	6.8e-13	0.05	-0.14		LECTIN (AGGLUTININ) WHEAT GERM A AGGLUTININ (ISOLECTIN 2)	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	9wga	A	586	749	3.4e-11	0.09	-0.19		9WGA 3 LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
108	1b08	A	211	312	3.4e-18	0.04	-0.19		LUNG SURFACTANT PROTEIN D; CHAIN: A, B, C;	SUGAR BINDING PROTEIN C-TYPE LECTIN, CRD, SP-D, COLECTIN, ALPHA-HELICAL COILED-2 COIL, LUNG SURFACTANT, SUGAR BINDING PROTEIN
108	1bj3	A	29	178	8.5e-33			69.74	COAGULATION FACTOR IX- BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX- BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX- BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
108	1bj3	A	32	177	8.5e-33	0.40	1.00		COAGULATION FACTOR IX- BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX- BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX- BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
108	1c3a	B	32	180	5.1e-31	0.38	0.81		FLAVOCETIN-A; ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A; BETA SUBUNIT;	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
108	1dv8	A	211	309	6.8e-21	0.00	-0.19		CHAIN: B ASIALOGLYCOPROT EIN RECEPTOR I; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN HI; C-TYPE LECTIN CRD
108	1dv8	A	33	177	5.1e-29	0.30	0.57		ASIALOGLYCOPROT EIN RECEPTOR I; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN HI; C-TYPE LECTIN CRD
108	1egg	A	33	177	3.4e-30	0.26	1.00		MACROPHAGE MANNOSE RECEPTOR; CHAIN: A, B;	SUGAR BINDING PROTEIN C-TYPE LECTIN, MANNOSE RECEPTOR
108	1egg	B	31	184	6.8e-31	0.14	0.98		MACROPHAGE MANNOSE RECEPTOR; CHAIN: A, B;	SUGAR BINDING PROTEIN C-TYPE LECTIN, MANNOSE RECEPTOR
108	1esl		45	187	3.4e-27	0.71	0.93		CELL ADHESION PROTEIN E; SELECTIN (LECTIN AND EGF DOMAINS, RESIDUES 1 - 157) IESL 3 (FORMERLY KNOWN AS ELAM-1) IESL 4	
108	1esl		46	214	3.4e-27			62.46	CELL ADHESION PROTEIN E; SELECTIN (LECTIN AND EGF DOMAINS, RESIDUES 1 - 157) IESL 3 (FORMERLY KNOWN AS ELAM-1) IESL 4	
108	1hm		15	181	3.4e-26			61.20	TETRALECTIN; CHAIN: NULL;	LECTIN TETRALECTIN, PLASMINOGEN BINDING, KRINGLE 4, ALPHA-HELICAL 2 COILED COIL,

Seq ID No:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqField Score	Compound	PDB annotation
108	1ixx	A	32	177	8.5e-31	0.38	1.00		COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F.	C-TYPE LECTIN, CARBOHYDRATE RECOGNITION DOMAIN
108	1ixx	A	33	178	8.5e-31			63.16	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F.	COAGULATION FACTOR BINDING
108	1ixx	B	32	180	3.4e-31	0.29	0.48		COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F.	COAGULATION FACTOR BINDING
108	1ixx	B	34	180	3.4e-31			55.73	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F.	COAGULATION FACTOR BINDING
108	1lit		33	179	1e-32	0.56	0.90		LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR, LECTIN
108	1lit		33	180	1e-32			76.77	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR, LECTIN
108	1qdd	A	20	180	5.1e-34			80.98	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN
108	1qdd	A	210	313	5.1e-19	0.20	-0.15		LITHOSTATHINE; CHAIN: A;	PANCREATIC STONE PROTEIN, PSP; LITHOSTATHINE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
108	1qdd	A	26	179	5.1e-34	0.42	0.99		LITHOSTATHINE; CHAIN: A;	PANCREATIC STONE INHIBITOR, LITHOSTATHINE
108	1m3		29	181	3.4e-26			68.02	TETRANEECTIN; CHAIN: NULL;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
108	2afp	A	210	309	3.4e-18	0.12	-0.15		SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	LECTIN TETRANEECTIN, PLASMINOGEN BINDING, KRINGLE 4, C-TYPE LECTIN, 2 CARBOHYDRATE RECOGNITION DOMAIN
109	1enn		243	328	3.4e-14	0.09	-0.17		FIBRILLIN; CHAIN: NULL;	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C-2 TYPE LECTIN, ANTIFREEZE PROTEIN
109	1f7e	A	38	72	5.1e-07	-0.02	0.04		BLOOD COAGULATION FACTOR VII; CHAIN: A;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
109	1klo		239	374	3.4e-17	0.09	-0.19		LAMININ; CHAIN: NULL;	BLOOD CLOTTING FACTOR VII, BLOOD COAGULATION, EGF-LIKE DOMAIN, BLOOD 2 CLOTTING
109	1klo		247	404	3.9e-10	0.09	0.10		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
109	1klo		247	406	3.4e-17			76.67	LAMININ; CHAIN:	GLYCOPROTEIN GLYCOPROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
109	1qfk	L	39	110	8.5e-10	0.07	-0.13		NULL; COAGULATION FACTOR VIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR, CHAIN: C;	SERINE PROTEASE FWIA; FWIA; BLOOD COAGULATION, SERINE PROTEASE
109	1qub	A	146	470	1.3e-14			91.30	HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
109	1xka	L	73	148	1.7e-08	0.08	-0.17		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
109	4m2		276	339	6.8e-09	0.13	-0.17		METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2 3	
109	9wga	A	64	232	3.4e-18	0.00	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
110	1ac6	A	16	123	8.5e-29			52.19	T-CELL RECEPTOR ALPHA; CHAIN: A;	RECEPTOR RECEPTOR, V ALPHA DOMAIN, SITE-DIRECTED

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									B;	MUTAGENESIS, 2 THREE-DIMENSIONAL STRUCTURE, GLYCOPROTEIN, SIGNAL
110	1b0w	A	14	123	1.7e-34			51.99	BENCE-JONES KAPPA 1 PROTEIN BRE; CHAIN: A, B, C;	IMMUNE SYSTEM BENCE-JONES; IMMUNOGLOBULIN, AMYLOID; IMMUNE SYSTEM
110	1b6d	A	16	122	3.4e-36	0.49	0.62		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN
110	1bj1	L	16	122	5.1e-38	0.33	0.83		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
110	1bw	A	13	122	8.5e-35			50.58	IG KAPPA CHAIN V-1 REGION REI; CHAIN: A, B;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
110	1dee	A	16	122	5.1e-39	0.74	0.82		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H;	IMMUNE SYSTEM FAB-1BP
110	1dfb	L	16	122	5.1e-36	0.65	0.83		IMMUNOGLOBULIN 3D6 FAB IDFB 3	COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPRANTIGEN FAB VH3 3 SPECIFICITY
110	1dql	L	16	122	3.4e-38	0.64	0.88		IGM MEZ	IMMUNE SYSTEM
110	1fgv	L	14	122	8.5e-37			52.50	IMMUNOGLOBULIN; CHAIN: L, IGM MEZ; IMMUNOGLOBULIN; CHAIN: H;	IMMUNOGLOBULIN FOLD, ANTIBODY, IGM, FV
									IMMUNOGLOBULIN FV FRAGMENT OF A	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									HUMANIZED VERSION OF THE ANTI-CD18 IFGV 3 ANTIBODY 'H52' (HUH52-AA FV) IFGV 4	
110	1fgv	L	16	122	8.5e-37	0.30	0.63		IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 IFGV 3 ANTIBODY 'H52' (HUH52-AA FV) IFGV 4	
110	1fve	A	16	122	8.5e-37	0.11	0.77		IMMUNOGLOBULIN FV FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 8 IFVC 3	
110	1fvd	A	16	122	3.4e-37	0.20	0.64		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 IFVD 3	
110	1kb5	A	15	123	1.7e-38	0.46	0.84		KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T- CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
110	1kb5	A	17	123	1.7e-38			55.34	KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T- CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
110	1mbb	L	14	123	1.4e-30			51.23	H ₂ N9 NEURAMINIDASE; INMB 4 CHAIN: N; INMB 5 FAB NCI0; INMB 9 CHAIN: L, H; INMB 10	(IMMUNOGLOBULIN/RECEPTOR) COMPLEX (HYDROLASE/IMMUNOGLOBULIN)
110	2fgw	L	16	122	5.1e-37	0.32	0.92		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	
111	1ac6	A	14	120	1e-26			50.92	T-CELL RECEPTOR ALPHA; CHAIN: A ₁ B ₁	RECEPTOR RECEPTOR, V ALPHA DOMAIN, SITE-DIRECTED MUTAGENESIS 2 THREE-DIMENSIONAL STRUCTURE, GLYCOPROTEIN, SIGNAL
111	1b6w	A	11	120	3.4e-35			51.25	BENCE-JONES KAPPA 1 PROTEIN BRE; CHAIN: A, B, C ₁	IMMUNE SYSTEM BENCE-JONES; IMMUNOGLOBULIN, AMYLOID, IMMUNE SYSTEM
111	1b6d	A	12	119	1.7e-37	0.60	0.98		IMMUNOGLOBULIN; CHAIN: A, B ₁	IMMUNOGLOBULIN
111	1b88	A	13	120	5.1e-36			50.11	T CELL RECEPTOR V-ALPHA DOMAIN; CHAIN: A, B ₁	IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER T CELL RECEPTOR TC; T CELL RECEPTOR, MHC CLASS I, HUMAN IMMUNODEFICIENCY VIRUS, 2 MOLECULAR RECOGNITION
111	1bj1	L	12	119	3.4e-39	0.37	1.00		FAB FRAGMENT; CHAIN: L, H, J, K ₁ VASCULAR	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN)

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	ANGIOGENIC FACTOR
111	1bw	A	9	119	1e-36			52.25	IG KAPPA CHAIN V-I REGION REI; CHAIN: A, B;	IMMUNE SYSTEM REIV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENICE-JONES 2 PROTEIN, IMMUNE SYSTEM
111	1dee	A	12	119	1.7e-40	0.72	0.96		IGM RF 2A2; CHAIN: A, C, E, IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H;	IMMUNE SYSTEM FAB-IBP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
111	1dfb	L	12	119	3.4e-37	0.42	0.77		IMMUNOGLOBULIN 3D6 FAB 1DFB 3	IMMUNE SYSTEM
111	1dql	L	12	119	1.2e-39	0.53	0.98		IGM MEZ IMMUNOGLOBULIN; CHAIN: L; IGM MEZ IMMUNOGLOBULIN; CHAIN: H;	IMMUNOGLOBULIN FOLD, ANTIBODY, IGM, FV
111	1fgv	L	11	119	6.8e-38			51.87	IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 IFGV 3 ANTIBODY 'H52' (HUH52-AA FV) IFGV 4	
111	1fgv	L	12	119	6.8e-38	0.77	0.96		IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 IFGV 3 ANTIBODY 'H52'	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
111	1fvc	A	12	119	1.2e-37	0.29	0.74		(HUH52-AA FV) IFGV 4	
111	1fvd	A	12	119	3.4e-38	0.23	0.39		IMMUNOGLOBULIN FV FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 8 1FVC 3	
111	1kx5	A	13	120	1.7e-38	0.51	0.90		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T-CELL RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;
111	1kx5	A	14	120	1.7e-38			54.13	KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T-CELL RECEPTOR; STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
111	1nmb	L	11	120	5.1e-32			50.60	N9 NEURAMINIDASE; INMB 4 CHAIN: N; INMB 5 FAB NC10; INMB 9 CHAIN: L, H; INMB 10	COMPLEX (HYDROLASE/IMMUNOGLOBULIN)
111	2fgw	L	12	119	3.4e-38	0.35	0.94		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									ANTI-CD18 2FGW 3 ANTIBODY 'H52 (HUH52-OZ FAB) 2FGW 4	
114	1elr	A	371	442	0.00026	-0.21	0.27		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
114	1elr	A	371	442	0.00026	-0.21	0.27		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
114	1elw	A	374	440	0.0052	-0.23	0.40		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
114	1elw	A	374	440	0.0052	-0.23	0.40		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
114	1fch	A	131	445	0.00013	-0.40	0.28		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1- PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRATRUCOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
114	1fch	A	131	445	0.00013	-0.40	0.28		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1- PEPTIDE; CHAIN: C,	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRATRUCOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
114	1feh	A	275	518	9.1e-09	-0.34	0.57		D; PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C; D;	SIGNALING PROTEIN PEROXISOME RECEPTOR 1, PTS1-BP; PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
114	1feh	A	275	518	9.1e-09	-0.34	0.57		D; PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C; D;	SIGNALING PROTEIN PEROXISOME RECEPTOR 1, PTS1-BP; PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
115	1ase		6	147	5.1e-14	0.04	-0.05		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
115	lawc	B	166	315	1.2e-31	0.93	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D; E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
115	lawc	B	195	349	1e-40	0.57	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D; E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
115	1awc	B	268	420	1.4e-36	-0.00	-0.06		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BETA 1; CHAIN: B; DNA; CHAIN: D; E;	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
115	1awc	B	40	215	3.4e-28	0.29	0.98		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BETA 1; CHAIN: B; DNA; CHAIN: D; E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABP BETA 1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
115	1awc	B	69	249	1.3e-35	0.30	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BETA 1; CHAIN: B; DNA; CHAIN: D; E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABP BETA 1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
115	1awc	B	6	181	5.1e-28	0.08	0.71		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BETA 1; CHAIN: B; DNA; CHAIN: D; E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABP BETA 1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
115	1bd8		237	386	3.4e-29	0.22	0.47		P19INK4D CDK4/6	TUMOR SUPPRESSOR TUMOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
115	1bd8		9	181	1e-26	0.10	0.03		INHIBITOR; CHAIN: NULL; P19NK4D CDK4/6	SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
115	1bi7	B	6	147	3.4e-14	-0.20	0.05		INHIBITOR; CHAIN: NULL; CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A; MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
115	1blx	B	132	287	5.2e-40	0.81	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19NK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
115	1blx	B	166	320	7.8e-39	0.44	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19NK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
115	1blx	B	198	348	5.2e-36	0.73	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19NK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
115	1blx	B	4	184	5.2e-27	0.44	1.00		CYCLIN-DEPENDENT	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
115	1bix	B	72	251	1.3e-36	0.59	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
115	1bu9	A	234	392	6.8e-31	0.37	0.28		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
115	1bu9	A	6	186	1.7e-29	0.12	0.59		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
115	1d9s	A	124	252	3.9e-29	0.37	0.99		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
115	1d9s	A	6	147	3.4e-14	0.08	-0.02		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
115	1d9s	A	9	151	1.3e-18	0.44	0.43		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
115	1ez3	A	804	880	3.9e-08	0.14	-0.19		CHAIN: A; SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
115	1ez3	A	817	880	1.3e-08	0.38	-0.05		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
115	1thb	A	234	391	3.4e-30	0.24	0.87		CYCLIN- DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
115	1thb	A	6	185	1e-28	0.03	0.77		CYCLIN- DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
115	1thb	A	80	215	1.7e-28	0.23	1.00		CYCLIN- DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
115	1tkn	D	161	348	3.4e-38	0.41	0.99		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; IKAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
115	1tkn	D	2	202	1.7e-28	-0.15	0.24		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	Seqfold Score	Coumpound	PDB annotation
115	likn	D	35	233	8.5e-35	0.04	0.70		IKAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
115	lmyo		2	56	1e-11	0.07	0.66		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
115	lnfi	E	159	348	3.4e-38	0.67	1.00		NF-KAPPA-B P65; CHAIN: A, C, NF- KAPPA-B P50; CHAIN: B, D, I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
115	lnfi	E	159	354	1.3e-47	0.48	1.00		NF-KAPPA-B P65; CHAIN: A, C, NF- KAPPA-B P50; CHAIN: B, D, I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
115	lnfi	E	261	463	3.4e-37	0.07	-0.14		NF-KAPPA-B P65; CHAIN: A, C, NF- KAPPA-B P50; CHAIN: B, D, I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
115	lnfi	E	34	233	3.4e-35	0.17	0.98		NF-KAPPA-B P65; CHAIN: A, C, NF- KAPPA-B P50; CHAIN: B, D, I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
115	Infi	E	39	250	3.9e-36	0.41	0.99		NF-KAPPA-B P65; CHAIN: A, C, NF- KAPPA-B P50; CHAIN: B, D, I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
115	Infi	E	4	165	5.1e-27	0.28	0.83		NF-KAPPA-B P65; CHAIN: A, C, NF- KAPPA-B P50; CHAIN: B, D, I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
115	Infi	E	69	289	1.2e-40	0.64	1.00		NF-KAPPA-B P65; CHAIN: A, C, NF- KAPPA-B P50; CHAIN: B, D, I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
115	1yes	B	2	57	3.4e-14	0.39	0.70		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)
116	lawc	B	166	315	1.7e-34	0.79	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A, GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS.

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
116	lawc	B	195	349	1e-40	0.57	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
116	lawc	B	200	348	1.7e-36	0.73	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
116	lawc	B	234	382	5.1e-34	0.43	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
116	lawc	B	268	399	1.7e-34	0.20	0.29		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
116	lawc	B	69	249	1.3e-35	0.30	1.00		GA BINDING PROTEIN ALPHA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; TRANSCRIPTION 3 FACTOR

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING; 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
116	lawc	B	6	181	1.4e-27	0.09	0.68		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING; 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
116	lawc	B	76	215	1.7e-29	0.26	0.99		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING; 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
116	lbd8		101	249	1.7e-27	0.28	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
116	lbd8		237	385	3.4e-31	0.50	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
116	lbd8		2	113	5.1e-12	0.10	0.17		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
116	lbd8	B	101	249	1e-25	0.57	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									P19INK4D; CHAIN: B;	KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
116	1blx	B	132	287	5.2e-40	0.81	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
116	1blx	B	166	320	7.8e-39	0.44	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
116	1blx	B	198	348	5.2e-36	0.73	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
116	1blx	B	237	385	1.4e-31	0.56	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
116	1blx	B	4	184	5.2e-27	0.44	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
116	1blx	B	72	251	1.3e-36	0.59	1.00		CYCLIN-	COMPLEX (INHIBITOR PROTEIN/KINASE)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	PROTEIN(KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
116	1bu9	A	132	288	1.5e-30	0.84	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
116	1bu9	A	234	387	1.4e-35	0.29	0.66		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
116	1bu9	A	6	186	5.1e-28	0.15	0.64		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
116	1d9s	A	9	151	1.3e-18	0.44	0.43		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
116	1ez3	A	746	822	3.9e-08	0.14	-0.19		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
116	1ez3	A	759	822	1.3e-08	0.38	-0.05		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
116	1hhb	A	132	287	6.8e-30	0.61	1.00		CYCLIN-	CELL CYCLE INHIBITOR P18-

Seq ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	INK4C(NK0); CELL CYCLE INHIBITOR, P18-INK4C(NK0), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
116	1ihb	A	234	386	5.1e-35	0.46	0.94		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(NK0); CELL CYCLE INHIBITOR, P18-INK4C(NK0), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
116	1ihb	A	6	185	1.7e-27	0.03	0.58		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(NK0); CELL CYCLE INHIBITOR, P18-INK4C(NK0), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
116	1ikn	D	127	299	6.8e-34	0.35	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
116	1ikn	D	161	348	1.5e-37	0.29	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
116	1ikn	D	229	399	1.7e-33	0.15	0.19		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
116	1ikn	D	2	199	5.1e-28	0.05	0.22		NF-KAPPA-B P65 SUBUNIT; CHAIN: A;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR,

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	IRB/NFKB COMPLEX
116	1mvo		2	58	3.4e-12	-0.09	0.87		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
116	1nfi	E	125	299	1.7e-34	0.76	1.00		NF-KAPPA-B P65; CHAIN: A, C, NF- KAPPA-B P50; CHAIN: B, D, I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
116	1nfi	E	139	356	7.8e-48	0.72	1.00		NF-KAPPA-B P65; CHAIN: A, C, NF- KAPPA-B P50; CHAIN: B, D, I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
116	1nfi	E	161	348	8.5e-38	0.58	1.00		NF-KAPPA-B P65; CHAIN: A, C, NF- KAPPA-B P50; CHAIN: B, D, I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
116	1nfi	E	228	399	3.4e-33	0.38	0.51		NF-KAPPA-B P65; CHAIN: A, C, NF- KAPPA-B P50; CHAIN: B, D, I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
116	1nfi	E	263	444	1.4e-33	0.10	-0.14		NF-KAPPA-B P65; CHAIN: A, C, NF- KAPPA-B P50; CHAIN: B, D, I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
116	1nfi	E	2	199	3.4e-28	0.28	0.19		KAPPA-B-ALPHA; CHAIN: E, F; NF-KAPPA-B P65; CHAIN: A, C, NF- KAPPA-B P50; CHAIN: B, D, I; KAPPA-B-ALPHA; CHAIN: E, F;	ANKYRIN 2 REPEAT HELIX COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
116	1nfi	E	39	250	3.9e-36	0.41	0.99		NF-KAPPA-B P65; CHAIN: A, C, NF- KAPPA-B P50; CHAIN: B, D, I; KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
116	1nfi	E	69	289	1.2e-40	0.64	1.00		NF-KAPPA-B P65; CHAIN: A, C, NF- KAPPA-B P50; CHAIN: B, D, I; KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
116	1yes	B	2	57	1.2e-13	0.39	0.70		P53, CHAIN: A; 53BP2, CHAIN: B; P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) P53BP2, ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)
117	1a5t		150	455	6.8e-14	0.25	-0.05		DELTA PRIME; CHAIN: NULL;	ZINC FINGER HOLB; ZINC FINGER, DNA REPLICATION
119	1d2n	A	401	566	3.4e-29	0.55	0.65		N-	HEXAMERIZATION DOMAIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									ETHYLENEIMIDE-SENSITIVE FUSION PROTEIN; CHAIN: A;	HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT
119	1e94	E	388	489	5.1e-13	-0.54	0.21		HEAT SHOCK PROTEIN HSLV; CHAIN: A, B, C, D; HEAT SHOCK PROTEIN HSLU; CHAIN: E, F;	CHAPERONE HSLV; HSLU CHAPERONE, HSLVU, CLPQY, AAA-ATPASE, ATP-DEPENDENT 2 PROTEOLYSIS, PROTEASOME
119	1e94	E	496	577	3.4e-05	-0.30	0.31		HEAT SHOCK PROTEIN HSLV; CHAIN: A, B, C, D; HEAT SHOCK PROTEIN HSLU; CHAIN: E, F;	CHAPERONE HSLV; HSLU CHAPERONE, HSLVU, CLPQY, AAA-ATPASE, ATP-DEPENDENT 2 PROTEOLYSIS, PROTEASOME
119	1g41	A	388	656	1.7e-18	-0.06	0.13		HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS
119	1shk	A	437	466	0.0024	-0.62	0.06		SHIKIMATE KINASE; CHAIN: A, B;	TRANSFERASE SHIKIMATE KINASE, PHOSPHORYL TRANSFER, ADP, SHIKIMATE 2 PATHWAY, P-LOOP PROTEIN, TRANSFERASE
119	3adk		434	599	3.9e-05	0.09	0.01		TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	
120	1cs8	A	19	333	0			497.56	HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE INHIBITION, HYDROLASE
120	1cs8	A	19	333	0			497.56	HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE INHIBITION, HYDROLASE

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
120	1cs8	A	21	333	0	0.83	1.00		HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
120	1cs8	A	21	333	0	0.83	1.00		HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
120	1icf	B	292	333	1.7e-17	-0.53	0.90		CATHEPSIN L; HEAVY CHAIN; CHAIN: A, C; CATHEPSIN L; LIGHT CHAIN; CHAIN: B, D; INVARIANT CHAIN; CHAIN: L, J;	HYDROLASE II FRAGMENT, CD74 FRAGMENT CYSTEINE PROTEINASE, CATHEPSIN, MHC CLASS II, INVARIANT 2 CHAIN, THYROGLOBULIN TYPE-1 DOMAIN
120	1icf	B	292	333	1.7e-17	-0.53	0.90		CATHEPSIN L; HEAVY CHAIN; CHAIN: A, C; CATHEPSIN L; LIGHT CHAIN; CHAIN: B, D; INVARIANT CHAIN; CHAIN: L, J;	HYDROLASE II FRAGMENT, CD74 FRAGMENT CYSTEINE PROTEINASE, CATHEPSIN, MHC CLASS II, INVARIANT 2 CHAIN, THYROGLOBULIN TYPE-1 DOMAIN
121	1dix	A	242	793	0			519.97	PHOSPHONOSITIDE -SPECIFIC PHOSPHOLIPASE C; CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHONOSITIDE-SPECIFIC
121	1dix	A	242	793	0			519.97	PHOSPHONOSITIDE -SPECIFIC PHOSPHOLIPASE C; CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
121	1dix	A	259	792	0	0.65	1.00		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, 3	CALCIUM-BINDING, PHOSPHOINOSITIDE-SPECIFIC
									LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3	
121	1dix	A	259	792	0	0.68	1.00		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B,	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
121	1dix	B	200	793	0			571.84	PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
121	1dix	B	200	793	0			571.84	PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
121	1dix	B	201	792	0	0.65	1.00		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B,	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
121	1dix	B	201	792	0	0.66	1.00		PHOSPHONOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHONOSITIDE-SPECIFIC LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHONOSITIDE-SPECIFIC
121	1eor	A	177	322	5.1e-36	0.18	0.07		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
121	1eor	A	177	322	5.1e-36	0.18	0.07		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
121	1mai		55	170	9.1e-29	0.89	1.00		PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN PLECKSTRIN, PHOSPHOLIPASE, INOSITOL TRISPHOSPHATE, 2 SIGNAL TRANSDUCTION PROTEIN, HYDROLASE
121	1mai		55	170	9.1e-29	0.89	1.00		PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN PLECKSTRIN, PHOSPHOLIPASE, INOSITOL TRISPHOSPHATE, 2 SIGNAL TRANSDUCTION PROTEIN, HYDROLASE
121	1mai		55	170	9.1e-29			110.09	PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN PLECKSTRIN, PHOSPHOLIPASE, INOSITOL TRISPHOSPHATE, 2 SIGNAL TRANSDUCTION PROTEIN, HYDROLASE
121	1mai		55	170	9.1e-29			110.09	PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN PLECKSTRIN, PHOSPHOLIPASE, INOSITOL TRISPHOSPHATE, 2 SIGNAL TRANSDUCTION PROTEIN, HYDROLASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PIRF Score	SeqFold Score	Compound	PDB annotation
121	1tnx	179	320	320	3.4e-34	0.07	0.09		TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	CALCIUM-BINDING PROTEIN EF-HAND ITNX 14
121	1tnx	179	320	320	3.4e-34	0.07	0.09		TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	CALCIUM-BINDING PROTEIN EF-HAND ITNX 14
121	1top	179	320	320	1.4e-34	0.26	0.84		CONTRACTILE SYSTEM PROTEIN TROPONIN C ITOP 3	
121	1top	179	320	320	1.4e-34	0.26	0.84		CONTRACTILE SYSTEM PROTEIN TROPONIN C ITOP 3	
121	1vrk	A	176	323	3.4e-36	0.07	0.33		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN; CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
121	1vrk	A	176	323	3.4e-36	0.07	0.33		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN; CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
122	12e8	H	35	247	5.1e-27			64.22	2E8 (GG1=KAPPA=) ANTIBODY; CHAIN: L, H, M, P;	IMMUNOGLOBULIN IMMUNOGLOBULIN
122	1a0q	H	40	245	5.1e-24			63.99	29G11 FAB; CHAIN: L, E;	CATALYTIC ANTIBODY, ESTERASE COMPLEX
122	1a3r	H	40	247	1.5e-27			68.09	IGG2A; CHAIN: L, H; HUMAN RHINOVIRUS CAPSID PROTEIN VP2; CHAIN: P;	(IMMUNOGLOBULIN/VIRAL PEPTIDE) ANTIBODY 3F5; IMMUNOGLOBULIN, ANTIBODY; RHINOVIRUS, NEUTRALIZATION, 2 CONTINUOUS EPTOPE, COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
122	1a3r	H	41	242	1.5e-27	0.10	0.48		IGG2; CHAIN: L, H; HUMAN RHINOVIRUS CAPSID PROTEIN VP2; CHAIN: P;	COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE) ANTIBODY 8F5; IMMUNOGLOBULIN, ANTIBODY, RHINOVIRUS, NEUTRALIZATION, 2 CONTINUOUS EPTOPE, COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE)
122	1a5f	H	39	245	1.7e-25			63.45	MONOCLONAL ANTI-P-SELECTIN 7A9 ANTIBODY; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB, ANTIBODY, ANTI-P-SELECTIN
122	1a66	H	35	245	6.8e-25			63.32	ANTIBODY CTM01; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB FRAGMENT, HUMANISATION
122	1a1f	L	37	231	1e-17	-0.20	0.42		ANTI-ID10TYPIC FAB 409.5.3 (IGG2A) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN IMMUNOGLOBULIN, C REGION, V REGION
122	1a1t	H	37	247	5.1e-27			65.91	IMMUNOGLOBULIN IGG2A; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY FAB, CATALYST, ALDOLASE REACTION
122	1a1y	H	35	247	1e-26			67.40	TP7 FAB; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY, FAB, ENZYME INHIBITOR, PCR, 2 HOT START
122	1ba1	H	35	247	1e-24			63.28	IMMUNOGLOBULIN FAB FRAGMENT OF MURINE MONOCLONAL ANTIBODY AN02 COMPLEX 1BAF 3 WITH ITS HAPTEN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									(2,2,6,6-TETRAMETHYL-1-PIPERIDINYL-OXY-IBAF 4 DINITROPHENYL) IBAF 5	
122	1bqg	B	35	247	3.4e-24			64.40	ANTIBODY (CB 4-1); CHAIN: A, B, PEPTIDE; CHAIN: C;	COMPLEX (ANTIBODY/PEPTIDE) POLYSPECIFICITY, CROSS REACTIVITY, FAB-FRAGMENT, PEPTIDE, 2 HIV-1, COMPLEX (ANTIBODY/PEPTIDE)
122	1bql	H	36	246	3.4e-24			64.73	COMPLEX (ANTIBODY/ANTIGEN) HYHEL-5 FAB COMPLEXED WITH BOBWHITE QUAIL LYSOZYME IBOQL 3 IBOQL 95	
122	1ee1	H	37	242	1.5e-27	0.09	0.34		CAMPATH-1H LIGHT CHAIN; CHAIN: L; CAMPATH-1H HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: F;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
122	1cf8	H	35	247	5.1e-27			64.05	CATALYTIC ANTIBODY 19A4 (LIGHT CHAIN); CHAIN: L; CATALYTIC ANTIBODY 19A4 (HEAVY CHAIN); CHAIN: H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, TERPENOID SYNTHASE, CARBOXYLATION, 2 CYCLIZATION CASCADE
122	1cf8	H	44	242	5.1e-27	0.08	0.16		CATALYTIC ANTIBODY 19A4	CATALYTIC ANTIBODY CATALYTIC ANTIBODY,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									(LIGHT CHAIN); CHAIN: L; CATALYTIC ANTIBODY 19A4 (HEAVY CHAIN); CHAIN: H;	TERPENOID SYNTHASE, CARBOXYATION, 2 CYCLIZATION CASCADE
122	1cf8	L	40	231	1.4e-17	-0.19	0.31		CATALYTIC ANTIBODY 19A4 (LIGHT CHAIN); CHAIN: L; CATALYTIC ANTIBODY 19A4 (HEAVY CHAIN); CHAIN: H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, TERPENOID SYNTHASE, CARBOXYATION, 2 CYCLIZATION CASCADE
122	1cr9	H	41	242	6.8e-30	0.20	0.57		FAB ANTIBODY LIGHT CHAIN; CHAIN: L; FAB ANTIBODY HEAVY CHAIN; CHAIN: H;	IMMUNE SYSTEM ANTI-PRION FAB 3F4, ANTI-PRION FAB 3F4 ANTI-PRION ANTIBODY, FAB 3F4
122	1ct8	B	37	247	3.4e-24			62.70	7C3 FAB FRAGMENT; SHORT CHAIN; CHAIN: A, C; 7C3 FAB FRAGMENT; LONG CHAIN; CHAIN: B, D	IMMUNE SYSTEM ABZYME TRANSITION STATE ANALOG, IMMUNE SYSTEM
122	1deq	B	44	242	6.8e-28	-0.13	0.07		ANTI-LYSOZYME ANTIBODY HYHEL-63 (LIGHT CHAIN); CHAIN: A, C; ANTI-LYSOZYME ANTIBODY HYHEL-63 (HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM ANTI-LYSOZYME ANTIBODY, HYHEL-63, HEN EGG WHITE LYSOZYME
122	1e6o	L	40	231	8.5e-18	-0.17	0.06		IMMUNOGLOBULIN LIGHT CHAIN;	IMMUNOGLOBULIN FAB, ANTIBODY, ANTIGEN, HIV-1, P24,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: L; IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H; CA	
122	1f5w	A	35	150	1.3e-24	0.36	0.98		COXSACKIE VIRUS AND ADENOVIRUS RECEPTOR; CHAIN: A, B;	VIRUS/VIRAL PROTEIN RECEPTOR IMMUNOGLOBULIN V DOMAIN FOLD, SYMMETRIC DIMER
122	1f5w	A	37	152	3.4e-22	0.22	0.92		COXSACKIE VIRUS AND ADENOVIRUS RECEPTOR; CHAIN: A, B;	VIRUS/VIRAL PROTEIN RECEPTOR IMMUNOGLOBULIN V DOMAIN FOLD, SYMMETRIC DIMER
122	1fig	H	35	244	8.5e-24			71.28	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (KAPPA LIGHT CHAIN) FAB FRAGMENT IFIG 3	
122	1fns	L	37	231	1.7e-18	-0.07	0.06		IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A; MAJOR FOLLEN ALLERGEN BET V 1- A; CHAIN: A, D, J; IMMUNOGLOBULIN KAPPA LIGHT CHAIN; CHAIN: B, B, H, K; ANTIBODY HEAVY CHAIN FAB; CHAIN: C, F, I, L;	IMMUNE SYSTEM VON WILLEBRAND FACTOR GLYCOPROTEIN IBA (A-ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN , BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE
122	1f5k	B	41	231	1e-17	0.03	0.00		IMMUNE SYSTEM BET V1-A, BETVI ALLERGEN; BV16 FAB-FRAGMENT, KAPPA MOPC21 CODING SEQUENCE; HEAVY CHAIN OF THE MONOCLONAL ANTIBODY MST2; BET V1, BV16 FAB FRAGMENT, ANTIBODY ALLERGEN COMPLEX	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
122	1ghf	H	40	245	1.7e-23			66.93	ANTI-ANTI-IDIOTYPE GHI002 FAB FRAGMENT; CHAIN: L, H	ANTIBODY FAB FRAGMENT ANTIBODY FAB FRAGMENT
122	1gpo	H	44	242	1.7e-28	0.04	-0.09		ANTIBODY M41; CHAIN: L, H, M ₁	IMMUNOGLOBULIN PROTEIN ENGINEERING, ANTIBODY DESIGN, IMMUNOGLOBULIN 2 STRUCTURE, ANTIGEN-BINDING SITE, CANONICAL CONFORMATION, 3 COMPLEMENTARITY - DETERMINING REGION
122	1lgi	B	36	246	1.7e-22			65.63	IMMUNOGLOBULIN FAB (JGG2A, KAPPA) FRAGMENT (26-10) COMPLEX WITH DIGOXIN 11GJA 1 11GJA 2	
122	1kso	H	35	247	6.8e-25			68.30	KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H ₂	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T- CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
122	1kso	L	37	231	1.7e-19	0.15	0.88		KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H ₂	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T- CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
122	1mfe	H	37	247	1.5e-22			64.30	IMMUNOGLOBULIN FAB FRAGMENT (MURINE SE155-4) COMPLEX WITH DODECASACCHARI DE 1MFE 3 1-	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									3)ALPHA-D-GALACTOSE(1-ABEQUOSE(1-3))ALPHA-1MFE 4 D-MANNOSE(1-4)ALPHA-L-RAHAMNOSE(1-5 CELL SURFACE CARBOHYDRATE OF PATHOGENIC SALMONELLA) IMFE 6	
122	1nld	H	35	246	1.2e-26			68.87	FAB1583; CHAIN: L, H	IMMUNOGLOBULIN FAB FRAGMENT, IMMUNOGLOBULIN
122	1nsn	H	39	244	1.7e-26			63.71	IGG FAB (GG1, KAPPA); INSN 4 CHAIN: L, H; INSN 5 STAPHYLOCOCCAL NUCLEASE; INSN 9 CHAIN: S; INSN 10	COMPLEX (IMMUNOGLOBULIN/HYDROLASE) N10 FAB IMMUNOGLOBULIN; INSN 7 STAPHYLOCOCCAL NUCLEASE RIBONUCLEASE, INSN 11 IMMUNOGLOBULIN, STAPHYLOCOCCAL NUCLEASE INSN 25
122	1psk	H	35	240	5.1e-23			62.61	ANTIBODY; CHAIN: L, H;	IMMUNOGLOBULIN FAB, GD2-GANGLIOSIDE, CARBOHYDRATE, MELANOMA, IMMUNOGLOBULIN
122	1sm3	H	35	247	6.8e-29			63.77	SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPITOPE)
122	1sm3	H	37	242	6.8e-29	0.00	0.35		SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE;	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
122	1tet	H	35	247	6.8e-25			62.73	CHAIN: F; IMMUNOGLOBULIN IGG1 MONOCLONAL FAB FRAGMENT (TE33) COMPLEX WITH CHOLERA ITET 3 TOXIN PEPTIDE 3 (CTP3) ITET 4	2 COMPLEX (ANTIBODY/PEPTIDE EPTOPE)
122	1wej	H	35	253	1.7e-25			66.09	E8 ANTIBODY; CHAIN: L, H; CYTOCHROME C; CHAIN: F;	COMPLEX (ANTIBODY/ELECTRON TRANSPORT) FAB E8; CYT C; ANTIGEN: IMMUNOGLOBULIN, IGG1 KAPPA, FAB FRAGMENT, HORSE 2 CYTOCHROME C; COMPLEX (ANTIBODY/ELECTRON TRANSPORT)
122	1wej	L	37	231	8.5e-19	-0.30	0.81		E8 ANTIBODY; CHAIN: L, H; CYTOCHROME C; CHAIN: F;	COMPLEX (ANTIBODY/ELECTRON TRANSPORT) FAB E8; CYT C; ANTIGEN: IMMUNOGLOBULIN, IGG1 KAPPA, FAB FRAGMENT, HORSE 2 CYTOCHROME C; COMPLEX (ANTIBODY/ELECTRON TRANSPORT)
122	25e8	H	35	245	1.2e-26			71.71	IGG 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
122	3lhm	H	35	247	1.4e-28			65.83	COMPLEX (ANTIBOD Y-ANTIGEN) IGG*G1 FAB FRAGMENT (HYHEL5-10) AND LYSOZYME (E.C.3.2.1.17) 3HEM 4 COMPLEX 3HEM 5	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
122	3hfm	H	44	242	1.4e-28	0.00	0.28		COMPLEX/ANTIBODY-ANTIGEN 1G*G1 FAB FRAGMENT (HY/HEL5-10) AND LYSOZYME (E.C.3.2.1.17) 3HFM 4 COMPLEX 3HFM 5	
123	1l99	A	176	303	2.6e-06	-0.08	0.06		CARBON MONOXIDE OXIDATION SYSTEM TRANSCRIPTION CHAIN: A, B;	TRANSCRIPTION COOA GENE PRODUCT; CARBON MONOXIDE, HEME SENSOR, CATABOLITE GENE ACTIVATOR 2 PROTEIN
123	1l99	A	181	319	3.4e-05	-0.21	0.05		CARBON MONOXIDE OXIDATION SYSTEM TRANSCRIPTION CHAIN: A, B;	TRANSCRIPTION COOA GENE PRODUCT; CARBON MONOXIDE, HEME SENSOR, CATABOLITE GENE ACTIVATOR 2 PROTEIN
123	1l99		135	288	1.4e-27	0.33	0.62		CAMP DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE RI(ALPHA), REGULATORY SUBUNIT, KINASE
123	2egp	A	171	319	1.7e-26	-0.25	0.23		CATABOLITE GENE ACTIVATOR PROTEIN; CHAIN: A; DNA (5'-D(CGP*TP*CP*AP*CP*AP*TP*TP*AP*AP*T)-3'); CHAIN: B; DNA (5'-CHAIN: C;	TRANSCRIPTION/DNA COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, CAMP- 2 BINDING, ACTIVATOR
127	153l		36	212	1e-47	0.70	1.00		HYDROLASE(O-GLYCOSYL)	

Seq ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
127	1531	36	212	1e-47	0.70	1.00			LYSOZYME (E.C.3.2.1.17) 153L 3	
									HYDROLASE(O-GLYCOSYL) LYSOZYME (E.C.3.2.1.17) 153L 3	
127	1531	36	212	1e-47				186.19	HYDROLASE(O-GLYCOSYL) LYSOZYME (E.C.3.2.1.17) 153L 3	
127	1531	36	212	1e-47				186.19	HYDROLASE(O-GLYCOSYL) LYSOZYME (E.C.3.2.1.17) 153L 3	
									HYDROLASE(O-GLYCOSYL) LYSOZYME (E.C.3.2.1.17) 153L 3	
128	1cdl	A	147	267	2.6e-11	0.10	0.87		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
128	1cdl	A	29	145	5.1e-18	0.05	-0.15		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
128	1cdl	A	87	201	1e-18	0.40	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
128	1cdl	A	87	204	1e-18			58.04	CD46; CHAIN: A, B,	GLYCOPROTEIN MEMBRANE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									C, D, E, F;	COFACTOR PROTEIN (MCP), VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
128	1e5g	A	29	141	1.7e-15	0.19	0.65		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
128	1e5g	A	87	201	7.8e-25	0.65	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
128	1e5g	A	87	202	1.4e-24	0.43	0.98		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
128	1hec		147	202	6.5e-16	0.55	1.00		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (CCPS) OF FACTOR H 1HCC 3	
128	1hec		87	141	1.3e-10	0.44	0.90		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (CCPS) OF FACTOR H 1HCC 3	
128	1hfh		143	266	3.4e-14	0.19	0.52		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFA 1 AVERAGED	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
128	1hh		28	141	1.7e-13	0.19	0.05		STRUCTURE) 1HFH 4 1HFHA 5	
									GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
128	1hh		83	202	3.4e-17			93.95	GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
128	1hh		87	202	3.4e-17	0.28	0.82		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
128	1hf		147	201	3.9e-16	0.68	0.98		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HF1 4	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
128	1hhf		87	140	5.2e-10	0.57	1.00		1HEIA 5 GLYCOPROTEIN FACTOR H. 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HEIA 1 STRUCTURE) 1HEI 4 1HEIA 5	
128	1pfx	L	104	192	5.1e-10	0.15	0.10		FACTOR IXA; CHAIN: C, L ₂ ; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/ECF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
128	1lqb	A	3	266	6.8e-39			95.32	HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
128	1lqb	A	8	266	6.8e-39	0.07	0.87		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
128	1yvc		145	266	3.4e-24	-0.22	0.21		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
128	1yvc		29	142	1.5e-17	0.07	-0.05		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
128	1vvc		86	203	3.4e-20			82.91	CHAIN: NULL; VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
128	1vvc		87	202	3.4e-20	0.30	1.00		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
129	1ata		834	896	5.2e-12	0.29	0.09		PROTEINASE INHIBITOR(TRYPSIN) TRYPSIN INHIBITOR (PH 4.75) IATA 3 (NMR, MINIMIZED AVERAGE STRUCTURE) IATA 4	
129	1aut	L	845	940	5.1e-11	0.29	-0.19		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO- MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION(INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION(INHIBITOR))
129	1dan	L	819	898	1.7e-10	0.49	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG-CHLOROMETHYLKE TONE (DFRCMK) WITH CHAIN: C;	PROTEASE/COFACTOR/LIGAND)
129	1dan	L	851	943	3.4e-12	0.08	-0.15		BLOOD COAGULATION FACTOR VIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG-CHLOROMETHYLKE TONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
129	1dan	L	939	1020	1.7e-10	0.01	-0.18		BLOOD COAGULATION FACTOR VIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG-CHLOROMETHYLKE TONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
129	1dva	L	330	427	8.5e-14	0.20	-0.18		DES-GLA FACTOR VIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SqFold Score	Compound	PDB annotation
129	1dva	L	819	898	1.7e-10	0.65	-0.12		DES-GLA FACTOR VIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
129	1dva	L	851	943	3.4e-12	0.30	-0.14		DES-GLA FACTOR VIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
129	1dx5	I	1167	1294	3.4e-11	0.02	-0.20		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
129	1dx5	I	1167	1294	3.4e-11	0.02	-0.20		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									N; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
129	1fak	L	819	898	1.7e-10	0.27	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
129	1fak	L	819	898	1.7e-10	0.27	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
129	1fak	L	851	943	3.4e-12	0.05	-0.14		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
129	1fak	L	851	943	3.4e-12	0.10	-0.15		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: F	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
129	1klo		333	472	1e-09	0.21	-0.15		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
129	1klo		755	902	3.4e-15	0.20	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
129	1klo		755	902	3.4e-15	0.20	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
129	1pfx	L	330	438	1.4e-10	0.15	-0.14		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
129	1pfx	L	772	920	2.6e-08	0.03	-0.18		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
129	1pfx	L	819	898	1.7e-09	0.09	-0.19		FACTOR IXA; CHAIN: C, L; D-PHE-	COMPLEX (BLOOD COAGULATION/INHIBITOR)

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PRO-ARG; CHAIN: I;	CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/ECF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
129	1qtk	L	1263	1339	5.1e-11	0.16	-0.19		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
129	1qtk	L	334	427	5.1e-13	0.32	-0.18		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
129	1qtk	L	822	898	6.8e-10	0.31	-0.18		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN);	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: H; TRYPEPTIDYL INHIBITOR; CHAIN: C;	
129	1qub	A	379	488	3.9e-08	0.20	-0.15		HUMAN BETA-2- GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI- DOMAIN, MEMBRANE ADHESION
129	1xka	L	334	427	3.4e-10	0.22	-0.07		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
129	1xka	L	822	898	1e-10	0.22	-0.13		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
129	1xka	L	855	940	3.4e-09	0.11	-0.19		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
129	9wga	A	1219	1364	5.1e-11	0.02	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9wga 3	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
129	9wga	A	1219	1364	5.1e-11	0.02	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
129	9wga	A	277	420	5.1e-14	0.08	-0.19		(ISOLECTIN 2) 9WGA 3	
									LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
129	9wga	A	277	420	5.1e-14	0.08	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
129	9wga	A	318	544	1.5e-11	0.31	-0.18		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
129	9wga	A	318	544	1.5e-11	0.31	-0.18		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
129	9wga	A	757	907	3.4e-12	0.13	-0.17		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
129	9wga	A	757	907	3.4e-12	0.13	-0.17		LECTIN (AGGLUTININ)	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
129	9wga	A	777	975	5.1e-13	0.29	-0.12		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
129	9wga	A	777	975	5.1e-13	0.29	-0.12		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
130	lapo		1210	1245	1.3e-06	0.37	0.53		COAGULATION FACTOR EGF-LIKE MODULE OF BLOOD COAGULATION FACTOR X (N-TERMINAL, IAPO 3 APO FORM) (NMR, 13 STRUCTURES) IAPO 4	
130	lapo		1210	1245	1.3e-06	0.37	0.53		COAGULATION FACTOR EGF-LIKE MODULE OF BLOOD COAGULATION FACTOR X (N-TERMINAL, IAPO 3 APO FORM) (NMR, 13 STRUCTURES) IAPO 4	

SEQ ID No.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
130	1ciu	39	385		5.2e-34	0.05	-0.19		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
130	1ciu	39	385		5.2e-34	0.05	-0.19		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
130	1ciu	404	783		1.3e-32	0.01	-0.18		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
130	1ciu	404	783		1.3e-32	0.01	-0.18		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
130	1ciu	669	1044		1.3e-26	0.05	-0.19		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
130	1ciu	669	1044		1.3e-26	0.05	-0.19		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
130	1ciu	863	1177		3.9e-22	0.03	-0.15		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14

Seq ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
130	1ciu		863	1177	3.9e-22	0.03	-0.15		7 CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
130	1cww	A	264	749	9.1e-60	0.05	-0.20		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN- BINDING PROTEIN, INV GENE
130	1cww	A	264	749	9.1e-60	0.05	-0.20		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN- BINDING PROTEIN, INV GENE
130	1cww	A	521	996	1.2e-61			101.45	INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN- BINDING PROTEIN, INV GENE
130	1cww	A	521	996	1.2e-61			101.45	INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN- BINDING PROTEIN, INV GENE
130	1cww	A	561	1082	1e-56	0.04	-0.19		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN- BINDING PROTEIN, INV GENE
130	1cww	A	561	1082	1e-56	0.04	-0.19		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN- BINDING PROTEIN, INV GENE
130	1dan	L	1210	1282	8.5e-10	0.15	0.04		BLOOD COAGULATION FACTOR VILA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG- CHLOROMETHYLKE TONE (DFFRCK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
130	1dan	L	1210	1282	8.5e-10	0.15	0.04		BLOOD COAGULATION FACTOR VILA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PIIF Score	SeqFold Score	Compound	PDB annotation
									U; D-PHE-PHE-ARG-CHLOROMETHYLKE TONE (DFRCMK) WITH CHAIN: C; FACTOR IX; CHAIN: B, C;	
130	1edm	B	1210	1242	5.1e-07	0.32	0.76			COAGULATION FACTOR CRYSTAL STRUCTURE, EPIDERMAL GROWTH FACTOR, EGF, 2 CALCIUM-BINDING, EGF-LIKE DOMAIN, STRUCTURE AND FUNCTION, 3 HUMAN FACTOR IX, COAGULATION FACTOR
130	1edm	B	1210	1242	5.1e-07	0.32	0.76		FACTOR IX; CHAIN: B, C;	COAGULATION FACTOR CRYSTAL STRUCTURE, EPIDERMAL GROWTH FACTOR, EGF, 2 CALCIUM-BINDING, EGF-LIKE DOMAIN, STRUCTURE AND FUNCTION, 3 HUMAN FACTOR IX, COAGULATION FACTOR
130	1fak	L	1210	1282	8.5e-10	-0.03	0.00		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4), PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
130	1fak	L	1210	1282	8.5e-10	-0.03	0.00		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	PROTEASE/COFACTOR/LIGAND, BLOOD CLOTTING
130	1pfx	L	1189	1242	5.2e-10	0.04	-0.11		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
130	1pfx	L	1189	1242	5.2e-10	0.04	-0.11		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
130	1pfx	L	1210	1273	1e-08	0.15	0.11		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
130	1pfx	L	1210	1273	1e-08	0.15	0.11		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
130	1qdk	L	1214	1282	3.4e-09	0.04	-0.13		COAGULATION FACTOR VILA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VILA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C.	SERINE PROTEASE FVILA; FVILA; BLOOD COAGULATION, SERINE PROTEASE
130	1qdk	L	1214	1282	3.4e-09	0.04	-0.13		COAGULATION FACTOR VILA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VILA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C.	SERINE PROTEASE FVILA; FVILA; BLOOD COAGULATION, SERINE PROTEASE
130	1tpg		1189	1242	2.6e-10	0.44	0.07		T-PLASMINOGEN ACTIVATOR FI-G; 1TPG 7 CHAIN; NULL; 1TPG 8	PLASMINOGEN ACTIVATION
130	1tpg		1189	1242	2.6e-10	0.44	0.07		T-PLASMINOGEN ACTIVATOR FI-G; 1TPG 7 CHAIN; NULL; 1TPG 8	PLASMINOGEN ACTIVATION
130	1tpg		1197	1246	1.7e-07	-0.12	0.03		T-PLASMINOGEN ACTIVATOR FI-G; 1TPG 7 CHAIN; NULL; 1TPG 8	PLASMINOGEN ACTIVATION
130	1tpg		1197	1246	1.7e-07	-0.12	0.03		T-PLASMINOGEN	PLASMINOGEN ACTIVATION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	
130	1whe		1189	1245	3.9e-10	0.29	-0.14		COAGULATION FACTOR X; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN, HYDROLASE, SERINE PROTEASE, PLASMA, BLOOD 2 COAGULATION FACTOR
130	1whe		1189	1245	3.9e-10	0.29	-0.14		COAGULATION FACTOR X; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN, HYDROLASE, SERINE PROTEASE, PLASMA, BLOOD 2 COAGULATION FACTOR
130	9wga	A	1191	1293	5.1e-08	0.22	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
130	9wga	A	1191	1293	5.1e-08	0.22	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
131	1b08	A	153	308	6.5e-42	0.45	0.89		LUNG SURFACTANT PROTEIN D; CHAIN: A, B, C;	SUGAR BINDING PROTEIN C-TYPE LECTIN, CRD, SP-D, COLECTIN, ALPHA-HELICAL COILED-2 COIL, LUNG SURFACTANT, SUGAR BINDING PROTEIN
131	1dv8	A	184	311	1e-39	1.03	1.00		ASIALOGLYCOPROTEIN RECEPTOR I; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN HI; C-TYPE LECTIN CRD
132	1ant	L	292	374	1e-11	-0.03	0.03		ACTIVATED	COMPLEX (BLOOD)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PIRF Score	SeqFold Score	Compound	PDB annotation
									PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
132	1cdl	A	155	267	2.6e-16	0.71	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1cdl	A	213	330	6.5e-20	0.10	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1cdl	A	272	387	1.3e-25	0.62	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1cdl	A	284	388	5.1e-12	0.53	0.99		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1cdl	A	2	80	1.4e-09	-0.18	0.23		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
132	1cdl	A	332	445	9.1e-28	0.86	0.99		CD46; CHAIN: A, B, C, D, E, F;	REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1cdl	A	390	505	7.8e-23	0.40	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP), VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1cdl	A	40	145	3.2e-20	0.43	0.99		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP), VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1cdl	A	448	562	2.6e-21	0.20	0.99		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP), VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1cdl	A	4	93	6.5e-22	0.63	0.77		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP), VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1cdl	A	97	211	5.1e-10	0.38	0.66		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP), VIRUS

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1e5g	A	154	260	3.9e-21	0.71	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	154	266	8.5e-18	0.48	0.98		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	212	321	5.2e-18	0.53	0.51		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	270	386	7.8e-27	0.75	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	331	444	6.5e-31	0.82	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	332	443	1.4e-16	0.75	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	388	501	1.7e-17	0.19	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	3	80	8.5e-10	-0.08	0.99		COMPLEMENT CONTROL PROTEIN;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
132	1e5g	A	40	145	9.1e-24	0.63	0.99		CHAIN: A; COMPLEMENT CONTROL PROTEIN; CHAIN: A;	MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	40	151	3.4e-11	0.70	0.72		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	448	560	1.2e-14	0.15	0.93		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	448	560	1.3e-26	0.26	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	4	93	1.2e-23	0.46	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	506	566	2.6e-12	0.68	0.42		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	97	209	6.5e-20	0.53	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	97	210	3.4e-15	0.54	0.75		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
132	1emm		289	370	5.1e-12	0.18	-0.19		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
132	1emm		503	585	6.8e-12	-0.23	0.04		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
132	1f5y	A	376	452	1e-10	0.37	-0.17		LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: A;	LIPID BINDING PROTEIN LDL RECEPTOR; BETA HARPIN, 3-10 HELIX, CALCIUM BINDING
132	1hec		154	208	5.2e-09	-0.09	0.47		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (/CCP5) OF FACTOR H 1HCC 3	
132	1hec		330	385	6.5e-13	0.16	0.46		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (/CCP5) OF FACTOR H 1HCC 3	
132	1hec		38	94	3.9e-12	0.71	0.70		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (/CCP5) OF FACTOR H 1HCC 3	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
132	1hec		4	35	1.2e-07	-0.64	0.01		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN ((CCPS) OF FACTOR H) HCC 3	
132	1hec		503	559	2.6e-15	0.10	0.13		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN ((CCPS) OF FACTOR H) HCC 3	
132	1hfh		151	267	5.1e-12	0.47	0.31		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED) IHFHA 1 AVERAGED STRUCTURE) IHFH 4 IHFHA 5	
132	1hfh		328	444	3.4e-11			83.97	GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED) IHFHA 1 AVERAGED STRUCTURE) IHFH 4 IHFHA 5	
132	1hfh		444	559	6.8e-12	0.30	0.76		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED) IHFHA 1 AVERAGED	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
132	1hfh	97	208	1e-09	0.32	0.75			STRUCTURE) 1HFH 4 1HFA 5	
									GLYCOPROTEIN FACTOR H, 15TH C- AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFA 1 AVERAGED STRUCTURE) 1HFH 4 1HFA 5	
132	1hfi	154	209	1.3e-10	0.55	0.95			GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFI 1 STRUCTURE) 1HFI 4 1HFA 5	
132	1hfi	330	386	1.3e-13	0.74	0.96			GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFI 1 STRUCTURE) 1HFI 4 1HFA 5	
132	1hfi	38	93	6.5e-12	0.87	0.68			GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFI 1 STRUCTURE) 1HFI 4 1HFA 5	
132	1hfi	4	36	1e-07	0.24	0.18			GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR	

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									(NMR, MINIMIZED AVERAGED IHFIA 1 STRUCTURE) IHFIA 1 IHFIA 5	
132	1hf		503	559	1e-16	0.24	0.59		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED IHFIA 1 STRUCTURE) IHFIA 4 IHFIA 5	
132	1klo		275	426	1e-13	0.00	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
132	1qub	A	111	329	1.7e-28	0.29	0.96		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
132	1qub	A	210	522	6.5e-39			189.59	HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
132	1qub	A	212	489	6.8e-28	0.41	1.00		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
132	1qub	A	288	503	1e-31	0.37	1.00		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
132	1qub	A	2	270	1.7e-35	0.06	0.86		HUMAN BETA2-	MEMBRANE ADHESION SHORT

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI- BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									GLYCOPROTEIN I; CHAIN: A;	CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI- DOMAIN, MEMBRANE ADHESION
132	1qub	A	331	576	1.7e-41	0.53	1.00		HUMAN BETA2- GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI- DOMAIN, MEMBRANE ADHESION
132	1qub	A	388	589	6.8e-22	0.30	1.00		HUMAN BETA2- GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI- DOMAIN, MEMBRANE ADHESION
132	1wvc		153	267	1.7e-14	0.48	1.00		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35; VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
132	1wvc		211	327	5.1e-14	0.28	0.75		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35; VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
132	1wvc		271	385	1.7e-12	0.44	0.34		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35; VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
132	1wvc		330	444	5.1e-17	0.53	0.92		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35; VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	Psi-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
132	1lvc		388	502	5.1e-15	0.33	1.00		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
132	1lvc		388	504	5.2e-21			91.84	VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
132	1lvc		446	559	6.8e-14	-0.10	0.35		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
132	1lvc		505	584	2.6e-15	0.02	0.18		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
132	1lvc		505	589	1.7e-10	-0.14	0.01		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
132	1lvc		97	208	3.4e-14	0.40	0.82		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
132	1lvc	L	180	260	3.4e-09	0.17	-0.17		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
132	9wga	A	369	547	1.4e-11	0.06	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	GROWTH FACTOR LIKE DOMAIN
132	9wga	A	7	178	1.7e-10	0.07	-0.20		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
133	1b8q	A	76	167	0.0026	-0.04	0.45		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
133	1be9	A	67	164	3.4e-12	0.48	0.69		PSD-95; CHAIN: A; CRPT; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
133	1by1	A	775	987	3.4e-30	-0.15	0.75		PTX; CHAIN: A;	TRANSPORT PROTEIN RHO-GTPASE EXCHANGE FACTOR, TRANSPORT PROTEIN
133	1by1	A	787	992	2.6e-42	0.03	0.93		PTX; CHAIN: A;	TRANSPORT PROTEIN RHO-GTPASE EXCHANGE FACTOR, TRANSPORT PROTEIN
133	1dbh	A	800	1129	5.1e-36	0.18	1.00		HUMAN SOS 1; CHAIN: A;	GENE REGULATION SON OF SEVENLESS PROTEIN; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GENE REGULATION
133	1f5x	A	785	979	3.4e-34	0.37	1.00		RHO-GEF VAV; CHAIN: A;	SIGNALING PROTEIN 11 ALPHA-HELICES

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
133	1li6		71	157	2.6e-17	0.61	0.55		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
133	1kwa	A	71	148	1.3e-16	0.58	0.92		HCASK/LIN-2 PROTEIN; CHAIN: A; B;	KINASE HCASK, GLOF REPEAT, DHR, PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
133	1pdr		69	153	6.8e-12	0.65	0.93		HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT
133	1pis		1021	1144	0.0034	0.01	0.33		PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOG DOMAIN) MUTANT IPLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS IPLS 4 (INS(G105-LEHHHHH)) (NMR, 25 STRUCTURES) IPLS 5	
133	1qav	A	67	147	5.1e-07	0.77	0.83		ALPHA-1 SYNTHROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA-FINGER, HETERODIMER
133	1qlc	A	73	149	1.4e-08	0.90	0.99		POSTSYNAPTIC	PEPTIDE RECOGNITION PSD-95; PDZ

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									DENSITY PROTEIN 95; CHAIN: A;	DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
133	3p4z	A	73	151	3.4e-10	0.75	0.99		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPT1E, PTP-BAS, SPECIFICITY 2 OF BINDING
134	1a17		104	249	6.8e-10	-0.12	0.00		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
134	1a17		149	283	6.8e-14	0.10	0.47		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
134	1a17		185	335	5.1e-13	0.16	0.25		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
134	1a17		227	343	1e-17	0.14	0.77		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
134	1a17		235	396	1.3e-07	-0.37	0.09		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
134	1a17		262	381	1e-09	-0.09	0.28		SERINE/THREONINE	HYDROLASE TETRATRICOPEPTIDE,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PROTEIN PHOSPHATASE 5; CHAIN: NULL;	TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
134	1a17		63	213	6.8e-10	0.04	-0.14		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRAPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
134	1d8d	A	150	422	5.1e-10	0.06	-0.08		FARNESYLTRANSFERASE (ALPHA SUBUNIT); CHAIN: A; FARNESYLTRANSFERASE (BETA SUBUNIT); CHAIN: B; K-RAS4B PEPTIDE SUBSTRATE; CHAIN: P;	TRANSFERASE FTASE; FTASE; FTASE, PFT, PFTASE, FARNESYLTRANSFERASE, FARNESYL 2 TRANSFERASE, CAA X, RAS, CANCER
134	1e96	B	114	239	0.0026	-0.23	0.15		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2); CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
134	1e96	B	152	340	3.4e-11	0.03	-0.15		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2); CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
134	1e96	B	229	389	3.4e-14	-0.02	0.13		RAS-RELATED C3 BOTULINUM TOXIN	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
134	1e96	B	315	481	5.1e-06	-0.24	0.12		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
134	1e96	B	34	204	3.4e-10	-0.15	0.04		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
134	1e1r	A	105	216	1.7e-10	0.17	0.12		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
134	1e1r	A	117	242	1.3e-05	-0.13	0.21		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
134	1e1r	A	151	256	5.1e-14	-0.08	0.52		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
134	1e1r	A	167	291	5.2e-10	0.25	0.10		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
134	1elr	A	227	343	3.4e-20	0.12	0.87		MEEVD; CHAIN: B; TPR2-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE	BINDING CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
134	1elr	A	269	389	1.7e-12	-0.30	0.33		MEEVD; CHAIN: B; TPR2-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
134	1elr	A	35	140	1e-11	-0.05	0.00		MEEVD; CHAIN: B; TPR2-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
134	1elr	A	70	183	1.2e-12	-0.05	0.18		MEEVD; CHAIN: B; TPR2-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
134	1elw	A	151	275	3.4e-12	0.22	0.77		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
134	1elw	A	214	303	1.5e-10	0.55	0.80		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
134	1elw	A	232	335	3.4e-17	0.13	0.63		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
134	1elw	A	274	398	3.4e-12	-0.50	0.06		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
134	1elw	A	440	486	6.8e-06	-0.40	0.04		TPR1-DOMAIN OF	CHAPERONE HOP, TPR-DOMAIN,

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
134	1fch	A	130	424	3.4e-23	0.04	0.54		HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D; PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
134	1fch	A	156	476	6.5e-32	-0.17	0.34		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
134	1fch	A	233	485	5.1e-28	-0.14	0.54		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
134	1fch	A	2	280	5.1e-26	-0.20	0.19		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
134	1fch	A	45	336	5.1e-34	0.07	0.37		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CONTAINING PEPTIDE; CHAIN: C, D;	TETRAPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
134	1qge	A	130	385	3.4e-07	-0.18	0.11		VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	PROTEIN TRANSPORT HELIX-TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT
137	1elr	A	371	442	0.00026	-0.21	0.27		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
137	1elr	A	371	442	0.00026	-0.21	0.27		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
137	1elw	A	374	440	0.0052	-0.23	0.40		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
137	1elw	A	374	440	0.0052	-0.23	0.40		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
137	1f6h	A	131	445	0.00013	-0.40	0.28		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-PEPTIDE COMPLEX, CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRAPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
137	1f6h	A	131	445	0.00013	-0.40	0.28		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-

SFO ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
137	1fch	A	275	518	9.1e-09	-0.34	0.57		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
137	1fch	A	275	518	9.1e-09	-0.34	0.57		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
138	1aye		1	244	1.4e-95			207.01	PROCARBOXYPEPTIDASE A2; CHAIN: NULL;	SERINE PROTEASE PCP A2; SERINE PROTEASE, ZYMOMEN, HYDROLASE
138	1aye		3	244	1.4e-95	0.61	1.00		PROCARBOXYPEPTIDASE A2; CHAIN: NULL;	SERINE PROTEASE PCP A2; SERINE PROTEASE, ZYMOMEN, HYDROLASE
138	1dtd	A	3	244	3.4e-94	0.66	1.00		CARBOXYPEPTIDASE A2; CHAIN: A; METALLOCARBOXY PEPTIDASE INHIBITOR; CHAIN: B	HYDROLASE/HYDROLASE INHIBITOR CARBOXYPEPTIDASE A2, LEECH CARBOXYPEPTIDASE INHIBITOR
138	1pca		1	244	3.4e-89			228.73	HYDROLASE(C-TERMINAL PEPTIDASE)	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PROCARBOXYPEPTIDASE A (E.C.3.4.12.2) IPCA 3	
138	1pca		3	242	3.4e-89	0.62	1.00		HYDROLASE(C-TERMINAL PEPTIDASE) PROCARBOXYPEPTIDASE A (E.C.3.4.12.2) IPCA 3	
138	2ctc		1	242	6.8e-95			292.46	HYDROLASE(C-TERMINAL PEPTIDASE) CARBOXYPEPTIDASE A (E.C.3.4.17.1) COMPLEX WITH L-PHENYL 2CTC 3 LACTATE (L-O-PHE) 2CTC 4	
138	2ctc		3	242	6.8e-95	0.61	1.00		HYDROLASE(C-TERMINAL PEPTIDASE) CARBOXYPEPTIDASE A (E.C.3.4.17.1) COMPLEX WITH L-PHENYL 2CTC 3 LACTATE (L-O-PHE) 2CTC 4	
139	1a5e		401	515	3.4e-24	0.10	0.99		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
139	1awc	B	401	535	6.8e-40	0.11	1.00		GA BINDING PROTEIN ALPHA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GA(B)ALPHA;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GABPETA1: COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
139	1bd8		371	518	8.5e-31	-0.36	0.16		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
139	1bd8		404	536	3.4e-31	0.10	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
139	1bi7	B	401	515	1.7e-25	-0.07	0.94		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADR
139	1biX	B	350	485	1.5e-27	-0.09	0.11		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
139	1biX	B	371	518	3.4e-29	-0.40	0.04		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
139	1biX	B	404	536	3.4e-31	0.03	1.00		CYCLIN-	COMPLEX (INHIBITOR PROTEIN/KINASE)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SafFold Score	Compound	PDB annotation
									DEPENDENT KINASE 6; CHAIN: A; P18INK4D; CHAIN: B;	PROTEIN(KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
139	1bu9	A	368	520	1.7e-37	-0.33	0.11		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
139	1bu9	A	401	538	1e-34	0.15	0.99		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
139	1d9s	A	401	521	5.1e-25	0.09	0.99		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
139	1d9s	A	434	536	1.7e-19	0.10	0.49		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
139	1hb	A	347	486	6.8e-29	-0.14	0.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
139	1hb	A	368	519	1e-36	-0.32	0.13		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
139	1lib	A	401	538	1e-34	0.11	0.99		A, B; CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B; NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	INHIBITOR CELL CYCLE INHIBITOR P18-INK4CQNK6; CELL CYCLE INHIBITOR, P18-INK4CQNK6, ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
139	1lkn	D	342	535	1.7e-41	-0.38	0.22			
139	1myo		435	533	8.5e-26	0.13	0.19		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
139	1sw6	A	389	537	1e-19	-0.25	0.10		REGULATORY PROTEIN SWI6; CHAIN: A, B;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE
139	1yes	B	401	515	3.4e-21	-0.21	0.80		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3
139	1yes	B	434	534	6.8e-23	-0.18	0.78		P53; CHAIN: A; 53BP2; CHAIN: B;	POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3
										POLYMORPHISM, COMPLEX (ANTI-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										ONCOGENE/ANKYRIN REPEATS)
141	1esd	A	15	95	5.1e-09	0.14	0.12		RUBREDOXIN-OXYGEN OXIDOREDUCTASE, DIIRON-CENTRE, 2 FLAVOPROTEINS, LACTAMASE-FOLD	OXIDOREDUCTASE OXIDOREDUCTASE, OXYGENREDUCTASE, DIIRON- CENTRE, 2 FLAVOPROTEINS, LACTAMASE-FOLD
141	1qht	A	5	96	6.8e-12	-0.03	0.27		HYDROXYACYLGLUTATHIONE HYDROLASE; CHAIN: A, B;	HYDROLASE GLYOXALASE II; METALLO-HYDROLASE
141	2bc2	A	12	100	1.4e-12	-0.03	0.01		METALLO BETA-LACTAMASE II; CHAIN: A, B;	HYDROLASE HYDROLASE, BETA-LACTAMASE, ANTIBIOTIC, METALLOENZYME
142	1cs8	A	19	333	0			497.56	HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
142	1cs8	A	19	333	0			497.56	HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
142	1cs8	A	21	333	0	0.83	1.00		HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
142	1cs8	A	21	333	0	0.83	1.00		HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
142	1icf	B	292	333	1.7e-17	-0.53	0.90		CATHEPSIN L; HEAVY CHAIN; CHAIN: A, C; CATHEPSIN L; LIGHT CHAIN; CHAIN: B, D; INVARIANT CHAIN;	HYDROLASE II FRAGMENT, CD74 FRAGMENT CYSTEINE PROTEINASE, CATHEPSIN, MHC CLASS II, INVARIANT 2 CHAIN, THYOGLOBULIN TYPE-1 DOMAIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
142	1icf	B	292	333	1.7e-17	-0.53	0.90		CHAIN: I, J; CATHEPSIN L; HEAVY CHAIN; CHAIN: A, C; CATHEPSIN L; LIGHT CHAIN; CHAIN: B, D; INVARIANT CHAIN; CHAIN: I, J;	HYDROLASE II FRAGMENT, CD74 FRAGMENT CYSTEINE PROTEINASE, CATHEPSIN, MHC CLASS II, INVARIANT 2 CHAIN, THYROGLOBULIN TYPE-1 DOMAIN
143	1ctq	A	22	197	6.8e-46			53.49	TRANSFORMING PROTEIN P21/H-RAS- 1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
143	1ctq	A	24	197	6.8e-46	0.44	0.89		TRANSFORMING PROTEIN P21/H-RAS- 1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
143	1d5c	A	24	194	5.1e-48	0.80	1.00		RAB6 GTPASE; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G- PROTEIN, GTPASE, RAB6, VESICULAR TRAFFICKING
143	1e0s	A	14	190	8.5e-53	0.90	1.00		ADP- RIBOSYLATION FACTOR 6; CHAIN: A;	G PROTEIN G PROTEIN RAS, ARF, ARF6, MEMBRANE TRAFFIC
143	1ek0	A	26	197	3.4e-47	0.34	0.63		GTP-BINDING PROTEIN YPT51; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G PROTEIN, VESICULAR TRAFFIC, GTP HYDROLYSIS, YPT/RAB 2 PROTEIN, ENDOCYTOSIS, HYDROLASE
143	1fzq	A	23	194	1.7e-45	1.00	1.00		ADP- RIBOSYLATION FACTOR-LIKE PROTEIN 3; CHAIN: A;	SIGNALING PROTEIN ARF-LIKE PROTEIN 3, ARF3; PROTEIN-GDP COMPLEX WITHOUT MAGNESIUM, ARF FAMILY, RAS 2 SUPERFAMILY,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
143	1hur	A	10	199	1e-58			118.41	HUMAN ADP-RIBOSYLATION FACTOR 1; IHUR 5 CHAIN: A, B; IHUR 7	G-DOMAIN PROTEIN TRANSPORT GDP-BINDING, MEMBRANE TRAFFICKING, NON-MYRISTOYLATED IHUR 16
143	1hur	A	9	196	1e-58	0.64	1.00		HUMAN ADP-RIBOSYLATION FACTOR 1; IHUR 5 CHAIN: A, B; IHUR 7	PROTEIN TRANSPORT GDP-BINDING, MEMBRANE TRAFFICKING, NON-MYRISTOYLATED IHUR 16
143	1zbd	A	13	200	1.7e-56	0.52	0.27		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
143	1zbd	A	21	202	1.7e-56			51.86	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
143	3rab	A	16	197	3.4e-56	0.15	0.51		RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
143	3rab	A	16	197	3.4e-56			59.67	RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SegFold Score	Compound	PDB annotation
148	1evj	F	71	155	3.4e-17	0.39	0.90		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R ^C *AP ^A *AP ^B *AP ^A *P ^A *AP ^B *AP ^A *A)-3'); CHAIN: M, N, O, P, Q, R, S, T.	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP 1; RRm, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
148	1evj	H	71	155	3.4e-17	0.37	0.94		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R ^C *AP ^A *AP ^B *AP ^A *P ^A *AP ^B *AP ^A *A)-3'); CHAIN: M, N, O, P, Q, R, S, T.	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP 1; RRm, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
148	1d8z	A	67	147	1.5e-15	0.19	0.35		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
148	1d9a	A	71	145	1.7e-15	0.21	0.34		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
148	1fht		64	146	5.1e-12	0.20	0.12		UI SMALL NUCLEAR RIBONUCLEOPROTEIN IN A; CHAIN: NULL;	RIBONUCLEOPROTEIN UIA117; RIBONUCLEOPROTEIN, RNP DOMAIN, SPliceosome
148	1fjc	A	70	153	1.7e-13	0.29	0.18		NUCLEOLIN RBD2; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
148	1hd1	A	71	145	1.2e-19	0.33*	0.47		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN IN D0; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
148	1skl		61	149	1.7e-17	-0.14	0.23		RNA-BINDING PROTEIN SEX-LETHAL PROTEIN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									(C-TERMINUS, OR SECOND RNA-BINDING DOMAIN ISXL 3 (RED-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) ISXL 4 (NMR, 17 STRUCTURES) ISXL 5	
148	2ms	A	71	145	5.1e-20	0.56	0.31		MOSASHI; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
148	2sx1		68	150	1.5e-15	0.29	0.66		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPLICING
148	2u2f	A	70	145	1.7e-12	-0.09	0.00		SPLICING FACTOR UZAF 65 KD SUBUNIT; CHAIN: A;	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN
149	1dix	A	242	793	0			519.97	PHOSPHONITIDE -SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
149	1dix	A	242	793	0			519.97	PHOSPHONITIDE -SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	PHOSPHONITIDE-SPECIFIC LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
149	1dix	A	259	792	0	0.65	1.00		PHOSPHONITIDE -SPECIFIC	PHOSPHONITIDE-SPECIFIC LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PHOSPHOLIPASE C, CHAIN: A, B;	HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
149	1dix	A	259	792	0	0.68	1.00		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
149	1dix	B	200	793	0			571.84	PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	PHOSPHOINOSITIDE-SPECIFIC LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
149	1dix	B	200	793	0			571.84	PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
149	1dix	B	201	792	0	0.65	1.00		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
149	1dix	B	201	792	0				PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
149	1dix	B	201	792	0	0.66	1.00		PHOSPHOINOSITIDE-SPECIFIC	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PHOSPHOLIPASE C, CHAIN: A, B;	HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
149	1exr	A	177	322	5.1e-36	0.18	0.07		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
149	1exr	A	177	322	5.1e-36	0.18	0.07		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
149	1mai		55	170	9.1e-29	0.89	1.00		PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN PLECKSTRIN, PHOSPHOLIPASE, INOSITOL TRISPHOSPHATE, 2
										SIGNAL TRANSDUCTION PROTEIN, HYDROLASE
149	1mai		55	170	9.1e-29	0.89	1.00		PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN PLECKSTRIN, PHOSPHOLIPASE, INOSITOL TRISPHOSPHATE, 2
										SIGNAL TRANSDUCTION PROTEIN, HYDROLASE
149	1mai		55	170	9.1e-29			110.09	PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN PLECKSTRIN, PHOSPHOLIPASE, INOSITOL TRISPHOSPHATE, 2
										SIGNAL TRANSDUCTION PROTEIN, HYDROLASE
149	1mai		55	170	9.1e-29			110.09	PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN PLECKSTRIN, PHOSPHOLIPASE, INOSITOL TRISPHOSPHATE, 2
										SIGNAL TRANSDUCTION PROTEIN, HYDROLASE
149	1lux		179	320	3.4e-34	0.07	0.09		TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1 ITNX 14
149	1lux		179	320	3.4e-34	0.07	0.09		TROPONIN C; ITNX 4 CHAIN: NULL;	CALCIUM-BINDING PROTEIN EF-HAND 1 ITNX 14

Seq ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
149	1top		179	320	1.4e-34	0.26	0.84		ITXN 5	
149	1top		179	320	1.4e-34	0.26	0.84		CONTRACTILE SYSTEM PROTEIN TROPONIN C I TOP 3	
149	1vrk	A	176	323	3.4e-36	0.07	0.33		CONTRACTILE SYSTEM PROTEIN TROPONIN C I TOP 3 CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX/CALCIUM-BINDING PROTEIN/PEPTIDE)
149	1vrk	A	176	323	3.4e-36	0.07	0.33		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX/CALCIUM-BINDING PROTEIN/PEPTIDE)
151	1qbj	A	32	89	0.0046	0.47	0.96		DOUBLE-STRANDED RNA SPECIFIC ADENOSINE DEAMINASE CHAIN: A, B, C; DNA (5'-D(*Tp* Cp* Cp* Gp* Cp* G)-3'); CHAIN: D, E, F;	HYDROLASE/DNA PROTEIN/Z-DNA COMPLEX, HYDROLASE/DNA
151	1qgp	A	32	89	0.0046	0.28	1.00		DOUBLE STRANDED RNA ADENOSINE DEAMINASE; CHAIN: A;	HYDROLASE Z-ALPHA-Z-DNA BINDING DOMAIN, RNA-EDITING, Z-DNA 2 RECOGNITION, ADAR1, HELIX-TURN-HELIX, HYDROLASE
153	1bkd		S451	606	2.6e-28	0.23	0.77		H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
153	1bkd		S900	1116	1e-64	0.53	1.00		H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR
153	1l9r	A	86	168	0.00065	-0.35	0.19		CARBON MONOXIDE OXIDATION SYSTEM TRANSCRIPTION CHAIN: A, B;	TRANSCRIPTION COOA GENE PRODUCT; CARBON MONOXIDE, HEME SENSOR, CATABOLITE GENE ACTIVATOR 2 PROTEIN
153	1i16		579	650	3.9e-14	0.24	0.98		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE
153	1kwa	A	577	659	2.6e-16	0.60	1.00		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	CHEMOATTRACTANT FACTOR, PDZ DOMAIN
153	1pdr		579	640	9.1e-12	0.72	0.80		HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
153	1rgs		256	414	6.8e-12	0.02	0.19		CAMP DEPENDENT PROTEIN KINASE; CHAIN: NULL;	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT
153	2egp	A	339	480	1.2e-16	-0.13	0.00		D(*GP*TP*CP*AP*CP*AP*TP*TP*AP*AP*JT)-3; CHAIN: B; DNA (5'-CHAIN: C;	KINASE RI(Alpha); REGULATORY SUBUNIT, KINASE
									TRANSCRIPTION/DNA COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, CAMP-2 BINDING, ACTIVATOR	

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									DNA (5'-D(*Tp*Tp* Cp*Ap* Cp* Tp*Tp* Cp*Ap* C P*(IDO) CHAIN: D, E, F;	
159	1bkd		S1	315	2.6e-76			74.57	H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR
159	1bkd		S23	293	2.6e-76	0.37	1.00		H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR
159	1bkd		S31	199	3.4e-52	0.05	1.00		H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR
159	1bm		392	491	9.1e-21	0.43	0.94		BETA-SPECTRIN; IBTN 4 CHAIN: NULL; IBTN 5	SIGNAL TRANSDUCTION PROTEIN
159	1fao	A	388	488	3.9e-07	0.31	0.59		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3- PHOSPHOINOSITIDES, INOSITOL TETRAPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
159	1fb8	A	385	496	6.5e-09	0.31	0.53		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3- PHOSPHOINOSITIDES, INOSITOL TETRAPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
159	1fgy	A	391	467	5.2e-06	0.23	0.75		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1

SSQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
159	1pm5		399	491	2.6e-10	0.18	0.16		SOS I; CHAIN: NULL;	GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION
159	1qgg	A	391	511	3.9e-12	0.18	-0.13		INSULIN RECEPTOR SUBSTRATE 1; CHAIN: A, B;	SIGNAL TRANSDUCTION IRS-1; BETA-SANDWICH, SIGNAL TRANSDUCTION
160	1dp7	P	108	183	6.8e-33	0.61	1.00		MHC CLASS II TRANSCRIPTION FACTOR HRFX1; CHAIN: P; DNA (5'-D'C'P*GP*(BRO)UP* T'P*AP*CP*CP*AP*(B RO) CHAIN: D;	TRANSCRIPTION/DNA REGULATORY FACTOR X; WINGED HELIX, MHC CLASS II TRANSCRIPTION FACTOR, PROTEIN-2 DNA COCRYSTAL STRUCTURE, NOVEL MODE OF DNA RECOGNITION
161	1bf7f	A	74	152	5.1e-18	0.43	0.12		SXL-LETHAL PROTEIN; CHAIN: A; B; RNA (5'-R(GP*Up*Up*Gp*R(GP*Up*Up*Up*Up*Up*U)p*Up*U)- CHAIN: P; Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
161	1cvj	A	70	154	3.4e-19	0.36	0.28		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(CAP*AP*AP*AP*A P*AP*AP*AP*AP*A P*A)-3); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PAPB 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
161	1d8z	A	79	153	5.1e-18	0.38	0.69		HU ANTIGEN C;	RNA BINDING PROTEIN RNA-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
161	1ha1		77	153	1e-26	0.57	0.57		CHAIN: A; HNRNP A1; CHAIN: NULL;	BINDING DOMAIN NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
161	1hd1	A	83	154	5.1e-24	0.87	0.86		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN IN D0; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
161	1sxl		74	152	5.1e-18	0.17	0.12		RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C-TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	RNA-BINDING PROTEIN RNA- BINDING DOMAIN
161	2mss	A	83	154	5.1e-19	0.72	0.46		MUSASHI1; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
161	2sxl		80	154	6.8e-17	0.34	0.59		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING
161	2up1	A	76	153	6.8e-27	0.68	0.40		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN IN A1; CHAIN: A; 12- NUCLEOTIDE SINGLE-STRANDED	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UPI, COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
161	3scl	A	72	153	1.7e-18	0.49	0.54		TELOMETRIC DNA; CHAIN: B;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
162	1edh	A	122	337	8.5e-30			75.74	E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
162	1edh	A	142	337	8.5e-30	0.39	0.94		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
162	1edh	A	243	351	8.5e-09	0.36	-0.01		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
162	1neg		142	226	0.0029	0.57	0.11		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
162	1neg		267	335	0.00068	0.11	0.49		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
162	1nci	B	176	228	0.0037	-0.12	0.45		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
162	1nci	B	270	337	0.00012	-0.15	0.37		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
162	1ncj	A	122	336	5.1e-31			79.80	N-CADHERIN;	CELL ADHESION PROTEIN CELL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
162	1ncj	A	142	337	5.1e-31	0.39	1.00		CHAIN: A; N-CADHERIN;	ADHESION PROTEIN
162	1ncj	A	243	345	8.5e-10	0.22	0.47		CHAIN: A; N-CADHERIN;	CELL ADHESION PROTEIN CELL
162	1ncj	A	30	228	1.7e-26	0.18	-0.14		CHAIN: A; N-CADHERIN;	ADHESION PROTEIN
162	1aah		142	232	1.2e-06	0.01	0.17		CHAIN: A; EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL
162	1aah		243	341	1e-05	-0.01	0.42		CHAIN: A; EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
163	1a25	A	1142	1217	5.2e-10	-0.28	0.18		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM-H-PROSOLIPID
163	1byn	A	1150	1251	3.9e-15	-0.21	0.13		SYNAPTOTAGMIN I; CHAIN: A;	BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
163	1dix	A	1029	1261	9.1e-76	0.36	1.00		PHOSPHOINOSITIDE -SPECIFIC PHOSPHOLIPASE C; CHAIN: A, B;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
163	1dix	A	605	807	2.6e-76	0.19	1.00		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, 3	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING
163	1dix	A							PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C; CHAIN: A, B;	PHOSPHORIC DIESTER HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER

Seq ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
163	1dix	B	1029	1261	1.3e-75	0.21	1.00		PHOSPHOINOSITIDE -SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC PHOSPHORIC DIESTER HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
163	1dix	B	526	781	1.4e-10	-0.14	0.92		PHOSPHOINOSITIDE -SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
163	1dix	B	605	807	5.2e-76	0.24	1.00		PHOSPHOINOSITIDE -SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
163	1rsy		1151	1250	9.1e-13	-0.41	0.13		CALCIUM/PHOSPHO LIPID BINDING PROTEIN SYNAPTOTAGMIN 1 (FIRST C2 DOMAIN) (CALE) IRSY 3	PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
164	1agq	B	299	406	1.2e-13	-0.42	0.28		GLIAL CELL-DERIVED NEUROTROPHIC	GROWTH FACTOR GDNF; GROWTH FACTOR, NEUROTROPHIC FACTOR, CYSTINE KNOT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
164	1bmp		301	406	3.4e-45	0.01	1.00		FACTOR; CHAIN: A, B, C, D; BONE MORPHOGENETIC PROTEIN-7; CHAIN: NULL;	TRANSFORMING GROWTH FACTOR OSTEOGENIC PROTEIN-1, HOP-1, BMP-7; MORPHOGEN, TRANSFORMING GROWTH FACTOR, CYTOKINE, BONE, 2 CARTILAGE, GLYCOPROTEIN
164	1bmp		301	407	3.4e-45			88.97	BONE MORPHOGENETIC PROTEIN-7; CHAIN: NULL;	TRANSFORMING GROWTH FACTOR OSTEOGENIC PROTEIN-1, HOP-1, BMP-7; MORPHOGEN, TRANSFORMING GROWTH FACTOR, CYTOKINE, BONE, 2 CARTILAGE GLYCOPROTEIN
164	1kla	A	290	407	1.3e-37			73.65	TRANSFORMING GROWTH FACTOR-BETA 1; CHAIN: A, B;	GROWTH FACTOR TGF-B1; GROWTH FACTOR, MITOGEN, GLYCOPROTEIN
164	1kla	A	296	407	1.3e-37	0.05	0.70		TRANSFORMING GROWTH FACTOR-BETA 1; CHAIN: A, B;	GROWTH FACTOR TGF-B1; GROWTH FACTOR, MITOGEN, GLYCOPROTEIN
164	1kla	A	302	407	1.7e-31	0.21	0.87		TRANSFORMING GROWTH FACTOR-BETA 1; CHAIN: A, B;	GROWTH FACTOR TGF-B1; GROWTH FACTOR, MITOGEN, GLYCOPROTEIN
164	1tgi		290	407	1.3e-37			77.32	TRANSFORMING GROWTH FACTOR-BETA 3; CHAIN: NULL;	GROWTH FACTOR TGF-BETA3; GROWTH FACTOR, MITOGEN, GLYCOPROTEIN, SIGNAL
164	1tgi		296	407	1.3e-37	0.38	0.81		TRANSFORMING GROWTH FACTOR-BETA 3; CHAIN: NULL;	GROWTH FACTOR TGF-BETA3; GROWTH FACTOR, MITOGEN, GLYCOPROTEIN, SIGNAL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
164	1tgi		298	407	1.4e-31	0.13	0.96		TRANSFORMING GROWTH FACTOR-BETA 3; CHAIN: NULL;	GROWTH FACTOR TGF-BETA3; GROWTH FACTOR, MITOGEN, GLYCOPROTEIN, SIGNAL
164	2tgi		290	407	6.8e-31			69.00	GROWTH FACTOR TRANSFORMING GROWTH FACTOR-BETA TWO (TGF-B2) 2TGI.3	
164	2tgi		302	407	6.8e-31	0.12	0.59		GROWTH FACTOR TRANSFORMING GROWTH FACTOR-BETA TWO (TGF-B2) 2TGI.3	
164	3bmp	A	300	406	3.4e-48	0.42	0.99		BONE MORPHOGENETIC PROTEIN 2 (BMP-2); CHAIN: A;	CYTOKINE CYTOKINE, BONE MORPHOGENETIC PROTEIN, CYSTIN-KNOT, TGFB-2 FAMILY
165	1a0a	A	58	113	1.7e-09	-0.45	0.11		PHOSPHATE SYSTEM POSITIVE REGULATORY PROTEIN CHAIN: A; B: DNA; CHAIN: C; D;	COMPLEX (TRANSCRIPTION FACTOR/DNA) BHLH; UAS2(17); TRANSCRIPTION FACTOR, BASIC HELIX LOOP HELIX, 2 COMPLEX (TRANSCRIPTION FACTOR/DNA)
165	1drrn	A	141	206	0.00026	0.04	0.17		SENSOR PROTEIN FIXL; CHAIN: A;	TRANSFERASE FIXL, HEME DOMAIN, CRYSTAL STRUCTURE, PAS FAMILY, TWO-2 COMPONENT SYSTEM, HISTIDINE KINASE
165	1mdy	A	51	116	1.2e-14	-0.50	0.04		TRANSCRIPTION ACTIVATION/DNA MYOD BASIC-HELIX-LOOP-HELIX (BHLH) DOMAIN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
166	1ha1		77	221	6.8e-29	0.22	0.19		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN RNA BINDING PROTEIN RNA- BINDING DOMAIN
166	1hd1	A	83	160	3.4e-22	0.69	0.87		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN IN D; CHAIN: A;	
166	2up1	A	1	166	5.1e-38	-0.15	0.15		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN IN A1; CHAIN: A; 12- NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
166	2up1	A	76	221	3.4e-31	-0.01	0.45		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN IN A1; CHAIN: A; 12- NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
166	3sd	A	82	227	8.5e-26	0.26	0.59		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
167	1cs6	A	11	307	2.6e-34	0.12	-0.01		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
167	1cs6	A	29	127	1.7e-08	0.15	-0.14		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
167	1cs6	C	150	277	1.2e-17	0.01	1.00		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
167	1cs6	C	35	246	1.4e-52	0.09	0.59		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
167	1cs6	D	150	277	1.2e-17	0.38	1.00		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
167	1cs6	D	150	293	5.2e-43	0.18	1.00		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
167	1cs6	D	35	246	5.1e-52	0.17	0.70		FIBROBLAST GROWTH FACTOR 2; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR

Seq ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
167	1epf	A	54	232	2.6e-18	0.36	0.94		NEURAL CELL ADHESION MOLECULE, CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
167	1ev2	E	34	246	3.4e-49	0.14	0.84		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
167	1ev2	G	150	297	6.8e-19	0.14	1.00		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
167	1ev2	G	34	247	1.7e-52	0.04	0.86		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
167	1evt	C	150	277	1.7e-17	0.19	1.00		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSE-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
167	1evt	C	35	246	1e-49	-0.01	0.84		RECEPTOR 1; CHAIN: C, D;	DOMAINS, B-TREFOIL FOLD
167	1f2q	A	45	126	7.8e-08	0.20	0.55		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
167	1f2q	A	54	247	9.1e-15	0.46	0.42		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
167	1feg	A	39	109	1.2e-07	0.49	0.03		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
167	1feg	A	54	245	1.3e-16	0.26	0.92		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
167	1fgk	A	346	644	0	1.00	1.00		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
167	1fgk	A	346	644	0			412.56	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1, FIBROBLAST GROWTH FACTOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
167	1fgk	B	343	643	0	0.82	1.00		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
167	1fgk	B	343	643	0			390.85	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
167	1fmk		289	646	0	0.39	1.00		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
167	litb	B	11	245	2.6e-21	0.09	0.13		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
167	litb	B	42	321	9.1e-38	0.19	0.40		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									INTERLEUKIN-1 RECEPTOR; CHAIN: B;	TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR) COMPLEX
167	1tib	B	42	367	9.1e-38			89.43	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	(IMMUNOGLOBULIN/RECEPTOR) TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
167	1nct		46	127	8.5e-09	0.00	-0.17		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTIN; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
167	1qcf	A	291	649	0	0.43	1.00		HAEMATOPHOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
167	1nm		46	127	8.5e-09	0.13	-0.18		MUSCLE PROTEIN (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	
167	1wit		54	110	2.6e-07	0.29	0.41		TWITCHIN 18TH IGSF MODULE; CHAIN: NULL;	MUSCLE PROTEIN IMMUNOGLOBULIN SUPERFAMILY, I SET, MUSCLE PROTEIN
167	2dli	A	54	247	2.6e-17	0.12	0.46		MHC CLASS I NK CELL RECEPTOR	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR, KIR,

Seq ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PRECURSOR; CHAIN: A;	NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
167	2fcb	A	54	249	2.6e-19	0.21	0.90		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
167	3ncm	A	54	110	1.3e-07	0.05	0.35		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
170	1c28	A	145	277	2.6e-45	0.76	1.00		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
170	1c28	A	145	277	2.6e-45			110.60	30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
170	1c28	A	149	277	1.2e-26	0.71	1.00		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
170	1c28	B	145	276	2.6e-39	0.57	0.99		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
170	1c28	B	145	276	2.6e-39			92.47	30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
170	1c28	B	159	276	6.8e-23	0.71	0.82		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 CIQ TNF TRIMER ALL-BETA, SERUM PROTEIN
170	1c28	C	145	276	1.3e-32	0.50	0.90		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 CIQ TNF TRIMER ALL-BETA, SERUM PROTEIN
170	1c28	C	145	276	1.3e-32			73.47	30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 CIQ TNF TRIMER ALL-BETA, SERUM PROTEIN
170	1c28	C	164	276	3.4e-16	0.35	1.00		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 CIQ TNF TRIMER ALL-BETA, SERUM PROTEIN
171	1884	A	4	167	1e-47	0.35	0.89		ANTICHYMOTRYPSIN N; CHAIN: A, B;	SERPIN ACT, SERPIN, SERINE PROTEASE INHIBITOR, ANTICHYMOTRYPSIN
171	1by7	A	2	168	1.7e-43	0.64	0.99		PLASMINOGEN ACTIVATOR INHIBITOR-2; CHAIN: A;	PROTEIN BINDING PAI-2; SERPIN, PROTEIN BINDING
171	1ezx	A	4	167	8.5e-48	0.31	0.95		ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1-ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1-ANTITRYPSIN, 2 TRYPSIN
171	1hle	A	1	167	8.5e-48	0.43	1.00		HYDROLASE INHIBITOR(SERINE PROTEINASE) HORSE LEUKOCYTE	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									ELASTASE INHIBITOR (HLEI) IHLE 3	
171	1ova	A	3	167	3.4e-40	0.45	0.99		SERPIN OVALBUMIN (EGG ALBUMIN) IOVA 3	
171	1qlp	A	4	167	8.5e-48	0.43	0.92		ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR, ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTIPROTEINASE, SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
171	1qmm	A	4	167	6.8e-46	0.02	0.70		ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERPIN AACT SERPIN, SERINE PROTEINASE INHIBITOR, PARTIAL LOOP 2 INSERTION, LOOP-SHEET POLYMERIZATION, EMPHYSEMA, DISEASE 3 MUTATION, ACUTE PHASE PROTEIN, CONFORMATIONAL DISEASE
171	2ant	I	4	145	1.3e-39	0.44	1.00		ANTITHROMBIN; CHAIN: L, I;	SERPIN SERPIN, HEPARIN, INHIBITOR
171	2ant	L	1	145	3.9e-40	0.22	0.95		ANTITHROMBIN; CHAIN: L, I;	SERPIN SERPIN, HEPARIN, INHIBITOR
171	2ant	L	3	167	5.1e-39	0.42	0.99		ANTITHROMBIN; CHAIN: L, I;	SERPIN SERPIN, HEPARIN, INHIBITOR
172	153l		36	212	1e-47	0.70	1.00		HYDROLASE(O-GLYCOSYL) LYSOZYME (E.C.3.2.1.17) 153L 3	
172	153l		36	212	1e-47	0.70	1.00		HYDROLASE(O-GLYCOSYL)	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
172	1531		36	212	1e-47			186.19	LYSOZYME (E.C.3.2.1.17) 1531.3	
172	1531		36	212	1e-47			186.19	HYDROLASE(O-GLYCOSYL) LYSOZYME (E.C.3.2.1.17) 1531.3	
									HYDROLASE(O-GLYCOSYL) LYSOZYME (E.C.3.2.1.17) 1531.3	
173	1a09	A	393	493	8.5e-19	0.80	0.84		C-SRC TYROSINE KINASE, CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU-(N,N-DIPENTYL AMINE), CHAIN: C, D;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)
173	1a02		394	496	1.7e-17	0.55	0.87		TRANSFERASE(PHOSPHOTRANSFERASE) PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1A02.3 (SRC HOMOMLOGY 2 DOMAIN) (ABELSON, SH2 ABL) 1A02.4 (NMR, 20 STRUCTURES) 1A02.5	
173	1a01	F	394	495	5.1e-18	0.88	0.46		FYN PROTEIN- TYROSINE KINASE; CHAIN: F; PHOSPHOTYROSYL PEPTIDE; CHAIN: P	COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN) SRC HOMOMLOGY 2 DOMAIN; SH2 DOMAIN, SIGNAL TRANSDUCTION, PEPTIDE COMPLEX, 2 COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
173	1aya	A	400	510	2.6e-17	0.56	0.59		HYDROLASE(SH2 DOMAIN) TYROSINE PHOSPHATASE SYP (N-TERMINAL SH2 DOMAIN) IAYA 3 (PTPID, SHPTP2) (E.C.3.1.3.48) COMPLEXED WITH THE PEPTIDE IAYA 4 PDGFR-1009 IAYA 5	(PROTO-ONCOGENE/EARLY PROTEIN)
173	1bfi		392	511	1.3e-19	0.36	0.49		P85 ALPHA; CHAIN: NULL;	SH2 DOMAIN PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY ALPHA SH2 DOMAIN, P85ALPHA, PI 3-KINASE, NMR, C-TERMINAL SH2 2 DOMAIN V-SRC SH2 DOMAIN SRC SH2; V-SRC SH2 DOMAIN, SRC SH2 DOMAIN, PHOSPHOTYROSINE RECOGNITION DOMAIN, PP60 2 SRC SH2 DOMAIN
173	1bdl		398	498	8.5e-18	0.76	0.39		PP60 V-SRC TYROSINE KINASE TRANSFORMING PROTEIN; CHAIN: NULL;	SH2 DOMAIN, SRC SH2 DOMAIN, PHOSPHOTYROSINE RECOGNITION DOMAIN, PP60 2 SRC SH2 DOMAIN
173	1blj		388	493	3.4e-17	0.40	0.45		P55 BLK PROTEIN TYROSINE KINASE; CHAIN: NULL;	PHOSPHORYLATION SIGNAL TRANSDUCTION, TYROSINE KINASE, TRANSFERASE, 2 PHOSPHOTRANSFERASE, PHOSPHORYLATION
173	1csy	A	387	511	2.6e-18	0.42	0.09		SVK PROTEIN TYROSINE KINASE; CHAIN: A; ACETYL-THR-PTR-GLU-THR-LEU-NH2; CHAIN: B;	COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE) PROTEIN-TYROSINE KINASE SH2 DOMAIN, COMPLEX 2 (PHOSPHOTRANSFERASE/PEPTIDE) SH2 DOMAIN GRB2, GRB2, SH2
173	1fhs		394	507	1.3e-17	0.38	0.07		GROWTH FACTOR	SH2 DOMAIN GRB2, GRB2, SH2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
173	1lck	A	374	493	5.1e-23	0.16	0.28		RECEPTOR BOUND PROTEIN-2; CHAIN: NULL; P56=ICK= TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO)YQ PQFA, ILCK 14 CHAIN: B; ILCK 15	DOMAIN, PROTEIN NMR, SOLUTION STRUCTURES COMPLEX (KINASE/PEPTIDE)
173	1lkk	A	395	493	1.2e-16	0.75	0.96		HUMAN P56 TYROSINE KINASE; ILKK 7 CHAIN: A; ILKK 8 PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU-ILE; ILKK 11 CHAIN: B; ILKK 12	COMPLEX (TYROSINE KINASE/PEPTIDE)
173	1lkk	A	395	509	2.6e-18	0.32	-0.09		HUMAN P56 TYROSINE KINASE; ILKK 7 CHAIN: A; ILKK 8 PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU-ILE; ILKK 11 CHAIN: B; ILKK 12	COMPLEX (TYROSINE KINASE/PEPTIDE)
173	1sha	A	398	493	1.4e-17	0.88	0.40		PHOSPHOTRANSFERASE V-SRC TYROSINE KINASE TRANSFORMING PROTEIN (PHOSPHOTYROSIN	

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									E ISHA 3 RECOGNITION DOMAIN SH2 (E.C.2.7.1.112) COMPLEX WITH ISHA 4 PHOSPHOPEPTIDE A (TYR-VAL-PRO- MET-LEU, PHOSPHORYLATED TYR) ISHA 5	
173	1tce	A	394	511	6.5e-17	0.74	0.88		SHC; CHAIN: A; PHOSPHOPEPTIDE OF THE ZETA CHAIN OF T CELL CHAIN: B ₁	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) SH2 DOMAIN; COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
173	2abl		379	492	1.7e-21	0.39	0.88		ABL TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH2, SH2, ONCOPROTEIN
173	2pna		395	512	2.6e-18	0.37	0.35		SIGNALING PROTEIN PHOSPHATIDYLINO SITOL 3-KINASE (E.C.2.7.1.137) (N- TERMINAL 2PNA 3 SH2 DOMAIN OF P85-ALPHA SUBUNIT) (NMR, 22 STRUCTURES) 2PNA 4	
178	1aut	L	168	260	8.5e-09	0.16	-0.13		ACTIVATED PROTEIN C; CHAIN: C; L; D-PHE-PRO- MAI; CHAIN: F;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
178	1aut	L	559	636	5.2e-16	-0.04	0.05		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR)
										PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
178	1eld	A	113	211	3.4e-09	0.26	0.87		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
										GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1eld	A	155	267	2.6e-16	0.71	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
										GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1eld	A	213	330	6.5e-20	0.10	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
										GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1eld	A	272	387	1.3e-25	0.62	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
178	1cdl	A	2	80	3.4e-10	0.32	0.65		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1cdl	A	332	445	3.4e-14	0.51	0.89		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1cdl	A	332	445	9.1e-28	0.86	0.99		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1cdl	A	390	505	7.8e-23	0.40	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1cdl	A	40	145	5.2e-20	0.43	0.99		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1cdl	A	448	562	2.6e-21	0.20	0.99		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1cd1	A	4	93	6.5e-22	0.63	0.77		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1dx5	I	566	654	3.9e-19	0.01	-0.02		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
178	1esg	A	154	260	3.9e-21	0.71	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1esg	A	154	268	1.2e-17	0.66	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1esg	A	212	321	5.2e-18	0.53	0.51		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1esg	A	213	324	1.2e-11	0.35	0.93		COMPLEMENT CONTROL PROTEIN;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
178	1e5g	A	270	386	7.8e-27	0.75	1.00		CHAIN: A; COMPLEMENT INHIBITOR VCP; SP35; COMPLEMENT, NMR; MODULES, PROTEIN STRUCTURE; VACCINIA VIRUS	MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	331	444	6.5e-31	0.82	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP; SP35; COMPLEMENT, NMR; MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	332	444	5.1e-18	0.83	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP; SP35; COMPLEMENT, NMR; MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	389	504	1.7e-17	0.44	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP; SP35; COMPLEMENT, NMR; MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	3	80	3.4e-10	-0.08	0.99		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP; SP35; COMPLEMENT, NMR; MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	40	145	9.1e-24	0.63	0.99		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP; SP35; COMPLEMENT, NMR; MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	40	151	6.8e-11	0.55	0.74		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP; SP35; COMPLEMENT, NMR; MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	448	560	1.3e-26	0.26	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP; SP35; COMPLEMENT, NMR; MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
178	1e5g	A	4	93	1.2e-23	0.46	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	506	566	2.6e-12	0.68	0.42		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	97	209	6.5e-20	0.53	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	98	210	6.8e-18	0.81	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1fak	L	566	633	1.3e-14	0.09	-0.08		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, BGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
178	1hec		154	208	5.2e-09	-0.09	0.47		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (CCP5) OF FACTOR H1HCC3	
178	1hec		330	385	6.5e-13	0.16	0.46		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
178	lhcc		38	94	3.9e-12	0.71	0.70		(CCPS) OF FACTOR H IHCC 3	
178	lhcc		390	443	3.9e-11	0.27	0.95		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (CCPS) OF FACTOR H IHCC 3	
178	lhcc		4	35	1.2e-07	-0.64	0.01		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (CCPS) OF FACTOR H IHCC 3	
178	lhcc		503	559	2.6e-15	0.10	0.13		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (CCPS) OF FACTOR H IHCC 3	
178	lhth		151	267	1.7e-10	0.38	0.94		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED IHFHA 1 AVERAGED STRUCTURE) IHFH 4 IHFHA 5	
178	lhth		328	444	5.1e-13	0.46	0.92		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
178	1hfh		328	444	5.1e-13			83.97	GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
178	1hfh		97	208	3.4e-11	0.60	0.86		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
178	1hfh		154	209	1.3e-10	0.55	0.95		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFHA 1 STRUCTURE) 1HFH 4 1HFHA 5	
178	1hfh		330	386	1.3e-13	0.74	0.96		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									AVERAGED 1HFIA 1 STRUCTURE) 1HFI 4 1HFIA 5	
178	1hfi	38	93		6.5e-12	0.87	0.68		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFIA 1 STRUCTURE) 1HFI 4 1HFIA 5	
178	1hfi	390	444		5.2e-12	0.59	0.65		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFIA 1 STRUCTURE) 1HFI 4 1HFIA 5	
178	1hfi	4	36		1e-07	0.24	0.18		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFIA 1 STRUCTURE) 1HFI 4 1HFIA 5	
178	1hfi	503	559		1e-16	0.24	0.59		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFIA 1 STRUCTURE) 1HFI 4 1HFIA 5	
178	1klo	532	639		6.5e-14	0.13	-0.18		LAMININ, CHAIN: HUMAN BETA2-NULL;	GLYCOPROTEIN GLYCOPROTEIN
178	1qub	A	116	329	1.7e-29	0.54	1.00		HUMAN BETA2-	MEMBRANE ADHESION SHORT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									GLYCOPROTEIN I; CHAIN: A;	CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI- DOMAIN, MEMBRANE ADHESION
178	1qub	A	212	443	1e-27	0.74	1.00		HUMAN BETA2- GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI- DOMAIN, MEMBRANE ADHESION
178	1qub	A	272	503	3.4e-31	0.29	1.00		HUMAN BETA2- GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI- DOMAIN, MEMBRANE ADHESION
178	1qub	A	2	267	1.7e-34	0.06	0.99		HUMAN BETA2- GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI- DOMAIN, MEMBRANE ADHESION
178	1qub	A	329	631	8.5e-42			190.64	HUMAN BETA2- GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI- DOMAIN, MEMBRANE ADHESION
178	1qub	A	331	586	8.5e-42	0.53	1.00		HUMAN BETA2- GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI- DOMAIN, MEMBRANE ADHESION
178	1qub	A	40	350	1.7e-25	0.49	1.00		HUMAN BETA2- GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI- DOMAIN, MEMBRANE ADHESION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
178	1qub	A	448	659	6.8e-19	-0.01	0.19		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
178	1vvc		153	268	5.1e-16	0.60	1.00		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
178	1vvc		211	325	6.8e-13	0.19	0.65		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
178	1vvc		270	385	5.1e-13	0.81	0.98		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
178	1vvc		330	444	3.4e-15	0.34	0.82		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
178	1vvc		388	504	5.1e-16		91.05		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
178	1vvc		390	502	5.1e-16	0.17	1.00		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
179	1btk	A	1765	1861	2.6e-10	0.42	0.47		BRUTON'S TYROSINE KINASE; CHAIN: A, B;	TRANSFERASE BRUTON'S AGAMMAGLOBULINEMIA TYROSINE KINASE, BTK; TRANSFERASE, PH DOMAIN, BTK MOTIF, ZINC BINDING, X-LINKED 2 AGAMMAGLOBULINEMIA, TYROSINE-PROTEIN KINASE
179	1btt		1765	1862	1.2e-07	0.01	0.57		BETA-SPECTRIN; IBTN 4 CHAIN: NULL; IBTN 5	SIGNAL TRANSDUCTION PROTEIN
179	1fao	A	1765	1865	1.3e-21	0.47	1.00		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32, PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
179	1b68	A	1765	1865	5.2e-22	0.73	1.00		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32, PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
179	1fgy	A	1761	1865	1.2e-20	0.00	0.45		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
179	1pms		1739	1864	1.3e-12	0.29	0.11		SOS 1; CHAIN: NULL;	SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
180	1ctu	A	115	447	1e-69	0.25	0.93		SOLUBLE QUINOPROTEIN GLUCOSE DEHYDROGENASE, CHAIN: A, B;	OXIDOREDUCTASE BETA-PROPELLER, SUPERBARREL, COMPLEX WITH THE COFACTOR PQ2 AND THE INHIBITOR METHYLHYDRAZINE, OXIDOREDUCTASE
181	1b8q	A	5	102	8.5e-13	-0.11	0.59		NEURONAL NITRIC OXIDE SYNTHASE, CHAIN: A; HEPTAPEPTIDE, CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
181	1be9	A	2	77	8.5e-20	0.73	1.00		PSD-95, CHAIN: A; CRIPT, CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
181	1il6	2	71	71	6.8e-14	0.34	0.78		INTERLEUKIN 16, CHAIN: NULL;	CYTOKINE LCF, CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
181	1kwa	A	1	77	1.7e-09	-0.10	0.63		HCASK/LIN-2 PROTEIN, CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
181	1kwa	A	2	73	1e-11	0.05	0.77		HCASK/LIN-2 PROTEIN, CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
181	1pdr		2	91	1.5e-19	0.48	1.00		HUMAN DISCS LARGE PROTEIN, CHAIN: NULL;	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN, SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT
181	1qau	A	5	102	8.5e-13	0.30	0.86		NEURONAL NITRIC OXIDE SYNTHASE	OXIDOREDUCTASE BETA-FINGER

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqPfold Score	Compound	PDB annotation
181	1qav	A	2	84	1e-18	0.59	0.98		(RESIDUES 1-130); CHAIN: A; ALPHA-1 SYNTHROPIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA-FINGER, HETERODIMER
181	1qlc	A	4	80	1.2e-21	0.48	1.00		POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
181	3pdx	A	2	77	1.7e-18	0.77	1.00		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTPIE, PTP-BAS, SPECIFICITY 2 OF BINDING
182	1e0s	A	8	177	3.4e-60	0.94	1.00		ADP-RIBOSYLATION FACTOR 6; CHAIN: A;	G PROTEIN G PROTEIN, RAS, ARF, ARF6, MEMBRANE TRAFFIC
182	1fzq	A	4	176	8.5e-51	0.95	1.00		ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3; CHAIN: A;	SIGNALING PROTEIN ARF-LIKE PROTEIN 3, ARF3; PROTEIN-GDP COMPLEX WITHOUT MAGNESIUM, ARF FAMILY, RAS 2 SUPERFAMILY, G-DOMAIN
182	1hur	A	2	177	8.5e-66	0.95	1.00		HUMAN ADP-RIBOSYLATION FACTOR 1; IHUR 5 CHAIN: A; B; IHUR 7	PROTEIN TRANSPORT GDP-BINDING, MEMBRANE TRAFFICKIN, NON-MYRISTOYLATED IHUR 16
182	1hur	A	2	179	8.5e-66			178.06	HUMAN ADP-RIBOSYLATION	PROTEIN TRANSPORT GDP-BINDING, MEMBRANE TRAFFICKIN,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									FACTOR I; 1HUR 5 CHAIN: A, B; 1HUR 7	NON-MYRISTOYLATED 1HUR 16
183	1ata		834	896	5.2e-12	0.29	0.09		PROTEINASE INHIBITOR(TRYPSIN) TRYPSIN INHIBITOR (PH 4.75) IATA 3 (NMR, MINIMIZED AVERAGE STRUCTURE) IATA 4	
183	1aut	L	845	940	5.1e-11	0.29	-0.19		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
183	1dan	L	819	898	1.7e-10	0.49	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETO (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
183	1dan	L	851	943	3.4e-12	0.08	-0.15		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									FACTOR; CHAIN: T; U; D-PHE-PHE-ARG-CHLOROMETHYLKE TONE (DFFRCMK) WITH CHAIN: C;	
183	1dan	L	939	1020	1.7e-10	0.01	-0.18		BLOOD COAGULATION FACTOR VIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG-CHLOROMETHYLKE TONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
183	1dva	L	330	427	8.5e-14	0.20	-0.18		DES-GLA FACTOR VIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C; D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
183	1dva	L	819	898	1.7e-10	0.65	-0.12		DES-GLA FACTOR VIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C; D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
183	1dva	L	851	943	3.4e-12	0.30	-0.14		DES-GLA FACTOR VIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C; D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: H, I; DES-GLA FACTOR VIA (LIGHT CHAIN); CHAIN: L, M, (DPN)- PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	COMPLEX
183	1dx5	I	1167	1294	3.4e-11	0.02	-0.20		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULI N; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L- GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
183	1dx5	I	1167	1294	3.4e-11	0.02	-0.20		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULI N; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L- GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
183	1fak	L	819	898	1.7e-10	0.27	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
183	1fak	L	819	898	1.7e-10	0.27	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
183	1fak	L	851	943	3.4e-12	0.05	-0.14		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
183	1fak	L	851	943	3.4e-12	0.10	-0.15		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
183	1ldo		333	472	1e-09	0.21	-0.15		LAMININ, CHAIN:	GLYCOPROTEIN GLYCOPROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
183	1klo		755	902	3.4e-15	0.20	-0.18		NULL; LAMININ; CHAIN:	GLYCOPROTEIN GLYCOPROTEIN
183	1klo		755	902	3.4e-15	0.20	-0.18		NULL; LAMININ; CHAIN:	GLYCOPROTEIN GLYCOPROTEIN
183	1pfx	L	330	438	1.4e-10	0.15	-0.14		FACTOR IXA; CHAIN: C, L; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
183	1pfx	L	772	920	2.6e-08	0.03	-0.18		FACTOR IXA; CHAIN: C, L; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
183	1pfx	L	819	898	1.7e-09	0.09	-0.19		FACTOR IXA; CHAIN: C, L; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
183	1qfk	L	1263	1339	5.1e-11	0.16	-0.19		COAGULATION FACTOR V (A) (LIGHT CHAIN); CHAIN: L; COAGULATION	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	
183	1qtk	L	334	427	5.1e-13	0.32	-0.18		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
183	1qtk	L	822	898	6.8e-10	0.31	-0.18		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
183	1qub	A	379	488	3.9e-08	0.20	-0.15		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD
183	1xka	L	334	427	3.4e-10	0.22	-0.07		BLOOD COAGULATION	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									FACTOR XA; CHAIN: L, C;	COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
183	1xka	L	822	898	1e-10	0.22	-0.13		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR
183	1xka	L	855	940	3.4e-09	0.11	-0.19		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
183	9wga	A	1219	1364	5.1e-11	0.02	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	BLOOD COAGULATION FACTOR
183	9wga	A	1219	1364	5.1e-11	0.02	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
183	9wga	A	277	420	5.1e-14	0.08	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
183	9wga	A	277	420	5.1e-14	0.08	-0.19		LECTIN (AGGLUTININ) WHEAT GERM	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
183	9wga	A	318	544	1.5e-11	0.31	-0.18		AGGLUTININ (ISOLECTIN 2) 9WGA 3	
183	9wga	A	318	544	1.5e-11	0.31	-0.18		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
183	9wga	A	757	907	3.4e-12	0.13	-0.17		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
183	9wga	A	757	907	3.4e-12	0.13	-0.17		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
183	9wga	A	777	975	5.1e-13	0.29	-0.12		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
183	9wga	A	777	975	5.1e-13	0.29	-0.12		LECTIN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSE-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									(AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLLECTIN 2) 9WGA.3	
184	1apo		1210	1245	1.3e-06	0.37	0.53		COAGULATION FACTOR EGF-LIKE MODULE OF BLOOD COAGULATION FACTOR X (N- TERMINAL, 1APO 3 APO FORM) (NMR, 13 STRUCTURES) 1APO.4	
184	1apo		1210	1245	1.3e-06	0.37	0.53		COAGULATION FACTOR EGF-LIKE MODULE OF BLOOD COAGULATION FACTOR X (N- TERMINAL, 1APO 3 APO FORM) (NMR, 13 STRUCTURES) 1APO.4	
184	1ciu	39		385	5.2e-34	0.05	-0.19		CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
184	1ciu	39		385	5.2e-34	0.05	-0.19		CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
184	1ciu		404	783	1.3e-32	0.01	-0.18		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
184	1ciu		404	783	1.3e-32	0.01	-0.18		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
184	1ciu		669	1044	1.3e-26	0.05	-0.19		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
184	1ciu		669	1044	1.3e-26	0.05	-0.19		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
184	1ciu		863	1177	3.9e-22	0.03	-0.15		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
184	1ciu		863	1177	3.9e-22	0.03	-0.15		CYCLODEXTRIN GLYCOSYLTRANSFERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
184	1ewv	A	264	749	9.1e-60	0.05	-0.20		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
184	1ewv	A	264	749	9.1e-60	0.05	-0.20		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	Fsi-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
184	1cww	A	521	996	1.2e-61			101.45	INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
184	1cww	A	521	996	1.2e-61			101.45	INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
184	1cww	A	561	1082	1e-56	0.04	-0.19		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
184	1cww	A	561	1082	1e-56	0.04	-0.19		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
184	1dan	L	1210	1282	8.5e-10	0.15	0.04		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
184	1dan	L	1210	1282	8.5e-10	0.15	0.04		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
184	1edm	B	1210	1242	5.1e-07	0.32	0.76		FACTOR IX; CHAIN: B, C;	COAGULATION FACTOR CRYSTALL STRUCTURE, EPIDERMAL GROWTH FACTOR, EGF, 2 CALCIUM-BINDING, EGF-LIKE DOMAIN, STRUCTURE AND FUNCTION, 3 HUMAN FACTOR IX,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
184	1edm	B	1210	1242	5.1e-07	0.32	0.76		FACTOR IX; CHAIN: B, C;	COAGULATION FACTOR CRYSTAL STRUCTURE, EPIDERMAL GROWTH FACTOR, EGF 2 CALCIUM-BINDING, EGF-LIKE DOMAIN, STRUCTURE AND FUNCTION, 3 HUMAN FACTOR IX, COAGULATION FACTOR
184	1fak	L	1210	1282	8.5e-10	-0.03	0.00		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
184	1fak	L	1210	1282	8.5e-10	-0.03	0.00		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
184	1pfx	L	1189	1242	5.2e-10	0.04	-0.11		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR: COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3

SEQ ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
184	1pfx	L	1189	1242	5.2e-10	0.04	-0.11		FACTOR IXA; CHAIN: C, L; D-PHE- PRO-ARG; CHAIN: I;	GLYCOPROTEIN COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3
184	1pfx	L	1210	1273	1e-08	0.15	0.11		FACTOR IXA; CHAIN: C, L; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3
184	1pfx	L	1210	1273	1e-08	0.15	0.11		FACTOR IXA; CHAIN: C, L; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3
184	1qfx	L	1214	1282	3.4e-09	0.04	-0.13		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN:	GLYCOPROTEIN SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
184	1qtk	L	1214	1282	3.4e-09	0.04	-0.13		C; COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
184	1tpg		1189	1242	2.6e-10	0.44	0.07		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
184	1tpg		1189	1242	2.6e-10	0.44	0.07		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
184	1tpg		1197	1246	1.7e-07	-0.12	0.03		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
184	1tpg		1197	1246	1.7e-07	-0.12	0.03		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
184	1twe		1189	1245	3.9e-10	0.29	-0.14		COAGULATION FACTOR X; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN, HYDROLASE, SERINE PROTEASE, PLASMA, BLOOD 2 COAGULATION FACTOR
184	1twe		1189	1245	3.9e-10	0.29	-0.14		COAGULATION FACTOR X; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN, HYDROLASE, SERINE PROTEASE,

SFO ID NO.	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
184	9wga	A	1191	1293	5.1e-08	0.22	-0.19		NULL;	PLASMA, BLOOD 2 COAGULATION FACTOR
									LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
184	9wga	A	1191	1293	5.1e-08	0.22	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
185	1c7j	A	1	83	3.4e-29	-0.84	0.40		PARA-NITROBENZYL ESTERASE; CHAIN: A;	HYDROLASE PNB ESTERASE; ALPHA-BETA HYDROLASE, DIRECTED EVOLUTION, ORGANIC ACTIVITY, 2 PNB ESTERASE
185	1c1e	A	1	83	1.5e-23	-0.66	0.33		CHOLESTEROL ESTERASE; ICLE 4 CHAIN: A, B, ICLE 5	LIPASE ESTERASE, SUBSTRATE/PRODUCT-BOUND ICLE 9
185	1dx4	A	1	83	1.7e-24	-0.91	0.10		ACETYLCHOLINESTERASE; CHAIN: A;	HYDROLASE (SERINE ESTERASE) HYDROLASE (SERINE ESTERASE), HYDROLASE, SERINE ESTERASE, 2 SYNAPSE, MEMBRANE, NERVE, MUSCLE, SIGNAL, NEUROTRANSMITTER 3 DEGRADATION, GLYCOPROTEIN, GPI-ANCHOR, ALTERNATIVE SPLICING
185	1e45	A	1	83	3.4e-30	-0.42	0.54		ACETYLCHOLINESTERASE; CHAIN: A;	CHOLINESTERASE SERINE HYDROLASE, NEUROTRANSMITTER CLEAVAGE,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
185	1f6w	A	1	83	5.1e-32	-0.93	0.25		BILE SALT ACTIVATED LIPASE; CHAIN: A;	CATALYTIC 2 TRIAD, ALPHA/BETA HYDROLASE
185	1lpp		1	83	8.5e-23	-0.93	0.16		HYDROLASE LIPASE (E.C.3.1.1.3) (TRIACYLGLYCERO LIPASE) COMPLEXED WITH ILPP 3 HEXADECANESULF ONATE ILPP 4 ILPP 71	HYDROLASE BILE SALT ACTIVATED LIPASE, ESTERASE, CATALYTIC DOMAIN
185	1maa	A	2	83	1.7e-29	-0.76	0.75		ACETYLCHOLINEST ERASE; CHAIN: A, B, C, D;	HYDROLASE MACHE; HYDROLASE, SERINE ESTERASE, ACETYLCHOLINESTERASE, TETRAMER, 2 HYDROLASE FOLD, GLYCOSYLATED PROTEIN
185	1qcz	A	1	83	1.7e-29	-0.51	0.48		PARA- NITROBENZYL ESTERASE; CHAIN: A;	HYDROLASE PNB ESTERASE; ALPHA-BETA HYDROLASE DIRECTED EVOLUTION
185	1thg		1	83	1.5e-25	-0.65	0.19		HYDROLASE(CARB OXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) TRIACYLGLYCEROL HYDROLASE ITHG 3	
185	2bee		1	83	3.4e-32	-0.93	0.36		CHOLESTEROL ESTERASE; CHAIN: NULL;	HYDROLASE BILE SALT ACTIVATED LIPASE, BILE SALT STIMULATED HYDROLASE, SERINE ESTERASE, LIPASE
186	1mrt		132	165	0.0052	-0.83	0.77		METALLOTHIONEIN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI- BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CD-7 METALLOTHIONEIN -2 (ALPHA DOMAIN) (NMES) IMETA 2	

TABLE 6

SEQ ID NO:	Position of Signal Peptide	Maximum score	Mean score
94	1-26	0.988	0.911
95	1-17	0.977	0.921
96	1-32	0.969	0.847
97	1-32	0.969	0.847
98	1-16	0.896	0.833
99	1-19	0.914	0.625
100	1-20	0.888	0.583
101	1-22	0.932	0.756
103	1-18	0.972	0.936
104	1-17	0.979	0.961
105	1-24	0.961	0.807
106	1-29	0.977	0.852
107	1-45	0.971	0.702
108	1-24	0.969	0.898
109	1-34	0.988	0.805
110	1-17	0.984	0.923
114	1-18	0.975	0.958
120	1-17	0.977	0.921
124	1-31	0.985	0.926
126	1-42	0.988	0.594
127	1-19	0.960	0.851
136	1-26	0.981	0.865
137	1-18	0.975	0.958
142	1-17	0.977	0.921
150	1-16	0.896	0.833
156	1-19	0.914	0.625
162	1-16	0.939	0.838
164	1-28	0.961	0.857
167	1-22	0.968	0.875
169	1-25	0.971	0.893
170	1-16	0.948	0.836
172	1-19	0.960	0.851
174	1-30	0.972	0.658
175	1-31	0.965	0.894
176	1-22	0.979	0.697
182	1-15	0.926	0.631
185	1-20	0.952	0.660
186	1-42	0.994	0.973

TABLE 7

SEQ ID NO:	Chromosomal Location
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3	20
4	20
5	20
7	17
10	17
11	19q13.3-q13.4
16	2p21
19	21
20	11q13
21	17
22	1p36.2
23	1p36.2
24	15
25	15
26	7
27	9q21-q22
28	17
31	1
32	13
36	11p15
37	7q22
38	17
40	11q23.3
41	10q25-q26
42	11q13
43	19p13.1
44	17
45	7q32
46	19
47	9q34
49	9q21-q22
50	20q13.3
51	2q35
52	9
54	9q34
55	9q34
56	17
57	14q32
58	20
60	5
61	16q24.3
62	16q24.3
64	4q34.1-q35.1
65	4q34.1-q35.1
66	9
67	15
68	11
69	14
70	10
71	2cen-q13
72	16
74	4p16.3

SEQ ID NO:	Chromosomal Location
75	13
76	1p36.2
77	4p16-p15
80	1
81	1p35-p31.3
82	1p35-p31.3
86	22q13.33
87	1q41
90	11p15
91	7q22
93	11p15.5

TABLE 8

SEQ ID NO: of Full-length Nucleotide Sequence	SEQ ID NO: of Full-length Peptide Sequence	SEQ ID NO: in Priority Application USSN 09/728,952
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16	109	22
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27	120	34
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31	124	38
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35	128	42
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39	132	46
40	133	47
41	134	48
42	135	49
43	136	50
44	137	51
45	138	52
46	139	53
47	140	54
48	141	55
49	142	57
50	143	58
51	144	59

SEQ ID NO: of Full-length Nucleotide Sequence	SEQ ID NO: of Full-length Peptide Sequence	SEQ ID NO: in Priority Application USSN 09/728,952
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53	146	61
54	147	62
55	148	63
56	149	64
57	150	65
58	151	66
59	152	67
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83	176	91
84	177	92
85	178	93
86	179	94
87	180	95
88	181	96
89	182	97
90	183	98
91	184	99
92	185	100
93	186	101

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-93, a mature protein coding portion of SEQ ID NO: 1-93, an active domain coding portion of SEQ ID NO: 1-93, and complementary sequences thereof.
- 5 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 10 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 15 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
- 20 7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 25 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - (a) a polypeptide encoded by any one of the polynucleotides of claim 1;
 - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-93; and
- 30

(c) a polypeptide of any one of SEQ ID NO: 94-186.

11. A composition comprising the polypeptide of claim 10 and a carrier.
- 5 12. An antibody directed against the polypeptide of claim 10.
13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
 - 10 b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with
 - 15 nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
 - c) detecting said product and thereby the polynucleotide of claim 1 in the
 - 20 sample.
15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 25 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
 - 30 b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
 - b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
 - b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from SEQ ID NO: 1-93, a mature protein coding portion of SEQ ID NO: 1-93, an active domain coding portion of SEQ ID NO: 1-93, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-93, under conditions sufficient to express the polypeptide in said cell; and
 - b) isolating the polypeptide from the cell culture or cells of step (a).
20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO: 94-186, the mature protein portion thereof, or the active domain thereof.
21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1-93.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
24. The collection of claim 23, wherein the array detects full-matches to any one of the
5 polynucleotides in the collection.
25. The collection of claim 23, wherein the array detects mismatches to any one of the
polynucleotides in the collection.
- 10 26. The collection of claim 22, wherein the collection is provided in a computer-readable
format.
27. A method of treatment comprising administering to a mammalian subject in need
thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20
15 and a pharmaceutically acceptable carrier.
28. A method of treatment comprising administering to a mammalian subject in need
thereof a therapeutic amount of a composition comprising an antibody that specifically binds
to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
20

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tac	cgc	ctt	ggg	gca	gca	cca	gag	gaa	gag	tct	gcc	tat	gtg	gca	gga	681
Tyr	Arg	Leu	Gly	Ala	Ala	Pro	Glu 200	Glu	Glu	Glu	Ser	Ala	Tyr	Val	Ala 210	
gaa	aag	agg	cag	cat	tcc	agc	caa	gat	gtt	cat	gta	gta	ttg	aaa	ctc	729
Glu	Lys	Arg	Gln	His	Ser	Ser	Asp 215	Val	His	Val	Val	Leu	Lys	Lys	Leu 225	
tgg	aag	agt	gga	ttc	agc	ctg	gat	aat	gga	gaa	ctc	aga	agc	tac	caa	777
Trp	Lys	Ser	Gly	Phe	Ser	Leu	Asp 230	Asn	Gly	Glu	Leu	Arg	Ser	Tyr	Gln 240	
gac	cca	tcc	aat	gcc	cag	ttt	ctg	gag	tct	atc	cgc	aga	ggg	gag	gtg	825
Asp	Pro	Ser	Asn	Ala	Gln	Phe	Leu 245	Glu	Ser	Ile	Arg	Arg	Gly	Glu	Val 255	
cca	gca	gag	ctt	cgg	agg	cta	gct	cac	ggg	gga	cag	gtg	aac	ttg	gat	873
Pro	Ala	Glu	Leu	Arg	Arg	Leu	Ala 260	His	Gly	Gly	Gln	Val	Asn	Leu	Asp 270	
atg	gag	gac	cat	cgg	gac	gag	gac	ttt	gtg	aag	ccc	aaa	gga	gcc	ctt	921
Met	Glu	Asp	His	Arg	Asp	Glu	Asp	Phe	Val	Lys	Pro	Lys	Gly	Ala	Leu	

275	280	285	290	
caa gcc ttc act ggc gag ggt cag aaa ctg ggc agc act gcc ccc cag				969
Gln Ala Phe Thr Gly Glu Gly Gln Lys Leu Gly Ser Thr Ala Pro Gln	295	300	305	
gtg ttg agt acc agc tct cca gcc caa cag gca gaa aat gaa gcc aaa				1017
Val Leu Ser Thr Ser Ser Pro Ala Gln Gln Ala Glu Asn Glu Ala Lys	310	315	320	
gcc agc tct tcc atc tta atc aac gaa tca gag cct acc aca aac atc				1065
Ala Ser Ser Ser Ile Leu Ile Asn Glu Ser Glu Pro Thr Thr Asn Ile	325	330	335	
caa att cgg ctt gca gac ggc ggg agg ctg gtg cag aaa ttt aac cac				1113
Gln Ile Arg Leu Ala Asp Gly Gly Arg Leu Val Gln Lys Phe Asn His	340	345	350	
agc cac agg atc agc gac atc cga ctc ttc atc gtg gat gcc cgg cca				1161
Ser His Arg Ile Ser Asp Ile Arg Leu Phe Ile Val Asp Ala Arg Pro	355	360	365	
gcc atg gct gcc acc agc ttt atc ctc atg act act ttc cgg aac aaa				1209
Ala Met Ala Ala Thr Ser Phe Ile Leu Met Thr Thr Phe Pro Asn Lys	375	380	385	
gag ctg gct gat gag agc cag acc ctg aag gaa gcc aac ctg ctc aat				1257
Glu Leu Ala Asp Glu Ser Gln Thr Leu Lys Glu Ala Asn Leu Leu Asn	390	395	400	
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			Met Cys Ser Thr Met Ser	
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gcc ccc acc tgc ctg gcc cac ttg cct ccc tgc ttc ctg ctg ctg gca				103
Ala Pro Thr Cys Leu Ala His Leu Pro Pro Cys Phe Leu Leu Ala	10	15	20	
ctg gtc ctt gtc ccc tca gat gcc tct ggg cag agc agc agg aat gac				151
Leu Val Leu Val Pro Ser Asp Ala Ser Gly Gln Ser Ser Arg Asn Asp	25	30	35	
tgg cag gtg cta cag ccc gag gcc ccc atg ctg gtg gca gaa ggt gag				199

Trp	Gln	Val	Leu	Gln	Pro	Glu	Gly	Pro	Met	Leu	Val	Ala	Glu	Gly	Glu	
40						45					50					
aca	ctt	cta	ctg	agg	tgt	atg	gtg	gtc	ggc	tcc	tgc	act	gat	ggg	atg	247
Thr	Leu	Leu	Leu	Arg	Cys	Met	Val	Val	Ala	Ser	Cys	Thr	Asp	Gly	Met	
55					60					65					70	
ata	aaa	tgg	gtg	aag	atc	gcg	cta	gcg	agc	ttt	tat	gag	gac	gga	ggg	295
Ile	Lys	Trp	Val	Lys	Ile	Ala	Leu	Ala	Ser	Phe	Tyr	Glu	Asp	Gly	Gly	
				75					80					85		
gat	gaa	gac	att	gtg	acc	att	tcg	cag	gca	acc	ccc	agt	tca	gtg	tcc	343
Asp	Glu	Asp	Ile	Val	Thr	Ile	Ser	Gln	Ala	Thr	Pro	Ser	Ser	Val	Ser	
				90				95					100			
aga	ggc	aca	gcc	ccc	agt	gat	aat	aga	gtg	aca	tcc	ttc	aga	gac	ctc	391
Arg	Gly	Thr	Ala	Pro	Ser	Asp	Asn	Arg	Val	Thr	Ser	Phe	Arg	Asp	Leu	
			105				110					115				
att	cat	gac	caa	gat	gaa	gat	gag	gag	gaa	gag	gaa	ggc	cag	agg	ttt	439
Ile	His	Asp	Gln	Asp	Glu	Asp	Glu	Glu	Glu	Glu	Gln	Gly	Gln	Arg	Phe	
			120			125						130				
tat	gct	ggg	ggc	tca	gag	aga	agt	gga	cag	cag	att	gtt	ggc	cct	ccc	487
Tyr	Ala	Gly	Gly	Ser	Glu	Arg	Ser	Gly	Gln	Ile	Val	Gly	Pro	Pro		
135					140					145				150		
agg	aag	aaa	agt	ccc	aac	gag	ctg	gtg	gat	gat	ctc	ttt	aaa	ggg	gcc	535
Arg	Lys	Lys	Ser	Pro	Asn	Glu	Leu	Val	Asp	Asp	Leu	Phe	Lys	Gly	Ala	
				155					160					165		
aaa	gag	cat	gga	gct	gta	gct	gtg	gag	cga	gtg	acc	aag	agc	cct	gga	583
Lys	Glu	His	Gly	Ala	Val	Ala	Val	Glu	Arg	Val	Thr	Lys	Ser	Pro	Gly	
			170					175					180			
gag	acc	agt	aaa	ccg	aga	gtt	cat	gta	gta	ttg	aaa	ctc	tgg	aag	agt	631
Glu	Thr	Ser	Lys	Pro	Arg	Val	His	Val	Val	Leu	Lys	Leu	Trp	Lys	Ser	
			185				190					195				
gga	ttc	agc	ctg	gat	aat	gga	gaa	ctc	aga	agc	tac	caa	gac	cca	tcc	679
Gly	Phe	Ser	Leu	Asp	Asn	Gly	Glu	Leu	Arg	Ser	Tyr	Gln	Asp	Pro	Ser	
			200			205					210					
aat	gcc	cag	ttt	ctg	gag	tct	atc	cgc	aga	ggg	gag	gtg	cca	gca	gag	727
Asn	Ala	Gln	Phe	Leu	Glu	Ser	Ile	Arg	Arg	Gly	Glu	Val	Pro	Ala	Glu	
215					220					225				230		
ctt	egg	agg	cta	gct	cac	ggg	gga	cag	gtg	aac	ttg	gat	atg	gag	gac	775
Leu	Arg	Arg	Leu	Ala	His	Gly	Gly	Gln	Val	Asn	Leu	Asp	Met	Glu	Asp	
				235				240						245		
cat	egg	gac	gag	gac	ttt	gtg	aag	ccc	aaa	gga	gcc	ttc	aaa	gcc	ttc	823
His	Arg	Asp	Glu	Asp	Phe	Val	Lys	Pro	Lys	Gly	Ala	Phe	Lys	Ala	Phe	
				250				255				260				
act	ggc	gag	ggg	cag	aaa	ctg	ggc	agc	act	gcc	ccc	cag	gtg	ttg	agt	871
Thr	Gly	Glu	Gly	Gln	Lys	Leu	Gly	Ser	Thr	Ala	Pro	Gln	Val	Leu	Ser	
			265			270						275				
acc	agc	tct	cca	gcc	caa	cag	gca	gaa	aat	gaa	gcc	aaa	gcc	agc	tct	919
Thr	Ser	Ser	Pro	Ala	Gln	Gln	Ala	Glu	Asn	Glu	Ala	Lys	Ala	Ser	Ser	

280	285	290	
tcc atc tta atc gac gaa tca gag cct acc aca aac atc caa att cgg			967
Ser Ile Leu Ile Asp Glu Ser Glu Pro Thr Thr Asn Ile Gln Ile Arg			
295	300	305	310
ctt gca gac ggc ggg agg ctg gtg cag aaa ttt aac cac agc cac agg			1015
Leu Ala Asp Gly Gly Arg Leu Val Gln Lys Phe Asn His Ser His Arg			
	315	320	325
atc agc gac atc cga ctc ttc atc gtg gat gcc cgg cca gcc atg gct			1063
Ile Ser Asp Ile Arg Leu Phe Ile Val Asp Ala Arg Pro Ala Met Ala			
	330	335	340
gcc acc agc ttt atc ctc atg act act ttc cgg aac aaa gag ctg gct			1111
Ala Thr Ser Phe Ile Leu Met Thr Thr Phe Pro Asn Lys Glu Leu Ala			
	345	350	355
gat gag agc cag acc ctg aag gaa gcc aac ctg ctc aat gct gtc atc			1159
Asp Glu Ser Gln Thr Leu Lys Glu Ala Asn Leu Leu Asn Ala Val Ile			
	360	365	370
gtg cag cgg tta aca taa ccgccc agccagctgc ctggcctccc tectgtgttt			1213
Val Gln Arg Leu Thr			
375			
cccatggcca gtggccatgc cccatgggga tcgccctcc tcgccctctg tgcaacccca			1273
gcagtcacagt gcaacgtctc ccccatagct ctgggttctt agatcttggt tggacgtttg			1333
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Met Ala Ala Glu Arg Gln Glu Ala Leu Arg	
1 5 10	
gag ttc gtg gcg gtg acg ggc gcc gag gag gac cgg gcc cgc ttc ttt	219
Glu Phe Val Ala Val Thr Gly Ala Glu Glu Asp Arg Ala Arg Phe Phe	
15 20 25	
ctc gag tcg gcc ggc tgg gac ttg cag atc gcg cta gcg agc ttt tat	267
Leu Glu Ser Ala Gly Trp Asp Leu Gln Ile Ala Leu Ala Ser Phe Tyr	
30 35 40	

gag gac gga ggg gat gaa gac att gtg acg att tcg cag gca acc ccc Glu Asp Gly Gly Asp Glu Asp Ile Val Thr Ile Ser Gln Ala Thr Pro 45 50 55	315
agt tca gtg tcc aga ggc aca gcc ccc agt gat aat aga gtg aca tcc Ser Ser Val Ser Arg Gly Thr Ala Pro Ser Asp Asn Arg Val Thr Ser 60 65 70	363
ttc aga gac ctc att cat gac caa gat gaa gat gag gag gaa gag gaa Phe Arg Asp Leu Ile His Asp Gln Asp Glu Asp Glu Glu Glu Glu Glu 75 80 85 90	411
ggc cag agg agc agg ttt tat gct ggg ggc tca gag aga agt gga cag Gly Gln Arg Ser Arg Phe Tyr Ala Gly Gly Ser Glu Arg Ser Gly Gln 95 100 105	459
cag att gtt ggc cct ccc agg aag aaa agt ccc aac gag ctg gtg gat Gln Ile Val Gly Pro Pro Arg Lys Lys Ser Pro Asn Glu Leu Val Asp 110 115 120	507
gat ctc ttt aaa ggt gcc aaa gag cat gga gct gta gct gtg gag cga Asp Leu Phe Lys Gly Ala Lys Glu His Gly Ala Val Glu Arg 125 130 135	555
gtg acc aag agc cct gga gag acc agt aaa ccg aga cca ttt gca gga Val Thr Lys Ser Pro Gly Glu Thr Ser Lys Pro Arg Pro Phe Ala Gly 140 145 150	603
ggg ggc tac cgc ctt ggg gcc agc acc aga gga aga gtc tgc cta tgt Gly Gly Tyr Arg Leu Gly Ala Ser Thr Arg Gly Arg Val Cys Leu Cys 155 160 165 170	651
ggc agg aga aaa gag gca gca ttc cag cca aga tgt tca tgt agt att Gly Arg Arg Lys Glu Ala Ala Phe Gln Pro Arg Cys Ser Cys Ser Ile 175 180 185	699
gaa act ctg gaa gag tgg att cag cct gga taa tggagaac tcagaagcta Glu Thr Leu Glu Glu Trp Ile Gln Pro Gly 190 195	750
ccaagaccga tccaatgcc agtttctgga gtctattcgc agaggggagg tgcagcagag	810
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agcactgccc ccagggtgtt gattaccagc tctccagccc aacaggcaga aaatgaagcc	990
aaagccagct cttccatctt aatcgacgaa tcagagccta ccacaaacat ccaaatccg	1050
cttgacagcg gcgggaggct ggtgcagaaa ttaaccaca gccacaggat cagcgacatc	1110
cgactcttca tcgtggatgc ccggccagcc atggctgcca ccagctttat cctcatgact	1170
actttccgga acaaagagct ggctgatgag agccagagccc tgaaggaagc caacctgctc	1230
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                                         1

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Phe Ala Pro Arg Leu Leu Asp Leu Gln Lys Thr Lys Tyr Ala Arg Phe
                    5                      10                      15

atg aac cac cga gtc cct gcc cac aag agg tac cag ccc aca gag tat      154
Met Asn His Arg Val Pro Ala His Lys Arg Tyr Gln Pro Thr Glu Tyr
                    20                      25                      30

gaa cat gcg gcc aac tgt gcc acc cat gct ttc tgg atc atc ccc agc      202
Glu His Ala Ala Asn Cys Ala Thr His Ala Phe Trp Ile Ile Pro Ser
                    35                      40                      45

atc ctg ggc agc tcc aac ctc tac ttc ctg tgc gac gat gac tgg gag      250
Ile Leu Gly Ser Ser Asn Leu Tyr Phe Leu Ser Asp Asp Asp Trp Glu
                    50                      55                      60                      65

acc atc tct gcc tgg atc tac ggc ctc ggc ctc tgc ggc ctc ttc gtg      298
Thr Ile Ser Ala Trp Ile Tyr Gly Leu Gly Leu Cys Gly Leu Phe Val
                    70                      75                      80

gtg tcc act gtg ttt cac acc atc tcc tgg aag aag agc cac ctc aga      346
Val Ser Thr Val Phe His Thr Ile Ser Trp Lys Lys Ser His Leu Arg
                    85                      90                      95

tgg gga ttc tga ggg ccaaggggtc ttggctggac agaggagccc agccctgcta      401
Trp Gly Phe
                    100

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ttcaagagca agacaggagg cgactgc atg aga cca tgg ctg aga cac cta 171
Met Arg Pro Trp Leu Arg His Leu
1 5

gtc ctc cag gca ctg agg aac tcc agg gca ttc tgt ggg tct cat ggg 219
Val Leu Gln Ala Leu Arg Asn Ser Arg Ala Phe Cys Gly Ser His Gly
10 15 20

aag cca gca cct cta cct gtt cct cag aag atc gtg gcc acc tgg gaa 267
Lys Pro Ala Pro Leu Pro Val Pro Gln Lys Ile Val Ala Thr Trp Glu
25 30 35 40

gcc atc agc ctg gga agg cag ctg gtg cct gag tac ttc aac ttc gcc 315
Ala Ile Ser Leu Gly Arg Gln Leu Val Glu Tyr Phe Asn Phe Ala
45 50 55

cat gat gtg ctg gat gtg tgg agt cgg ctg gaa gag gct gga cac cgc 363
His Asp Val Leu Asp Val Trp Ser Arg Leu Glu Glu Ala Gly His Arg
60 65 70

ccc cca aat cct gcc ttc tgg tgg gtc aat ggc aca gga gca gag atc 411
Pro Pro Asn Pro Ala Phe Trp Trp Val Asn Gly Thr Gly Ala Glu Ile
75 80 85

aag tgg agc ttt gag gag ctg ggg aag cag tcc agg aag gca gcc aat 459
Lys Trp Ser Phe Glu Glu Leu Gly Lys Gln Ser Arg Lys Ala Ala Asn
90 95 100

gtg ctg ggg ggt gca tgc ggc ctg cag cct ggg gac aga atg atg ctg 507
Val Leu Gly Gly Ala Cys Gly Leu Gln Pro Gly Asp Arg Met Met Leu
105 110 115 120

gta ctc cca cgg ctc ccg gag tgg tgg ctg gtc agt gtg gct tgc atg 555
Val Leu Pro Arg Leu Pro Glu Trp Trp Leu Val Ser Val Ala Cys Met
125 130 135

cgg aca ggg act gtg atg att ccg ggt gtg act cag ctg aca gag aag 603
Arg Thr Gly Thr Val Met Ile Pro Gly Val Thr Gln Leu Thr Glu Lys
140 145 150

gac ctc aag tac cgg ctg cag gcg tcc agg gcc aag tcc att atc acc 651
Asp Leu Lys Tyr Arg Leu Gln Ala Ser Arg Ala Lys Ser Ile Ile Thr
155 160 165

agt gac tcc cta gct cca agg gtg gat gcc atc agt gcc gaa tgc ccc 699
Ser Asp Ser Leu Ala Pro Arg Val Asp Ala Ile Ser Ala Glu Cys Pro
170 175 180

tcc ctc cag acc aag ctg ctg gtg tca gac agc agt cgg cca ggc tgg 747
Ser Leu Gln Thr Lys Leu Leu Val Ser Asp Ser Ser Arg Pro Gly Trp
185 190 195 200

ttg aac ttc agg gaa ctc ctc cgg gag gct tct aca gag cac aac tgc 795
Leu Asn Phe Arg Glu Leu Leu Arg Glu Ala Ser Thr Glu His Asn Cys

205										210										215									
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Met	Arg	Thr	Lys	Ser	Arg	Asp	Pro	Leu	Ala	Ile	Tyr	Phe	Thr	Lys	Arg														843
			220						225				230																
gaa	cca	ccg	ggg	gcc	ccc	aag	atg	gtc	gag	cac	tcc	cag	agc	agc	tac														891
Glu	Pro	Pro	Gly	Ala	Pro	Lys	Met	Val	Glu	His	Ser	Gln	Ser	Ser	Tyr														
			235					240					245																
gga	ctg	ggt	ttt	gtg	gcc	agc	gga	aga	cgg	tgg	gtg	gcc	ttg	acc	gaa														939
Gly	Leu	Gly	Phe	Val	Ala	Ser	Gly	Arg	Arg	Trp	Val	Ala	Leu	Thr	Glu														
			250				255						260																
tct	gac	atc	ttc	tgg	aac	acg	act	gac	act	ggc	tgg	gtg	aag	gca	gcc														987
Ser	Asp	Ile	Phe	Trp	Asn	Thr	Thr	Asp	Thr	Gly	Trp	Val	Lys	Ala															
			265				270						275																
tgg	act	ctc	ttc	tct	gcc	tgg	cct	aat	gga	tct	tgc	att	ttt	gtg	cat														1035
Trp	Thr	Leu	Phe	Ser	Ala	Trp	Pro	Asn	Gly	Ser	Cys	Ile	Phe	Val	His														
							285						295																
gag	ctg	ccc	cga	gtt	gat	gcc	aaa	gtt	atc	ctg	aat	act	ctc	tcc	aaa														1083
Glu	Leu	Pro	Arg	Val	Asp	Ala	Lys	Val	Ile	Leu	Asn	Thr	Leu	Ser	Lys														
							300						310																
ttc	ccg	ata	acc	acc	ctc	tgc	tgt	gtc	cca	acc	atc	ttt	cgg	ctg	ctt														1131
Phe	Pro	Ile	Thr	Thr	Leu	Cys	Cys	Val	Pro	Thr	Ile	Phe	Arg	Leu	Leu														
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gtg	cag	gag	gat	ctg	acc	agg	tac	cag	ttt	cag	agc	ttg	agg	cac	tgt														1179
Val	Gln	Glu	Asp	Leu	Thr	Arg	Tyr	Gln	Phe	Gln	Ser	Leu	Arg	His	Cys														
							330						340																
ctg	acc	gga	gga	gag	gcc	ctc	aac	cct	gac	gtg	agg	gag	aag	tgg	aaa														1227
Leu	Thr	Gly	Gly	Glu	Ala	Leu	Asn	Pro	Asp	Val	Arg	Glu	Lys	Trp	Lys														
							350						355																
cac	cag	act	ggt	gtg	gag	ctg	tac	gaa	ggc	tat	ggc	cag	tct	gaa	acg														1275
His	Gln	Thr	Gly	Val	Glu	Leu	Tyr	Glu	Gly	Tyr	Gly	Gln	Ser	Glu	Thr														
							365						370																
gtt	gtc	atc	tgt	gcc	aat	cca	aaa	ggc	atg	aaa	atc	aag	tct	gga	tcc														1323
Val	Val	Ile	Cys	Ala	Asn	Pro	Lys	Gly	Met	Lys	Ile	Lys	Ser	Gly	Ser														
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atg	ggg	aag	gcg	tcc	cca	ccc	tac	gat	gtg	cag	att	gtg	gat	gat	gag														1371
Met	Gly	Lys	Ala	Ser	Pro	Pro	Tyr	Asp	Val	Gln	Ile	Val	Asp	Asp	Glu														
							400						405																
ggc	aac	gtc	ctg	cct	cct	gga	gaa	gag	ggg	aat	gtt	gcc	gtc	cgt	atc														1419
Gly	Asn	Val	Leu	Pro	Pro	Gly	Glu	Glu	Gly	Asn	Val	Ala	Val	Arg	Ile														
							410						420																
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Arg	Pro	Thr	Arg	Pro	Phe	Cys	Phe	Phe	Asn	Cys	Tyr	Leu	Asp	Asn	Pro														
							430						435																
gag	aag	aca	gct	gca	tca	gaa	caa	ggg	gac	ttt	tac	atc	aca	ggg	gac														1515
Glu	Lys	Thr	Ala	Ala	Ser	Glu	Gln	Gly	Asp	Phe	Tyr	Ile	Thr	Gly	Asp														
							445																						

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gaa agt gcc ctg gca gag cat cct gct gtc ctg gag tgg gct gtg gtc Glu Ser Ala Leu Ala Glu His Pro Ala Val Leu Glu Ser Ala Val Val 490 495 500	1659
agc agc cca gac ccc atc agg gga gag gtg gta aag gca ttt ata gtc Ser Ser Pro Asp Pro Ile Arg Gly Glu Val Val Lys Ala Phe Ile Val 505 510 515 520	1707
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aag gtg gcc ttt gtt tca gaa ctg cca aag acg gtt tct gga aag atc Lys Val Ala Phe Val Ser Glu Leu Pro Lys Thr Val Ser Gly Lys Ile 555 560 565	1851
caa agg agt aaa ttg cga agt cag gag tgg ggg aaa tga ggtgcacccc Gln Arg Ser Lys Leu Arg Ser Gln Glu Trp Gly Lys 570 575 580	1900
aggaaggccc cgtagacctc cgaagactcc acaagaaact aatggatcac tggtcagtc	1960
ccatggggag catcatctct tcgacctaa agatgtcaaa ggtgtgcagc ttccaaacgg	2020
catccccagg atcactgggc aatgctggaa agagcaaaag aatatcattg gccctgatca	2080
catagatgct gcgcgcctca gcaaatgctt ggtggttcga cttctccctc tgtctggggg	2140
caggctcagc atctgccac tggtctcact aagagcttcc agattccct ccataggaca	2200
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cttcatcctt tgtatgtaac catttggcaa aagtatgcag gaacataaaa taaaatatcc	2320
tttagctcag aaattctatc ttcgggagtc accacaaaag aaaaaataca aaatgcagaa	2380
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 <211> 783
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (50) .. (379)

<400> 8

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                               Met Asp
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ctg ccc agg ggc ctg gtg gtg gcc tgg gcg ctc agc ctg tgg cca ggg      103
Leu Pro Arg Gly Leu Val Val Ala Trp Ala Leu Ser Leu Trp Pro Gly
                    5                    10                    15

ttc acg gac acc ttc aac atg gac acc agg aag ccc cgg gtc atc cct      151
Phe Thr Asp Thr Phe Asn Met Asp Thr Arg Lys Pro Arg Val Ile Pro
                    20                    25                    30

ggc tcc agg acc gcc ttc ttt ggc tac aca gtg cag cag cac gac atc      199
Gly Ser Arg Thr Ala Phe Phe Gly Tyr Thr Val Gln Gln His Asp Ile
                    35                    40                    45                    50

agt ggc aat aag tgg ctg gtc gtg ggc gcc cca ctg gaa acc aat ggc      247
Ser Gly Asn Lys Trp Leu Val Val Gly Ala Pro Leu Glu Thr Asn Gly
                    55                    60                    65

tac cag aag acg gga gac gtg tac aag tgt cca gtg atc cac ggg aac      295
Tyr Gln Lys Thr Gly Asp Val Tyr Lys Cys Pro Val Ile His Gly Asn
                    70                    75                    80

tgc acc aaa ctc aac ctg ggt aac gtg ggc tgg tgg tct ctt cac aat      343
Cys Thr Lys Lys Leu Asn Leu Gly Asn Val Gly Trp Trp Ser Leu His Asn
                    85                    90                    95

gag gcc agc ggt tgt cta aca caa ggc agg ctc tga tga cgcccatgtc      393
Glu Ala Ser Gly Cys Leu Thr Gln Gly Arg Leu
                    100                    105

catggtcaca ctgactcctt cctgctactc catgagatga ccagctgat atcactgcc      453

ccactttaca catgaggaag ctgaggccag ggagaggagg caactttttcc acagtcacac      513

agcttgccag gggctcacca ggaatcaacc caggccctag ctgtcccgaga ccattctctt      573

ttctgactca gccactgccc ttcaactcaa agttttctct cccaggagaa aaaaccaaac      633

caaagggggc ggcggtttta gaggatccag gtttacttcc cccggcatgc aacgcaataa      693

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<211> 1830

<212> DNA

<213> Homo sapiens

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ggcatggtgg ctacgacctg taatcccaac actttgggag gtcgaggtga gagaatggct	180
tgaagcctcc cggcctcaag accagcttcg acaacataat gagaaccccc ccaacccccca	240
ctcccccatc tctacaaaaa ataaaaataa agtaggtgat caataagatg gcagatgaga	300
aaactggggc agatgacaca aagagagggc aggttaaggt ggggtgggcc agctctgggt	360
gacaaggcgg cgctccctgt ttctagacaa aacccactgg ccagtggtat agcagaatct	420
gggtccctg tacaccattg agggccacag ctatgggctc	475
atg cag aag ctg gag Met Gln Lys Leu Glu 1 5	
ctg ggc cgg tac aat gag aca cac gcc ata gcc aag tgg cta cta gag	523
Leu Gly Arg Tyr Asn Glu Thr His Ala Ile Ala Lys Trp Leu Leu Glu	
10 15 20	
aag cag gag ctg gga gga ggc ttc agg tcc acc cag acc acg gtg gtg	571
Lys Gln Glu Leu Gly Gly Gly Phe Arg Ser Thr Gln Thr Thr Val Val	
25 30 35	
gcc ctt gaa gct ctg acc cgc ttc cgc gaa gct gtc ccc ttc aag ggc	619
Ala Leu Glu Ala Leu Thr Arg Phe Arg Glu Ala Val Pro Phe Lys Gly	
40 45 50	
atc cag gat ctc cac gtc cag atc aga gcc ccc aag aca gcc ctg aat	667
Ile Gln Asp Leu His Val Gln Ile Arg Ala Pro Lys Thr Ala Leu Asn	
55 60 65	
gtg aat tgg tac att gat cac agc aat gcc tac caa cag cgg tca gca	715
Val Asn Trp Tyr Ile Asp His Ser Asn Ala Tyr Gln Gln Arg Ser Ala	
70 75 80 85	
aag ttc ctt gcc cag gac gac cta gag atc aaa gcc agt ggc aac ggg	763
Lys Phe Leu Ala Gln Asp Asp Leu Glu Ile Lys Ala Ser Gly Asn Gly	
90 95 100	
aga ggc acc atc tgc atc ctg aca atg tat cac aag tcc cca gag tcc	811
Arg Gly Thr Ile Ser Ile Leu Thr Met Tyr His Lys Ser Pro Glu Ser	
105 110 115	
cgg gag gac aac tgc aac ctg tac cac ctg aat ggc act ctc cac agt	859
Arg Glu Asp Asn Cys Asn Leu Tyr His Leu Asn Ala Thr Leu His Ser	
120 125 130	
gcc cta gaa gaa aat aaa aag gga ggt gag act ttt cgg ctc cgg atg	907
Ala Leu Glu Glu Asn Lys Lys Gly Gly Glu Thr Phe Arg Leu Arg Met	
135 140 145	
gaa aca agg ttc cag aac aat tga gaggccacaa tgactatcat ggaggtctcc	961
Glu Thr Arg Phe Gln Asn Asn	
150 155	
ctgtctcagg gcttctaccc caaccaggat gacctcaaac agctcacgag tgatgtggag	1021

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aggtacgcct ttcagtacaa aaccaagaca agtaccagcg acagcactgt tgcctctac 1081
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<210> 10
<211> 885
<212> DNA
<213> Homo sapiens

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<222> (242) .. (838)

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ctgcagggct cagctgagcc catgagctcc cagagctaac ccctgaacac ccaggcgggc 180
aaagggtcga tgcggtagt ccccatcctg gaggggcagg ctctgcgcac ctgctcctgg 240
c   atg gcg ctg cgg cac ctc gcc ctc ctg gct ggc ctt ctc gtg gga 286
    Met Ala Leu Arg His Leu Ala Leu Leu Ala Gly Leu Leu Val Gly
    1             5             10             15

gtc gcc agc aag tcc atg gag aac acg gcc cag ctg ccc gag tgc tgt 334
Val Ala Ser Lys Ser Met Glu Asn Thr Ala Gln Leu Pro Glu Cys Cys
           20             25             30

gta gat gtg gtg ggc gtc aac gcc agc tgc cca ggc gca agt ctg tgt 382
Val Asp Val Val Gly Val Asn Ala Ser Cys Pro Gly Ala Ser Leu Cys
           35             40             45

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ggt cca ggc tgt tac agg cgc tgg aac gcg gac ggg agc gcc agc tgc Gly Pro Gly Cys Tyr Arg Arg Trp Asn Ala Asp Gly Ser Ala Ser Cys 50 55 60	430
gtc cgc tgt ggg aac gga acc ctc cca gcc tac aac ggc tcc gag tgt Val Arg Cys Gly Asn Gly Thr Leu Pro Ala Tyr Asn Gly Ser Glu Cys 65 70 75	478
aga agc ttt gct ggc ccg ggt gcg cca ttc ccc atg aac aga agc tca Arg Ser Phe Ala Gly Pro Gly Ala Pro Phe Pro Met Asn Arg Ser Ser 80 85 90 95	526
ggg acc ccc ggg cgg cca cat cct ggg gct ccg cgc gtg gcc gcc tcc Gly Thr Pro Gly Arg Pro His Pro Gly Ala Pro Arg Val Ala Ala Ser 100 105 110	574
ctc ttc ctg ggc acg ttc ttc att agc tcc ggc ctc atc ctc tcc gta Leu Phe Leu Gly Thr Phe Phe Ile Ser Ser Gly Leu Ile Leu Ser Val 115 120 125	622
gct ggg ttc ttc tac ctc aag cgc tcc agt aaa ctc ccc agg gcc tgc Ala Gly Phe Phe Tyr Leu Lys Arg Ser Ser Lys Leu Pro Arg Ala Cys 130 135 140	670
tac aga aga aac aaa gct ccg gcc ctg cag cct ggc gaa gcc gct gca Tyr Arg Arg Asn Lys Ala Pro Ala Leu Gln Pro Gly Glu Ala Ala Ala 145 150 155	718
atg atc ccc ccg cca cag tcc tca gta cgg aag ccg cgc tac gtc agg Met Ile Pro Pro Pro Gln Ser Ser Val Arg Lys Pro Arg Tyr Val Arg 160 165 170 175	766
cgg gag cgg ccc ctg gac agg gcc acg gat ccc gct gcc ttc ccg ggg Arg Glu Arg Pro Leu Asp Arg Ala Thr Asp Pro Ala Ala Phe Pro Gly 180 185 190	814
gag gcc cgt atc agc aat gtc tga cctggaggcc gagaccacgc cagcacttg Glu Ala Arg Ile Ser Asn Val 195	868
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gca gcc aca ccg aag att ttc aat ggc act gag tgt ggg cgt aac tca Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg Asn Ser 20 25 30	213
cag ccg tgg cag gtg ggg ctg ttt gag ggc acc agc ctg cgc tgc ggg Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu Arg Cys Gly 35 40 45	261
ggg gtc ctt att gac cac agg tgg gtc ctc aca gcg gct cac tgc agc Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala Ala His Cys Ser 50 55 60	309
ggc agc agg tac tgg gtg cgc ctg ggg gaa cac agc ctc agc cag ctc Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His Ser Leu Ser Gln Leu 65 70 75 80	357
gac tgg acc gag cag atc cgg cac agc ggc ttc tct gtg acc cat ccc Asp Trp Thr Glu Gln Ile Arg His Ser Gly Phe Ser Val Thr His Pro 85 90 95	405
ggc tac ctg gga gcc tcg acg agc cac gag cac gac ctc cgg ctg ctg Gly Tyr Leu Gly Ala Ser Thr Ser His Glu His Asp Leu Arg Leu Leu 100 105 110	453
cgg ctg cgc ctg ccc gtc cgc gta acc agc agc gtt caa ccc ctg ccc Arg Leu Arg Leu Pro Val Arg Val Thr Ser Ser Val Gln Pro Leu Pro 115 120 125	501
ctg ccc aat gac tgt gca acc gct ggc acc gag tgc cac gtc tca ggc Leu Pro Asn Asp Cys Ala Thr Ala Gly Thr Glu Cys His Val Ser Gly 130 135 140	549
tgg ggc atc acc aac cac cca cgg aac cca ttc ccg gat ctg ctc cag Trp Gly Ile Thr Asn His Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln 145 150 155 160	597
tgc ctc aac ctc tcc atc gtc tcc cat gcc acc tgc cat ggt gtg tat Cys Leu Asn Leu Ser Ile Val Ser His Ala Thr Cys His Gly Val Tyr 165 170 175	645
ccc ggg aga atc acg agc aac atg gtg tgt gca ggc ggc gtc ccg ggg Pro Gly Arg Ile Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly 180 185 190	693
cag gat gcc tgc cag ggt gat tct ggg ggc ccc ctg gtg tgt ggg gga Gln Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly 195 200 205	741
gtc ctt caa ggt ctg gtg tcc tgg ggg tct gtg ggg ccc tgt gga caa Val Leu Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln 210 215 220	789
gat ggc atc cct gga gtc tac acc tat att tgc agc tcc act ctt gtt Asp Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Ser Ser Thr Leu Val 225 230 235 240	837
ggc ctg gga act tct tgg aac ttt aac tcc tgc cag ccc ttc taa gac Gly Leu Gly Thr Ser Trp Asn Phe Asn Ser Cys Gln Pro Phe 245 250	885

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<210> 12
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 <222> (646) .. (1860)
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 <222> (1) ... (2422)
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 ctacgccac tagcgctgct tccactgctt ctacctcccc tcccaggacc ccgagacacc 180
 cggggcgga gcggcagtgc tgcttgcttg ctctctctct cccccagccc ttccctcccg 240
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 cgggcgcgg gaggaggaca ccagcggagc cctgcactct cgtgccccgc tcaccagcat 600
 ctacttgccc cctcgcttct tcccagccc ttagagaag ggacc atg att tgg 654
 Met Ile Trp
 1
 aaa cgc agc gcc gtt ctg cgc ttc tac agt gtc tgc ggg ctg ctg cta 702
 Lys Arg Ser Ala Val Leu Arg Phe Tyr Ser Val Cys Gly Leu Leu Leu
 5 10 15
 caa gcg gct gct tca aag aat aaa gtt aaa ggc agc caa ggg cag ttt 750
 Gln Ala Ala Ala Ser Lys Asn Lys Val Lys Gly Ser Gln Gly Gln Phe
 20 25 30 35
 cca cta aca cag aat gta acc gtt gtt gaa ggt gga act gca att ttg 798
 Pro Leu Thr Gln Asn Val Thr Val Val Glu Gly Gly Thr Ala Ile Leu
 40 45 50
 acc tgc agg gtt gat caa aat gat aac acc tcc ctg cag tgg tca aat 846
 Thr Cys Arg Val Asp Gln Asn Asp Asn Thr Ser Leu Gln Trp Ser Asn
 55 60 65
 cca gct caa cag act ctg tac ttt gac gac aag aaa gct tta agg gac 894

Pro	Ala	Gln	Gln	Thr	Leu	Tyr	Phe	Asp	Asp	Lys	Lys	Ala	Leu	Arg	Asp	
	70						75					80				
aat	agg	atc	gag	ctg	gtt	cgc	gct	tcc	tgg	cat	gaa	ttg	agt	att	agt	942
Asn	Arg	Ile	Glu	Leu	Val	Arg	Ala	Ser	Trp	His	Glu	Leu	Ser	Ile	Ser	
	85					90					95					
gtc	agt	gat	gtg	tct	ctc	tct	gat	gaa	gga	cag	tac	acc	tgt	tct	tta	990
Val	Ser	Asp	Val	Ser	Leu	Ser	Asp	Glu	Gly	Ala	Tyr	Thr	Cys	Ser	Leu	
	100				105					110					115	
ttt	aca	atg	cct	gtc	aaa	act	tcc	aag	gca	tat	ctc	acc	gtt	ctg	ggg	1038
Phe	Thr	Met	Pro	Val	Lys	Thr	Ser	Lys	Ala	Tyr	Leu	Thr	Val	Leu	Gly	
					120				125					130		
gtt	cct	gaa	aag	cct	cag	att	agt	gga	ttc	tca	tca	cca	gtt	atg	gag	1086
Val	Pro	Glu	Lys	Pro	Gln	Ile	Ser	Gly	Phe	Ser	Ser	Pro	Val	Met	Glu	
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Gly	Asp	Leu	Met	Gln	Leu	Thr	Cys	Lys	Thr	Ser	Gly	Ser	Lys	Pro	Ala	
	150						155					160				
gct	gat	ata	aga	tgg	ttc	aaa	aat	gac	aaa	gag	att	aaa	gat	gta	aaa	1182
Ala	Asp	Ile	Arg	Trp	Phe	Lys	Asn	Asp	Lys	Glu	Ile	Lys	Asp	Val	Lys	
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tat	tta	aaa	gaa	gag	gat	gca	aat	cgc	aag	aca	ttc	act	gtc	agc	agc	1230
Tyr	Leu	Lys	Glu	Glu	Asp	Ala	Asn	Arg	Lys	Thr	Phe	Thr	Val	Ser	Ser	
	180				185				190						195	
aca	ctg	gac	ttc	cga	gtg	gac	cgg	agt	gat	gat	gga	gtg	gcg	gtc	atc	1278
Thr	Leu	Asp	Phe	Arg	Val	Asp	Arg	Ser	Asp	Asp	Gly	Val	Ala	Val	Ile	
				200					205					210		
tgc	aga	gta	gat	cac	gaa	tcc	ctc	aat	gcc	acc	cct	cag	gta	gcc	atg	1326
Cys	Arg	Val	Asp	His	Glu	Ser	Leu	Asn	Ala	Thr	Pro	Gln	Val	Ala	Met	
			215					220					225			
cag	gtg	cta	gaa	ata	cac	tat	aca	cca	tca	gtt	aag	att	ata	cca	tcg	1374
Gln	Val	Leu	Glu	Ile	His	Tyr	Thr	Pro	Ser	Val	Lys	Ile	Ile	Pro	Ser	
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Thr	Pro	Phe	Pro	Gln	Glu	Gly	Gln	Pro	Leu	Ile	Leu	Thr	Cys	Glu	Ser	
	245					250					255					
aaa	gga	aaa	cca	ctg	cca	gaa	cct	gtt	ttg	tgg	aca	aag	gat	ggc	gga	1470
Lys	Gly	Lys	Pro	Leu	Pro	Glu	Pro	Val	Leu	Trp	Thr	Lys	Asp	Gly	Gly	
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gaa	tta	cca	gat	cct	gac	cga	atg	gtt	gtg	agt	ggg	agg	gag	cta	aac	1518
Glu	Leu	Pro	Asp	Pro	Asp	Arg	Met	Val	Val	Ser	Gly	Arg	Glu	Glu	Asn	
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att	ctt	ttc	ctg	aac	aaa	acg	gat	aat	ggg	aca	tat	cga	tgt	gaa	gcc	1566
Ile	Leu	Phe	Leu	Asn	Lys	Thr	Asp	Asn	Gly	Thr	Tyr	Arg	Cys	Glu	Ala	
			295				300					305				
aca	aac	acc	att	ggc	caa	agc	agt	gcg	gaa	tat	gtt	ctc	att	gtg	cat	1614
Thr	Asn	Thr	Ile	Gly	Gln	Ser	Ser	Ala	Glu	Tyr	Val	Leu	Ile	Val	His	

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Asp Pro Asn Ala Leu Ala Gly Gln Asn Gly Pro Asp His Ala Leu Ile			
325	330	335	
gga gga ata gtg gct gta gtt gta ttt gtc acg ctg tgt tct atc ttt			1710
Gly Gly Ile Val Ala Val Val Phe Val Thr Leu Cys Ser Ile Phe			
340	345	350	355
ctg ctt ggt cga tat ctg gca agg cat aaa gga acg tat tta aca aat			1758
Leu Leu Gly Arg Tyr Leu Ala Arg His Lys Gly Thr Tyr Leu Thr Asn			
360	365	370	
gaa gct aad gga gct gaa gat gca cca gat gct gat aca gcc att atc			1806
Glu Ala Lys Gly Ala Glu Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile			
375	380	385	
aat gct gaa ggc agc caa gtc aat gct gaa gag aaa aaa gag tat ttc			1854
Asn Ala Glu Gly Ser Gln Val Asn Ala Glu Glu Lys Lys Glu Tyr Phe			
390	395	400	
att taa gatgcagggc aagattctga gttttactac caggctgaat gctggagaaa			1910
Ile			
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 <211> 4857
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(4803)

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1 5 10 15	

ctg ctg gcc tgg tgg gcc ctg ttg tgc atg gca ggt ggc caa ggc cgc Leu Leu Ala Trp Ser Ala Leu Leu Cys Met Ala Gly Gly Gln Gly Arg 20 25 30	96
tgg gac ggg gcc ttg gag gct gca ggt cct gga cgt gtg cgg agg cgg Trp Asp Gly Ala Leu Glu Ala Ala Gly Pro Gly Arg Val Arg Arg Arg 35 40 45	144
ggc agc cca ggc atc ttg cag ggg tgc gtg gta cct ggg atg ctg gga Gly Ser Pro Gly Ile Leu Gln Gly Cys Val Val Pro Gly Met Leu Gly 50 55 60	192
gac ccc ttc ggt gtg gat tgg gct gtc ctg ggg cca gcg gaa tac cgg Asp Pro Phe Gly Val Asp Trp Ala Val Leu Gly Pro Ala Glu Tyr Pro 65 70 80	240
ggg gga tgt cca cac ggg cag ggg ctc acc aga ccc atc tgc ctg tcc Gly Gly Cys Pro His Gly Gln Gly Leu Thr Arg Pro Ile Ser Leu Ser 85 90 95	288
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Thr	Gln	Asp	Val	Arg	Gly	Glu	Cys	Ile	Asp	Val	Asp	Glu	Cys	Thr	Ser	
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Ser	Pro	Cys	His	His	Gly	Asp	Cys	Val	Asn	Ile	Pro	Gly	Thr	Tyr	His	

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Pro Gly Ser Arg Leu Asp Pro Ser Gly Thr Phe Cys Leu Asp Ser Thr	
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tga gcgg ggaggctgcc aaccaggcca ggctgcgctc agaacacacc cccccaacaa	639
gaatgaaatg cccacacctt gcccatggac cctctccttg ctgcttgaga gatttggggn	699
nnnnnnnnnn anacannngn nctnnnctgn ngactctgct gtgcggagcac actgctcatc	759
ccagcaacct gatgccccagg ccagcgtggg ccctcctgcc ttgcatacac ccgtgggctg	819
agtgaacttc tcgggggatt ccaggagcac agtggcctga ctgtgatggt gcccttgagc	879
ctcccttcat cactcaacat cagaccacc gagggcagga cactctgtgc ccgtcctaca	939
gaaccaggaa gggaagtcca gcctctgtgc cttgtggggc ttgggggact caggggccaaa	999
aagggtgggt taggtctca tcacacctcc atactgcgcc gcgcaactgg gaggttgtga	1059
ggtaaaacta tcggagaccc cactgtttga atccatcgat ttggaaagt cccccaagcc	1119
tgcgttgtt ccgtgtggtt ttcttaattg gtggcccccg gtgcctccac ctc	1173

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<210> 15
<211> 1672
<212> DNA
<213> Homo sapiens

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<222> (41) .. (1165)

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                               Met Met Pro Gly Thr
                               1                               5

cgc ctg gag ggc gtg ctg ctg gcc gtg ctg ctg ggc ctg cag acc      103
Ala Leu Glu Gly Val Leu Leu Ala Val Leu Leu Val Gly Leu Gln Thr
                               10                               20

cgc acg ggt cgc ctg ctg agt ggg cag cca gtc tgc cgg gga ggg aca      151
Ala Thr Gly Arg Leu Leu Ser Gly Gln Pro Val Cys Arg Gly Gly Thr
                               25                               35

cag agg cct tgt tat aaa gtc att tac ttc cat gat act tct cga aga      199
Gln Arg Pro Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg
                               40                               50

ctg aac ttt gag gaa gcc aaa gaa gcc tgc agg agg gat gga ggc cag      247
Leu Asn Phe Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln
                               55                               60

cta gtc agc atc gag tct gaa gat gaa cag aaa ctg ata gaa aag ttc      295
Leu Val Ser Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe
                               70                               75                               80                               85

att gaa aac ctc ttg cca tct gat ggt gac ttc tgg att ggg ctc agg      343
Ile Glu Asn Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg
                               90                               95                               100

agg cgt gag gag aaa caa agc aat agc aca gcc tgc cag gac ctt tat      391
Arg Arg Glu Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr
                               105                               110                               115

gct tgg act gat ggc agc ata tca caa ttt agg aac tgg tat gtg gat      439
Ala Trp Thr Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp
                               120                               125                               130

gag ccg tcc tgc ggc agc gag gtc tgc gtg gtc atg tac cat cag cca      487
Glu Pro Ser Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro
                               135                               140                               145

tcg gca ccc gct ggc atc gga ggc ccc tac atg ttc cag tgg aat gat      535
Ser Ala Pro Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp
                               150                               155                               160                               165

gac cgg tgc aac atg aag aac aat ttc att tgc aaa tat tct gat gag      583
Asp Arg Cys Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu
                               170                               175                               180

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aaa cca gca gtt cct tct aga gaa gct gaa ggt gag gaa aca gag ctg	631
Lys Pro Ala Val Pro Ser Arg Glu Ala Glu Gly Glu Thr Glu Leu	
185 190 195	
aca aca cct gta ctt cca gaa gaa aca cag gaa gaa gat gcc aaa aaa	679
Thr Thr Pro Val Leu Pro Glu Glu Thr Gln Glu Asp Ala Lys Lys	
200 205 210	
aca ttt aaa gaa agt aga gaa gct gcc ttg aat ctg gcc tac atc cta	727
Thr Phe Lys Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu	
215 220 225	
atc ccc agc att ccc ctt ctc ctc ctc ctt gtg gtc acc aca gtt gta	775
Ile Pro Ser Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val	
230 235 240 245	
tgt tgg gtt tgg atc tgt aga aaa aga aaa cgg gag cag cca gac cct	823
Cys Trp Val Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro	
250 255 260	
agc aca aag aag caa cac acc atc tgg ccc tct cct cac cag gga aac	871
Ser Thr Lys Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn	
265 270 275	
agc cgg gac cta gag gtc tac aat gtc ata aga aaa caa agc gaa gct	919
Ser Pro Asp Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala	
280 285 290	
gac tta gct gag acc cgg cca gac ctg aag aat att tca ttc cga gtg	967
Asp Leu Ala Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val	
295 300 305	
tgt tcg gga gaa gcc act ccc gat gac atg tct tgt gac tat gac aac	1015
Cys Ser Gly Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn	
310 315 320 325	
atg gct gtg aac cca tca gaa agt ggg ttt gtg act ctg gtg agc gtg	1063
Met Ala Val Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val	
330 335 340	
gag agt gga ttt gtg acc aat gac att tat gag ttc tcc cca gac caa	1111
Glu Ser Gly Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln	
345 350 355	
atg ggg agg agt aag gag tct gga tgg gtg gaa aat gaa ata tat ggt	1159
Met Gly Arg Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly	
360 365 370	
tat tag gacatataaa aaactgaaac tgacaacaat ggaaaagaaa tgataagcaa	1215
Tyr	
aatcctctta ttttctataa ggaaaatata cagaagggtct atgaacaagc ttagatcagg	1275
tcctgtggat gagcatgtgg tccccacgac ctccgtgttg accccacagt tttggctgta	1335
tcctttatcc cagccagta tccagctcga ccttatgaga aggtaccttg cccaggtctg	1395
gcacatagta gagtctcaat aaatgtcact tgggtggttg tatctaactt ttaagggaca	1455

gagctttacc tggcagtgat aaagatgggc tgtggagctt ggaaaccac ctctgttttc 1515
 cttgctctat acagcagcac atattatcat acagacagaa aatccagaat cttttcaaaag 1575
 cccacatatg gtacacacagg ctggcctgtg catcggaat tctcatatct gtttttttca 1635
 aagaataaaa tcaataaaag agcaaaaaaa aaaaaaa 1672

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(1512)

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 Met Tyr Leu Val Ala Gly Asp Arg Gly Leu Ala Gly Cys Gly His Leu
 1 5 10 15
 ctg gtc tcg ctg ctg ggg ctg ctg ctg ctg ctg ggc cgc tcc ggc acc 96
 Leu Val Ser Leu Leu Gly Leu Leu Leu Leu Ala Arg Ser Gly Thr
 20 25 30
 cgg gcg ctg gtc tgc ctg ccc tgt gac gag tcc aag tgc gag gag ccc 144
 Arg Ala Leu Val Cys Leu Pro Cys Asp Glu Ser Lys Cys Glu Glu Pro
 35 40 45
 agg aac tgc ccg ggg agc atc gtg cag ggc gtc tgc ggc tgc tgc tac 192
 Arg Asn Cys Pro Gly Ser Ile Val Gln Gly Val Cys Gly Cys Cys Tyr
 50 55 60
 acg tgc gcc agc cag agg aac gag agc tgc ggc ggc acc ttc ggg att 240
 Thr Cys Ala Ser Gln Arg Asn Glu Ser Cys Gly Gly Thr Phe Gly Ile
 65 70 75 80
 tac gga acc tgc gac cgg ggg ctg cgt tgt gtc atc cgc ccc ccg ctc 288
 Tyr Gly Thr Cys Asp Arg Gly Leu Arg Cys Val Ile Arg Pro Pro Leu
 85 90 95
 aat ggc gac tcc ctc acc gag tac gaa gcg ggc gtt tgc gaa gat gag 336
 Asn Gly Asp Ser Leu Thr Glu Tyr Glu Ala Gly Val Cys Glu Asp Glu
 100 105 110
 aac tgg act gat gac caa ctg ctt ggt ttt aaa cca tgc aat gaa aac 384
 Asn Trp Thr Asp Asp Gln Leu Leu Gly Phe Lys Pro Cys Asn Glu Asn
 115 120 125
 ctt att gct ggc tgc aat ata atc aat ggg aaa tgt gaa tgt aac acc 432
 Leu Ile Ala Gly Cys Asn Ile Ile Asn Gly Lys Cys Glu Cys Asn Thr
 130 135 140
 att cga acc tgc agc aat ccc ttt gag ttt cca agt cag gat atg tgc 480
 Ile Arg Thr Cys Ser Asn Pro Phe Glu Phe Pro Ser Gln Asp Met Cys
 145 150 155 160

ctt tca gct tta aag aga att gaa gaa gag aag cca gat tgc tcc aag	528
Leu Ser Ala Leu Lys Arg Ile Glu Glu Lys Pro Asp Cys Ser Lys	
165 170 175	
gcc cgc tgt gaa gtc cag ttc tct cca cgt tgt cct gaa gat tct gtt	576
Ala Arg Cys Glu Val Gln Phe Ser Pro Arg Cys Pro Glu Asp Ser Val	
180 185 190	
ctg atc gag ggt tat gct cct cct ggg gag tgc tgt ccc tta ccc agc	624
Leu Ile Glu Gly Tyr Ala Pro Pro Gly Glu Cys Cys Pro Leu Pro Ser	
195 200 205	
cgc tgc gtg tgc aac ccc gca ggc tgt ctg cgc aaa gtc tgc cag ccg	672
Arg Cys Val Cys Ash Pro Ala Gly Cys Leu Arg Lys Val Cys Gln Pro	
210 215 220	
gga aac ctg aac ata cta gtg tca aaa gcc tca ggg aag ccg gga gag	720
Gly Asn Leu Asn Ile Leu Val Ser Lys Ala Ser Gly Lys Pro Gly Glu	
225 230 235 240	
tgc tgt gac ctc tat gag tgc aaa cca gtt ttc ggc gtg gac tgc agg	768
Cys Cys Asp Leu Tyr Glu Cys Lys Pro Val Phe Gly Val Asp Cys Arg	
245 250 255	
act gtg gaa tgc cct cct gtt cag cag acc gcc cgg tgt ccc ccg gac	816
Thr Val Glu Cys Pro Pro Val Gln Gln Thr Ala Arg Cys Pro Pro Asp	
260 265 270	
agc tat gaa act caa gtc aga cta act gca gat ggt tgc tgt cct ttg	864
Ser Tyr Glu Thr Gln Val Arg Leu Thr Ala Asp Gly Cys Pro Leu	
275 280 285	
cca cca aga tgc gag tgt ctc tct ggc tta tgt ggt ttc ccc gtg tgt	912
Pro Pro Arg Cys Glu Cys Leu Ser Gly Leu Cys Gly Phe Pro Val Cys	
290 295 300	
gag gtg gga tcc act ccc cgc ata gtc tct cgt ggc gat ggg aca cct	960
Glu Val Gly Ser Thr Pro Arg Ile Val Ser Arg Gly Asp Gly Thr Pro	
305 310 315 320	
gga aag tgc tgt gat gtc ttt gaa tgt gtt aat gat aca aag cca gcc	1008
Gly Lys Cys Cys Asp Val Phe Glu Cys Val Asn Asp Thr Lys Pro Ala	
325 330 335	
tgc gta ttt aac aat gtg gaa tat tat gat gga gac atg ttt cga atg	1056
Cys Val Phe Asn Asn Val Glu Tyr Tyr Asp Gly Asp Met Phe Arg Met	
340 345 350	
gac aac tgt cgg ttc tgt cga tgc caa ggg ggc gtt gcc atc tgc ttc	1104
Asp Asn Cys Cys Arg Phe Cys Arg Cys Gln Gly Gly Val Ala Ile Cys Phe	
355 360 365	
act gcc cag tgt ggt gag ata aac tgc gag agg tac tac gtg ccc gaa	1152
Thr Ala Gln Cys Gly Glu Ile Asn Cys Glu Arg Tyr Tyr Val Pro Glu	
370 375 380	
gga gag tgc tgc cca gtg tgt gaa gat cca gtg tat cct ttt aat aat	1200
Gly Glu Cys Cys Pro Val Cys Glu Asp Pro Val Tyr Pro Phe Asn Asn	
385 390 395 400	
ccc gct ggc tgc tat gcc aat ggc ctg atc ctt gcc cac gga gac cgg	1248

Pro	Ala	Gly	Cys	Tyr	Ala	Asn	Gly	Leu	Ile	Leu	Ala	His	Gly	Asp	Arg		
			405						410						415		
tgg	cgg	gaa	gac	gac	tgc	aca	ttc	tgc	cag	tgc	gtc	aac	ggg	gaa	cgc	1296	
Trp	Arg	Glu	Asp	Asp	Cys	Thr	Phe	Cys	Gln	Cys	Val	Asn	Gly	Glu	Arg		
			420					425					430				
cac	tgc	gtt	gcg	acc	gtc	tgc	gga	cag	acc	tgc	aca	aac	cct	gtg	aaa	1344	
His	Cys	Val	Ala	Thr	Val	Cys	Gly	Gln	Thr	Cys	Thr	Asn	Pro	Val	Lys		
			435				440					445					
gtg	cct	ggg	gag	tgt	tgc	cct	gtg	tgc	gaa	gaa	cca	acc	atc	atc	aca	1392	
Val	Pro	Gly	Glu	Cys	Cys	Pro	Val	Cys	Glu	Glu	Pro	Thr	Ile	Ile	Thr		
			450			455					460						
gtt	gat	cca	cct	gca	tgt	ggg	gag	tta	tca	aac	tgc	act	ctg	aca	ggg	1440	
Val	Asp	Pro	Pro	Ala	Cys	Gly	Glu	Leu	Ser	Asn	Cys	Thr	Leu	Thr	Gly		
					470					475					480		
aag	gac	tgc	att	aat	ggg	ttc	aaa	cgc	gat	cac	aat	ggg	tgt	cgg	acc	1488	
Lys	Asp	Cys	Ile	Asn	Gly	Phe	Lys	Arg	Asp	His	Asn	Gly	Cys	Arg	Thr		
				485				490						495			
tgt	cag	tgc	ata	aac	agt	gag	tag	acagaagact	gtatgttttt	tctgaggcct						1542	
Cys	Gln	Cys	Ile	Asn	Ser	Glu											
						500											
aatatgatata	tgctaaagca	tattatgtaa	ttgaatatct	ttttcacttc	tgttcagaca											1602	
ttcccttgac	aacctgaaaa	aaaggggaaa	aaa													1635	
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<213> Homo sapiens																	
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atg	tgg	ctg	ccc	cct	gct	ctg	ctc	ctt	ctc	agc	ctc	tca	ggc	tgt	ttc	168	
Met	Trp	Leu	Pro	Pro	Ala	Leu	Leu	Leu	Ser	Leu	Ser	Gly	Cys	Phe			
1				5					10				15				
tcc	atc	caa	ggc	cca	gag	tct	gtg	aga	gcc	cca	gag	cag	ggg	tcc	ctg	216	
Ser	Ile	Gln	Gly	Pro	Glu	Ser	Val	Arg	Ala	Pro	Glu	Gln	Gly	Ser	Leu		
				20				25					30				
acg	gtt	caa	tgc	cac	tat	aag	caa	gga	tgg	gag	acc	tac	att	aag	tgg	264	
Thr	Val	Gln	Cys	His	Tyr	Lys	Gln	Gly	Trp	Glu	Thr	Tyr	Ile	Lys	Trp		
			35				40					45					
tgg	tgc	cga	ggg	gtg	cgc	tgg	gat	aca	tgc	aag	atc	ctc	att	gaa	acc	312	

Trp Cys Arg Gly Val Arg Trp Asp Thr Cys Lys Ile Leu Ile Glu Thr	
50 55 60	
aga ggg tgc gag caa gga gag aag agt gac cgt gtg tcc atc aag gac	360
Arg Gly Ser Glu Gln Gly Glu Lys Ser Asp Arg Val Ser Ile Lys Asp	
65 70 75 80	
aat cag aaa gac cgc acg ttc act gtg acc atg gag ggg ctc agg cga	408
Asn Gln Lys Asp Arg Thr Phe Thr Val Thr Met Glu Gly Leu Arg Arg	
85 90 95	
gat gac gca gat gtt tac tgg tgt ggg att gaa aga aga gga cct gac	456
Asp Asp Ala Asp Val Tyr Trp Cys Gly Ile Glu Arg Arg Gly Pro Asp	
100 105 110	
ctt ggg act caa gtg aaa gtg att gtt gac cca tag ggag cgggtctctc	506
Leu Gly Thr Gln Val Lys Val Ile Val Asp Pro	
115 120	
aacagcaagc tcacctacca acagcaatat ggcagtgttg atcggtctccc acaagaggaa	566
ccactacatg ctccctggat ttgtgaaggt gcccatcttg etcatcttgg tcaactgccat	626
ctctctggttg aaggggtctc agagggtccc tgaggagcca ggggaacagc ctatctacat	686
gaacttctcc gaacctctga ctaa	710

<210> 18
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (108)..(470)

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Met Ser Cys	116
1	
atc ttg gga ttc tgt ttt cca ggc tgt ttc tcc atc caa ggc cca gag	164
Ile Leu Gly Phe Cys Phe Pro Gly Cys Phe Ser Ile Gln Gly Pro Glu	
5 10 15	
tct gtg aga gcc cca gag cag ggg tcc ctg acg gtt caa tgc cac tat	212
Ser Val Arg Ala Pro Glu Gln Gly Ser Leu Thr Val Gln Cys His Tyr	
20 25 30 35	
aag caa gga tgg gag acc tac att aag tgg tgg tgc cga ggg gtg cgc	260
Lys Gln Gly Trp Glu Thr Tyr Ile Lys Trp Trp Cys Arg Gly Val Arg	
40 45 50	
tgg gat aca tgc aag atc etc att gaa acc aga ggg tgc gag caa gga	308
Trp Asp Thr Cys Lys Ile Leu Ile Glu Thr Arg Gly Ser Glu Gln Gly	
55 60 65	


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gag aag agt gac cgt gtg tcc atc aag gac aat cag aaa gac cgc acg      356
Glu Lys Ser Asp Arg Val Ser Ile Lys Asp Asn Gln Lys Asp Arg Thr
      70              75              80

ttc act gtg acc atg gag ggg ctc agg cga gat gac gca gat gtt tac      404
Phe Thr Val Thr Met Glu Gly Leu Arg Arg Asp Asp Ala Asp Val Tyr
      85              90              95

tgg tgt ggg att gaa aga aga gga cct gac ctt ggg act caa gtg aaa      452
Trp Cys Gly Ile Glu Arg Arg Gly Pro Asp Leu Gly Thr Gln Val Lys
     100             105             110             115

gtg att gtt gac cca tag ggagcg gcttctctcaa cagcaagctc acctaccaac      506
Val Ile Val Asp Pro
              120

agcaatatgg cagtgttgat cggtctccac aagaggaacc actacatgct cctggatttt      566

gtgaagggtgc ccatcttgct catcttggtc actgccatcc tctggttgaa ggggtctcag      626

agggtccctg aggagccagg ggaacagcct atctacatga acttctccga acctctgact      686

aa                                                                    688

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<210> 19
<211> 1700
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (232)..(1272)

<220>
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<222> (1)...(1700)
<223> n = a,t,c or g

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<400> 19
tttcgtaaga ccacagaaac cctcctgtaa tggaacaagt tggctttggt actaattgca      60
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acagcatagg gaaaactagg ttntnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      180
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnagg c atg gag      237
                               Met Glu
                               1

aga aaa ttt atg tcc ttg caa cca tcc atc tcc gta tca gaa atg gaa      285
Arg Lys Phe Met Ser Leu Gln Pro Ser Ile Ser Val Ser Glu Met Glu
      5              10              15

cca aat ggc acc ttc agc aat aac aac agc agg aac tgc aca att gaa      333
Pro Asn Gly Thr Phe Ser Asn Asn Ser Arg Asn Cys Thr Ile Glu
      20              25              30

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aac ttc aag aga gaa ttt ttc cca att gta tat ctg ata ata ttt ttc Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile Phe Phe 35 40 45 50	381
tgg gga gtc ttg gga aat ggg ttg tcc ata tat gtt ttc ctg cag cct Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu Gln Pro 55 60 65	429
tat aag aag tcc aca tct gtg aac gtt ttc atg cta aat ctg gcc att Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu Ala Ile 70 75 80	477
tca gat ctc ctg ttc ata agc acg ctt ccc ttc agg gct gac tat tat Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp Tyr Tyr 85 90 95	525
ctt aga ggc tcc aat tgg ata ttt gga gac ctg gcc agg att atg Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg Ile Met 100 105 110	573
tct tat tcc ttg tat gtc aac atg tac agc agt att tat ttc ctg acc Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ile Tyr Phe Leu Thr 115 120 125 130	621
gtg ctg agt gtt gtg cgt ttc ctg gca atg gtt cac ccc ttt cgg ctt Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe Arg Leu 135 140 145	669
ctg cat gtc acc agc atc agg agt gcc tgg atc ctc tgt ggg atc ata Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly Ile Ile 150 155 160	717
tgg atc ctt atc atg gct tcc tca ata atg ctc ctg gac agt ggc tct Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser Gly Ser 165 170 175	765
gag cag aac ggc agt gtc aca tca tgc tta gag ctg aat ctc tat aaa Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu Tyr Lys 180 185 190	813
att gct aag ctg cag acc atg aac tat att gcc ttg gtg gtg ggc tgc Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val Gly Cys 195 200 205 210	861
ctg ctg cca ttt ttc aca ctc agc atc tgt tat ctg ctg atc att cgg Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile Ile Arg 215 220 225	909
gtt ctg tta aaa gtg gag gtc cca gaa tcg ggg ctg cgg gtt tct cac Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val Ser His 230 235 240	957
agg aag gca ctg acc acc atc atc atc acc ttg atc atc ttc ttc ttg Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe Phe Leu 245 250 255	1005
tgt ttc ctg ccc tat cac aca ctg agg acc gtc cac ttg acg aca tgg Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr Thr Trp 260 265 270	1053
aaa gtg ggt tta tgc aaa gac aga ctg cat aaa gct ttg gtt atc aca	1101

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<210> 20
<211> 1671
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (417)..(1628)
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agacgcggca cgcgcctct cgcacacct gaactctgac ccagctccc acactgtcgc		120
ctatcacccg cccactctcc gtgcccgctg tccctaaaa gctggggcct gggacaggaa		180
cgcagacaaa tgcagccaat ggcgtcacgc gcggtgcccc tactcccaat cgaaaggcgt		240
ggctgagggg aacgcggtgg gaaccgcccc cgactccagg cgactcctg gccggcgagg		300
ggagagcgtc cccgtcagct gagagcatcc tactcggtc agttcctcg gcgagttacg		360
gggacgacct gcgggagcac gcgggcagtg gccgcagcct gaagcccagg agagcg		416
atg gag acg tat gcg gag gtt ggg aag gag ggc aag cct tcc tgt gca		464
Met Glu Thr Tyr Ala Glu Val Gly Lys Glu Gly Lys Pro Ser Ser Cys Ala		

1	5	10	15	
tcg gtg gat ctg cag gga gac agc tcc tta cag gtg gag att tct gac				512
Ser Val Asp Leu Gln Gly Asp Ser Ser Leu Gln Val Glu Ile Ser Asp	20	25	30	
gca gtg agt gag cgg gac aag gtg aaa ttc act gtt caa aca aag agc				560
Ala Val Ser Glu Arg Asp Lys Val Lys Phe Thr Val Gln Thr Lys Ser	35	40	45	
tgk ctc cct cac ttc gcc cag acc gag ttc tca gtc gtg cgg cag cac				608
Cys Leu Pro His Phe Ala Gln Thr Glu Phe Ser Val Val Arg Gln His	50	55	60	
gag gag ttc atc tgg ctg cat gat gcc tac gtg gag aat gag gag tac				656
Glu Glu Phe Ile Trp Leu His Asp Ala Tyr Val Glu Asn Glu Glu Tyr	65	70	75	80
gcc ggc ctc atc atc ccc cca gcc cct ccg agg cca gac ttt gag gct				704
Ala Gly Leu Ile Ile Pro Pro Ala Pro Pro Arg Pro Asp Phe Glu Ala	85	90	95	
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Ser Arg Glu Lys Leu Gln Lys Leu Gly Glu Gly Asp Ser Ser Val Thr	100	105	110	
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Arg Glu Glu Phe Ala Lys Met Lys Gln Glu Leu Glu Ala Glu Tyr Leu	115	120	125	
gcc atc ttt aag aag aca gtt gcg atg cac gaa gtc ttt ctg cag cgc				848
Ala Ile Phe Lys Lys Thr Val Ala Met His Glu Val Phe Leu Gln Arg	130	135	140	
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Leu Ala Ala His Pro Thr Leu Arg Arg Asp His Asn Phe Phe Val Phe	145	150	155	160
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Leu Glu Tyr Gly Gln Asp Leu Ser Val Arg Gly Lys Asn Arg Lys Glu	165	170	175	
ctc ctc gga ggg ttt ctg agg aat att gtg aag tcc gcg gat gaa gcc				992
Leu Leu Gly Gly Phe Leu Arg Asn Ile Val Lys Ser Ala Asp Glu Ala	180	185	190	
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Leu Ile Thr Gly Met Ser Gly Leu Lys Glu Val Asp Asp Phe Phe Glu	195	200	205	
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His Glu Arg Thr Phe Leu Leu Glu Tyr His Thr Arg Ile Arg Asp Ala	210	215	220	
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Cys Leu Arg Ala Asp Arg Val Met Arg Ala His Lys Cys Leu Ala Asp	225	230	235	240
gat tat atc cct atc tca gct gcg ctg agc agt ctg gga aca cag gaa				1184
Asp Tyr Ile Pro Ile Ser Ala Ala Leu Ser Ser Leu Gly Thr Gln Glu	245	250	255	

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Val Asn Gln Leu Arg Thr Ser Phe Leu Lys Leu Ala Glu Leu Phe Glu	
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Arg Leu Arg Lys Leu Glu Gly Arg Val Ala Ser Asp Glu Asp Leu Lys	
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Leu Ser Asp Met Leu Arg Tyr Tyr Met Arg Asp Ser Gln Ala Ala Lys	
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Asn Lys Ala Leu Asp Lys Ala Arg Thr Arg Asn Arg Glu Val Arg Pro	
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Ala Glu Ser His Gln Gln Leu Cys Cys Gln Arg Phe Glu Arg Leu Ser	
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Asp Ser Ala Lys Gln Glu Leu Met Asp Phe Lys Ser Arg Arg Val Ser	
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Ser Phe Arg Lys Asn Leu Ile Glu Leu Ala Glu Leu Glu Leu Lys His	
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gcc gct gcc tcc caa gcc gag gtc gag tcc gag gca gga tgg gcc atg	96
Ala Ala Ala Ser Gln Ala Glu Val Glu Ser Glu Ala Gly Trp Gly Met	

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cgg gca gcc ctc cgc gcc ctt cgc ctg cgc tgc cgc acc cag tgt gcc Arg Ala Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala 65 70 75 80			240
gcc gac ttc cgg tgg gag ctg gac ccc gac tgg tcc ccc agc ccg gcc Ala Asp Phe Pro Gly Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala 85 90 95			288
cag gcc tcg ggc gcc gcc gcc ctg cgc gac ctg agc ttc ttc ggg ggc Gln Ala Ser Gly Ala Ala Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly 100 105 110			336
ctt ctg cgt cgc gct gcc tgc ctg cgc cgc tgc ctc ggg ccg ccg gcc Leu Leu Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala 115 120 125			384
gcc cac tcg ctc agc gaa gag atg gag ctg gag ttc cgc aag cgg agc Ala His Ser Leu Ser Gln Glu Met Glu Leu Glu Phe Arg Lys Arg Ser 130 135 140			432
ccc tac aac tac ctg cag gtc gcc tac ttc aag gtg cag acc tgc ctg Pro Tyr Asn Tyr Leu Leu Val Ala Tyr Phe Lys Val Gln Thr Cys Leu 145 150 155 160			480
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305 310 315 320	
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Val	Leu	Arg	Ser	Leu	His	Ala	Ala	Gly	Leu	Leu	Gly	Pro	Ser	Leu	Arg		
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Asp	Pro	Leu	Asp	Ala	Leu	Pro	Val	His	His	Ala	Ala	Arg	Ala	Gly	Lys		
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Gln Leu Pro Pro Pro Pro Pro Gly Tyr Pro Ala Pro Lys Pro Pro Val	
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			675					680					685			
acc	ggc	agc	acc	aag	tct	ttc	aac	atg	atg	tcc	ccg	acg	ggc	gac	aac	2112
Thr	Gly	Ser	Thr	Lys	Ser	Phe	Asn	Met	Met	Ser	Pro	Thr	Gly	Asp	Asn	
			690				695				700					
tgc	gag	cta	ctg	gct	gag	att	aag	gca	ggc	aag	agc	ctg	aag	ccg	acg	2160
Ser	Glu	Leu	Leu	Ala	Glu	Ile	Lys	Ala	Gly	Lys	Ser	Leu	Lys	Pro	Thr	
	705					710				715				720		
ccc	cag	agc	aag	ggg	ctg	acc	aca	gtg	ttc	tca	ggc	atc	ggg	cag	ccg	2208
Pro	Gln	Ser	Lys	Gly	Leu	Thr	Thr	Val	Phe	Ser	Gly	Ile	Gly	Gln	Pro	
				725					730					735		
gcc	ttc	cag	ccc	gat	tcg	ccg	ctg	cct	tct	gtg	tca	cct	gca	ctg	tca	2256
Ala	Phe	Gln	Pro	Asp	Ser	Pro	Leu	Pro	Ser	Val	Ser	Pro	Ala	Leu	Ser	
				740					745				750			
cca	gtc	cgg	agc	ccc	aca	ccg	cca	gct	gcg	ggg	ttt	cag	ccg	ctg	ctc	2304
Pro	Val	Arg	Ser	Pro	Thr	Pro	Pro	Ala	Ala	Gly	Phe	Gln	Pro	Leu	Leu	
		755						760				765				
aat	gga	agc	ttg	gtt	ccc	gtg	ccg	ccc	act	act	cct	gcg	ccg	gga	gtg	2352
Asn	Gly	Ser	Leu	Val	Pro	Val	Pro	Pro	Thr	Thr	Pro	Ala	Pro	Gly	Val	
			770				775					780				
cag	ctg	gac	gtg	gag	gct	ctc	atc	ccc	acg	cac	gat	gag	cag	ggc	cgg	2400
Gln	Leu	Asp	Val	Glu	Ala	Leu	Ile	Pro	Thr	His	Asp	Glu	Gln	Gly	Arg	
	785					790				795					800	
ccc	atc	ccc	gag	tgg	aag	cgc	cag	gtg	atg	gtg	cgc	aag	atg	cag	ctg	2448
Pro	Ile	Pro	Glu	Trp	Lys	Arg	Gln	Val	Met	Val	Arg	Lys	Met	Gln	Leu	
				805					810					815		
aag	atg	cag	gag	gag	gag	gag	cag	agg	cgg	aag	gag	gag	gag	gag	gag	2496
Lys	Met	Gln	Glu	Glu	Glu	Glu	Gln	Arg	Arg	Lys	Glu	Glu	Glu	Glu	Glu	

820	825	830	
gcc cgg ctg gcc agc atg ccc gcc tgg agg cgg gac ctc ctg cgg aag			2544
Ala Arg Leu Ala Ser Met Pro Ala Trp Arg Arg Asp Leu Leu Arg Lys	840	845	
835			
aag ctg gaa gaa gag agg gag cag aag cgg aaa gag gag gag cga cag			2592
Lys Leu Glu Glu Glu Arg Glu Gln Lys Arg Lys Glu Glu Glu Arg Gln	855	860	
850			
aag cag gag gag ctg cgg cgg gag aag gaa cag tca gag aag ctg cgg			2640
Lys Gln Glu Glu Leu Arg Arg Glu Lys Glu Gln Ser Glu Lys Leu Arg	870	875	
865		880	
acg ctg ggc tac gat gag agc aag ctg gcg ccc tgg cag cga cag gtc			2688
Thr Leu Gly Tyr Asp Glu Ser Lys Leu Ala Pro Trp Gln Arg Gln Val	885	890	
		895	
atc ctg aag aag ggg gac atc gct aag tac tag aggccgca gactcctgtc			2739
Ile Leu Lys Lys Gly Asp Ile Ala Lys Tyr	900	905	
cgcagcctcg cagctccgtg gggccctccg cccagcccc agccagccag gccctggtgg			2799
aaaggctggg agccgcacag cccctccctc ctgcgctgga aaccctccct gaacccacc			2859
ctggcccccc gtatccccag cctctggcaa cactggagtg cacacgccgc caagggtgcc			2919
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 <213> Homo sapiens

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gtg ctg agg tcg ctg cac gcc gca ggc ctc ctg ggg ccc tgg ctg cgc	96
Val Leu Arg Ser Leu His Ala Ala Gly Leu Leu Gly Pro Ser Leu Arg	
20 25 30	
gac cgg ctg gac gcg ctg ccc gtg cac cac gcg gcc cgc gct ggg aag	144
Asp Pro Leu Asp Ala Leu Pro Val His His Ala Ala Arg Ala Gly Lys	
35 40 45	
ctg cac tgt ctg cgc ttc ctg gtg gag gaa gcc gcc ctc ccc gcc gcg	192
Leu His Cys Leu Arg Phe Leu Val Glu Glu Ala Ala Leu Pro Ala Ala	
50 55 60	

gcc cgc gcc cgc aac ggc gcc aca cgc gcc cac gac gcc tcc gcc acc Ala Arg Ala Arg Asn Gly Ala Thr Pro Ala His Asp Ala Ser Ala Thr 65 70 75 80	240
ggc cac ctc gcc tgc ctg cag tgg ctg ctg tcg cag ggc ggc tgc aga Gly His Leu Ala Cys Leu Gln Trp Leu Ser Gln Gly Gly Cys Arg 85 90 95	288
gtg cag gca ttc cct gag tcc ctg gga gtc agg gct gtg gcc ctg ggc Val Gln Ala Phe Pro Glu Ser Leu Gly Val Arg Ala Val Ala Leu Gly 100 105 110	336
ctg gtg cca gtc tcc tgc cgt gac aac cag gac aaa gac aat tct ggt Leu Val Pro Val Ser Cys Arg Asp Asn Gln Asp Lys Asp Asn Ser Gly 115 120 125	384
gcc aca gtc ttg cat ctg gct gcc cgc ttc ggc cac ccc gag gtg gtg Ala Thr Val Leu His Leu Ala Ala Arg Phe Gly His Pro Glu Val Val 130 135 140	432
aac tgg ctc ttg cat cat ggc ggt ggg gac ccc acc gcg gcc aca gac Asn Trp Leu Leu His His Gly Gly Asp Pro Thr Ala Ala Thr Asp 145 150 155 160	480
atg ggc gcc ctg cct atc cac tac gct gcc gcc aaa gga gac ttc ccc Met Gly Ala Leu Pro Ile His Tyr Ala Ala Lys Gly Asp Phe Pro 165 170 175	528
tcc ctg agg ctt ctc gtc gag cac tac cct gag gga gtg aat gcc caa Ser Leu Arg Leu Leu Val Glu His Tyr Pro Glu Gly Val Asn Ala Gln 180 185 190	576
acc aag aac ggt gcc acg ccc ctg tac ctg gcg tgc cag gag ggc cac Thr Lys Asn Gly Ala Thr Pro Leu Tyr Leu Ala Cys Gln Glu Gly His 195 200 205	624
ctg gag gtg acc cag tac ctg gtg cag gaa tgc ggc gca gac ccg cac Leu Glu Val Thr Gln Tyr Leu Val Gln Glu Cys Gly Ala Asp Pro His 210 215 220	672
gcg cgc gcc cac gac ggc atg acc cgc ctg cac gcc gcg gcg cag atg Ala Arg Ala His Asp Gly Met Thr Pro Leu His Ala Ala Ala Gln Met 225 230 235 240	720
ggc cac agc cca gtc atc gtg tgg ttg gtg agc tgc acc gac gtg agc Gly His Ser Pro Val Ile Val Trp Leu Val Ser Cys Thr Asp Val Ser 245 250 255	768
ctg tcc gag cag gac aaa gac ggc gcc acc gcc atg cac ttc gcg gcg Leu Ser Glu Gln Asp Lys Asp Gly Ala Thr Ala Met His Phe Ala Ala 260 265 270	816
agc cgc ggc cac acc aag gtg ctc agc tgg ctg ctg ctg cac ggc ggg Ser Arg Gly His Thr Lys Val Leu Ser Trp Leu Leu Leu His Gly Gly 275 280 285	864
gag atc tcg gct gac ctg tgg ggc ggg acc ccg ctg cac gac gcc gcc Glu Ile Ser Ala Asp Leu Trp Gly Gly Thr Pro Leu His Asp Ala Ala 290 295 300	912
gag aac ggg gag cta gag tgc tgc cag atc ctg gta gtg aac ggc gcg	960

Glu Asn Gly Glu Leu Glu Cys Cys Gln Ile Leu Val Val Asn Gly Ala	
305 310 315 320	
gag ctg gac gtc cgc gac cgc gac ggg tac acg gcc gcc gac ctg tgc	1008
Glu Leu Asp Val Arg Asp Arg Asp Gly Tyr Thr Ala Ala Asp Leu Ser	
325 330 335	
gac ttc aac ggc cac agc cac tgc acc cgc tac ctg cgc acg gtg gag	1056
Asp Phe Asn Gly His Ser His Cys Thr Arg Tyr Leu Arg Thr Val Glu	
340 345 350	
aac ctg agc gtg gag cac cgc gtg ctt tcc cgg gat cca tcc gca gag	1104
Asn Leu Ser Val Glu His Arg Val Leu Ser Arg Asp Pro Ser Ala Glu	
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ctg gag gct aag cag ccg gat tca ggc atg tcc tca ccc aat acc acg	1152
Leu Glu Ala Lys Gln Pro Asp Ser Gly Met Ser Pro Asn Thr Thr	
370 375 380	
gtg tcg gtc cag ccg ctg aac ttt gac ctg agc tcg cct acc agc acc	1200
Val Ser Val Gln Pro Leu Asn Phe Asp Leu Ser Ser Pro Thr Ser Thr	
385 390 395 400	
ctc tcc aac tac gac tcc tgc tcc tcc agc cac tcc agc atc aag ggc	1248
Leu Ser Asn Tyr Asp Ser Cys Ser Ser Ser His Ser Ser Ile Lys Gly	
405 410 415	
cag cac cct cca tgt ggg ctt tcc agc gct aga gct gca gac ata cag	1296
Gln His Pro Pro Cys Gly Leu Ser Ser Ala Arg Ala Ala Asp Ile Gln	
420 425 430	
agc tac atg gac atg ctg aac ccg gag ctg ggc ctg cct cgg ggc acg	1344
Ser Tyr Met Asp Met Leu Asn Pro Glu Leu Gly Leu Pro Arg Gly Thr	
435 440 445	
att ggg aag ccc aca ccc cca cca ccc cca agc ttc ccc ccg cca	1392
Ile Gly Lys Pro Thr Pro Pro Pro Pro Pro Pro Ser Phe Pro Pro Pro	
450 455 460	
ccc ccg ccc cca ggc acc caa ctg ccc cca ccc cca cct ggc tac cca	1440
Pro Pro Pro Pro Gly Thr Gln Leu Pro Pro Pro Pro Pro Gly Tyr Pro	
465 470 475 480	
gct ccc aag cct cct gta gga cca cag gca gct gac atc tac atg cag	1488
Ala Pro Lys Pro Pro Val Gly Pro Gln Ala Ala Asp Ile Tyr Met Gln	
485 490 495	
acc aag aac aaa ctc cgc cac gtg gag aca gag gcc ctc aag aag gag	1536
Thr Lys Asn Lys Leu Arg His Val Glu Thr Glu Ala Leu Lys Lys Glu	
500 505 510	
ctg agc tcc tgt gac ggc cac gac ggg ctg cgg agg cag gac tcc agc	1584
Leu Ser Ser Cys Asp Gly His Asp Gly Leu Arg Arg Gln Asp Ser Ser	
515 520 525	
cgc aag ccc cgc gcc ttc agc aag cag ccc agc acg ggg gac tac tac	1632
Arg Lys Pro Arg Ala Phe Ser Lys Gln Pro Ser Thr Gly Asp Tyr Tyr	
530 535 540	
cgg cag ctg ggc cgc tgc ccc ggc gag acg ctg gcc gca cgc ccg ggc	1680
Arg Gln Leu Gly Arg Cys Pro Gly Glu Thr Leu Ala Ala Arg Pro Gly	

545	550	555	560	
atg gcg cac agc gag gag gcg gcg ctg ctt cct ggg aac cat gtt cct Met Ala His Ser Glu Glu Ala Ala Leu Leu Pro Gly Asn His Val Pro	565	570	575	1728
aac ggc tgc gcc gcg gac ccc aag gcg tcc agg gag ctg cca ccg ccg Asn Gly Cys Ala Ala Asp Pro Lys Ala Ser Arg Glu Leu Pro Pro Pro	580	585	590	1776
ccc cca ccg ccg ccg ccg ccc ctg ccg gag gcc gcg agt tgc cca ccg Pro Pro Pro Pro Pro Pro Pro Leu Pro Glu Ala Ala Ser Ser Pro Pro	595	600	605	1824
ccg gcc ccg cct ctg ccc ctc gag agc gct ggc cct ggc tgc ggg cag Pro Ala Pro Pro Leu Pro Leu Glu Ser Ala Gly Pro Gly Cys Gly Gln	610	615	620	1872
cgc cgc tcc tcc tgc tcc acc gcc agc acc aag tct ttc aac atg atg Arg Arg Ser Ser Ser Ser Thr Gly Ser Thr Lys Ser Phe Asn Met Met	625	630	635	1920
tcc ccg acg ggc gac aac tgc gag cta ctg gct gag att aag gca ggc Ser Pro Thr Gly Asp Asn Ser Glu Leu Leu Ala Glu Ile Lys Ala Gly	645	650	655	1968
aag agc ctg aag ccg acg ccc cag agc aag ggg ctg acc aca gtg ttc Lys Ser Leu Lys Pro Thr Pro Gln Ser Lys Gly Leu Thr Val Phe	660	665	670	2016
tca ggc atc ggg cag ccg gcc ttc cag ccc gat tgc ccg ctg cct tct Ser Gly Ile Gly Gln Pro Ala Phe Gln Pro Asp Ser Pro Leu Pro Ser	675	680	685	2064
gtg tca cct gca ctg tca cca gtc cgg agc ccc aca ccg cca gct gcg Val Ser Pro Ala Leu Ser Pro Val Arg Ser Pro Thr Pro Pro Ala Ala	690	695	700	2112
ggg ttt cag ccg ctg ctc aat gga agc ttg gtt ccc gtg ccg ccc act Gly Phe Gln Pro Leu Leu Asn Gly Ser Leu Val Pro Val Pro Pro Thr	705	710	715	2160
act cct gcg ccg gga gtg cag ctg gac gtg gag gct ctc atc ccc acg Thr Pro Ala Pro Gly Val Gln Leu Asp Val Glu Ala Leu Ile Pro Thr	725	730	735	2208
cac gat gag cag ggc cgg ccc atc ccc gag tgg aag cgc cag gtg atg His Asp Glu Gln Gly Arg Pro Ile Pro Glu Trp Lys Arg Gln Val Met	740	745	750	2256
gtg cgc aag atg cag ctg aag atg cag gag gag gag gag cag agg ccg Val Arg Lys Met Gln Leu Lys Met Gln Glu Glu Glu Glu Gln Arg Arg	755	760	765	2304
aag gag gag gag gag gag gcc ccg ctg gcc agc atg ccc gcc tgg agg Lys Glu Glu Glu Glu Glu Ala Arg Leu Ala Ser Met Pro Ala Trp Arg	770	775	780	2352
cgg gac ctc ctg cgg aag aag ctg gaa gaa gag agg gag cag aag ccg Arg Asp Leu Leu Arg Lys Lys Leu Glu Glu Glu Arg Glu Gln Lys Arg	785	790	795	2400


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aaa gag gag gag cga cag aag cag gag gag ctg cgg cgg gag aag gaa      2448
Lys Glu Glu Glu Arg Gln Lys Gln Glu Glu Leu Arg Arg Glu Lys Glu
      805                      810                      815

cag tca gag aag ctg cgg acg ctg ggc tac gat gag agc aag ctg gcg      2496
Gln Ser Glu Lys Leu Arg Thr Leu Gly Tyr Asp Glu Ser Lys Leu Ala
      820                      825                      830

ccc tgg cag cga cag gtc atc ctg aag aag ggg gac atc gct aag tac      2544
Pro Trp Gln Arg Gln Val Ile Leu Lys Lys Gly Asp Ile Ala Lys Tyr
      835                      840                      845

tag aggc cgcagactcc tgctcgcagc ctgcagctc cgtggggccc tccgccccag      2601

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<222> (189) .. (1955)

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agccgcgaag gcgccaggcc ctgcgcaccg cggagctgag cctgggtcgc aactagcgcc      180
gcgagttg atg ctg cgg ctg caa gcg cca ggg ccc gcg ggg cgg ccg cgc      230
      Met Leu Arg Leu Gln Ala Pro Gly Pro Ala Gly Arg Pro Arg
      1                      5                      10

tgc ttc cct ctg cgc gcc gcg cgc ctc ttc acg cgt ttc gcc gag gcc      278
Cys Phe Pro Leu Arg Ala Ala Arg Leu Phe Thr Arg Phe Ala Glu Ala
      15                      20                      25                      30

ggg cgc agc acc ctg cgg ctc ccc gcc cac gac acc ccc ggg gcc ggc      326
Gly Arg Ser Thr Leu Arg Leu Pro Ala His Asp Thr Pro Gly Ala Gly
      35                      40                      45

gca gtg cag ctg ctg ctc tog gac tgc ccc cca gac cgc ctg cgc cgc      374
Ala Val Gln Leu Leu Ser Asp Cys Pro Pro Asp Arg Leu Arg Arg
      50                      55                      60

ttc ctg cgc aca ttg cgc ctc aag ctg gct gcg gcc ccg ggt ccc ggg      422
Phe Leu Arg Thr Leu Arg Leu Lys Leu Ala Ala Ala Pro Gly Pro Gly
      65                      70                      75

ccg gcc tcc gcc cga gcg cag ctg ctg ggc ccg cgg ccc cgc gac ttc      470
Pro Ala Ser Ala Arg Ala Gln Leu Leu Gly Pro Arg Pro Arg Asp Phe
      80                      85                      90

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gtc acc atc agc cct gtg cag ccc gag gag cgg cgg ctc agg gcg gcc	518
Val Thr Ile Ser Pro Val Gln Pro Glu Glu Arg Arg Leu Arg Ala Ala	
95 100 105 110	
acc egg gtt ccg gac act acg ctg gtg aag cgg cct gtg gag ccc cag	566
Thr Arg Val Pro Asp Thr Thr Leu Val Lys Arg Pro Val Glu Pro Gln	
115 120 125	
gct ggg gcc gag cct agc aca gaa gcc cca agg tgg ccc ctg cct gtg	614
Ala Gly Ala Glu Pro Ser Thr Glu Ala Pro Arg Trp Pro Leu Pro Val	
130 135 140	
aag agg ctg agc ttg ccc tcc acc aag cca cag ctt tct gag gaa cag	662
Lys Arg Leu Ser Leu Pro Ser Thr Lys Pro Gln Leu Ser Glu Glu Gln	
145 150 155	
gct gct gtg ctg agg gcc gcc ctg aaa ggc cag agc atc ttc ttc act	710
Ala Ala Val Leu Arg Ala Ala Leu Lys Gly Gln Ser Ile Phe Phe Thr	
160 165 170	
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Gly Ser Ala Gly Thr Gly Lys Ser Tyr Leu Lys Arg Ile Leu Gly	
175 180 185 190	
tca ctg ccc ccc aca ggc act gag gcc act gcc agc act ggg gtg gca	806
Ser Leu Pro Pro Thr Gly Thr Glu Ala Thr Ala Ser Thr Gly Val Ala	
195 200 205	
gcc tgc cac atc ggg ggc acc acc ctc cat gcc ttt gca ggc atc ggc	854
Ala Cys His Ile Gly Gly Thr Thr Leu His Ala Phe Ala Gly Ile Gly	
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Ser Gly Gln Ala Pro Leu Ala Gln Cys Val Ala Leu Ala Gln Arg Pro	
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Gly Val Arg Gln Gly Trp Leu Asn Cys Gln Arg Leu Val Ile Asp Glu	
240 245 250	
atc tca atg gtg gag gca gac ctg ttt gac aaa ctg gag gcc gtg gcc	998
Ile Ser Met Val Glu Ala Asp Leu Phe Asp Lys Leu Glu Ala Val Ala	
255 260 265 270	
aga gct gtc cgg cag cag aac aag cca ttc gga ggg atc cag ctc atc	1046
Arg Ala Val Arg Gln Gln Asn Lys Pro Phe Gly Gly Ile Gln Leu Ile	
275 280 285	
atc tgt ggg gac ttt ctg cag ctg cca cct gtg acc aag ggc tcc cag	1094
Ile Cys Gly Asp Phe Leu Gln Leu Pro Pro Val Thr Lys Gly Ser Gln	
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Pro Pro Arg Phe Cys Phe Gln Ser Lys Ser Trp Lys Arg Gly Val Pro	
305 310 315	
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Val Thr Leu Glu Leu Thr Lys Gly Gly Arg Gln Ala Asn Gln Thr Phe	
320 325 330	
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Phe	Phe	Leu	Leu	Gln	Ala	Val	Arg	Leu	Gly	Arg	Cys	Ser	Asp	Glu	Val	
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Thr	Arg	Gln	Leu	Gln	Ala	Thr	Ala	Ser	His	Lys	Val	Gly	Arg	Asp	Gly	
				355				360						365		
att	gtg	gcc	acg	agg	ctc	tgc	acc	cac	cag	gat	gat	gtg	gcc	ctc	acc	1334
Ile	Val	Ala	Thr	Arg	Leu	Cys	Thr	His	Gln	Asp	Asp	Val	Ala	Leu	Thr	
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aac	gag	agg	cgg	ctt	cag	gag	ctg	cca	ggt	aag	gta	cac	aga	ttt	gag	1382
Asn	Glu	Arg	Arg	Leu	Gln	Glu	Leu	Pro	Gly	Lys	Val	His	Arg	Phe	Glu	
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gct	atg	gac	agc	aac	cct	gag	ctg	gcc	agt	acc	ctg	gat	gcc	cag	tgt	1430
Ala	Met	Asp	Ser	Asn	Pro	Glu	Leu	Ala	Ser	Thr	Leu	Asp	Ala	Gln	Cys	
				400				405						410		
cct	gtt	agc	cag	ctc	ctt	caa	cta	aag	ctg	ggg	gcc	cag	gtg	atg	ctg	1478
Pro	Val	Ser	Gln	Leu	Leu	Gln	Leu	Lys	Leu	Gly	Ala	Gln	Val	Met	Leu	
				415				420						425		
gtg	aaa	aac	tta	tgc	gtg	tct	cgg	ggc	ctg	gtg	aat	ggt	gcc	cga	ggg	1526
Val	Lys	Asn	Leu	Ser	Val	Ser	Arg	Gly	Leu	Val	Asn	Gly	Ala	Arg	Gly	
				435					440					445		
gtg	gta	gtt	ggg	ttc	gag	gca	gaa	ggg	aga	ggg	cta	ccc	cag	gtg	cgg	1574
Val	Val	Val	Gly	Phe	Glu	Ala	Glu	Gly	Arg	Gly	Leu	Pro	Gln	Val	Arg	
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ttc	ctg	tgt	gga	gtc	act	gag	gtc	atc	cac	gct	gac	cgc	tgg	acg	gtg	1622
Phe	Leu	Cys	Gly	Val	Thr	Glu	Val	Ile	His	Ala	Asp	Arg	Trp	Thr	Val	
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cag	gcc	acc	ggg	ggc	cag	ctc	ctc	agt	cgg	cag	cag	ctg	ccc	ctc	cag	1670
Gln	Ala	Thr	Gly	Gly	Gln	Leu	Leu	Ser	Arg	Gln	Gln	Leu	Pro	Leu	Gln	
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ctg	gcc	tgg	gcg	atg	tcc	atc	cac	aag	agc	caa	ggc	atg	acc	ctg	gat	1718
Leu	Ala	Trp	Ala	Met	Ser	Ile	His	Lys	Ser	Gln	Gly	Met	Thr	Leu	Asp	
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Cys	Val	Glu	Ile	Ser	Leu	Gly	Arg	Val	Phe	Ala	Ser	Gly	Gln	Ala	Tyr	
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gtg	gcc	ctt	tct	cgg	gcc	cgc	agc	ctg	cag	ggc	cta	cgt	gtg	ctg	gac	1814
Val	Ala	Leu	Ser	Arg	Ala	Arg	Ser	Leu	Gln	Gly	Leu	Arg	Val	Leu	Asp	
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Phe	Asp	Pro	Met	Ala	Val	Arg	Cys	Asp	Pro	Arg	Val	Leu	His	Phe	Tyr	
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Ala	Thr	Leu	Arg	Arg	Gly	Arg	Ser	Leu	Ser	Leu	Ser	Pro	Pro	Asp	Asp	
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gat	gag	gca	gcc	tca	gac	cag	gag	aac	atg	gac	cca	atc	ctc	tga	gcc	1958
Asp	Glu	Ala	Ala	Ser	Asp	Gln	Glu	Asn	Met	Asp	Pro	Ile	Leu			

575	580	585	
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Met Leu Arg Leu Gln Ala Pro Gly Pro Ala Gly Arg Pro Arg	
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Cys Phe Pro Leu Arg Ala Ala Arg Leu Phe Thr Arg Phe Ala Glu Ala	
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Gly Arg Ser Thr Leu Arg Leu Pro Ala His Asp Thr Pro Gly Ala Gly	
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Ala Val Gln Leu Leu Leu Ser Asp Cys Pro Pro Asp Arg Leu Arg Arg	
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Phe	Leu	Arg	Thr	Leu	Arg	Leu	Lys	Leu	Ala	Ala	Ala	Pro	Gly	Pro	Gly	
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Pro	Ala	Ser	Ala	Arg	Ala	Gln	Leu	Leu	Gly	Pro	Arg	Pro	Arg	Asp	Phe	
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Val	Thr	Ile	Ser	Pro	Val	Gln	Pro	Glu	Glu	Arg	Arg	Leu	Arg	Ala	Ala	
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Thr	Arg	Val	Pro	Asp	Thr	Thr	Leu	Val	Lys	Arg	Pro	Val	Glu	Pro	Gln	
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Ala	Gly	Ala	Glu	Pro	Ser	Thr	Glu	Ala	Pro	Arg	Trp	Pro	Leu	Pro	Val	
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Lys	Arg	Leu	Ser	Leu	Pro	Ser	Thr	Lys	Pro	Gln	Leu	Ser	Glu	Glu	Gln	
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Gly	Ser	Ala	Gly	Thr	Gly	Lys	Ser	Tyr	Leu	Leu	Lys	Arg	Ile	Leu	Gly	
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tca	ctg	ccc	ccc	aca	ggc	act	gag	gcc	act	gcc	agc	act	ggg	gtg	gca	806
Ser	Leu	Pro	Pro	Thr	Gly	Thr	Glu	Ala	Thr	Ala	Ser	Thr	Gly	Val	Ala	
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Ser	Gly	Gln	Ala	Pro	Leu	Ala	Gln	Cys	Val	Ala	Leu	Ala	Gln	Arg	Pro	
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Gly	Val	Arg	Gln	Gly	Trp	Leu	Asn	Cys	Gln	Arg	Leu	Val	Ile	Asp	Glu	
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Ile	Ser	Met	Val	Glu	Ala	Asp	Leu	Phe	Asp	Lys	Leu	Glu	Ala	Val	Ala	
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Arg	Ala	Val	Arg	Gln	Gln	Asn	Lys	Pro	Phe	Gly	Gly	Ile	Gln	Leu	Ile	
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Ile	Cys	Gly	Asp	Phe	Leu	Gln	Leu	Pro	Pro	Val	Thr	Lys	Gly	Ser	Gln	
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Pro	Pro	Arg	Phe	Cys	Phe	Gln	Ser	Ser	Pro	Asn	Arg	Cys	Ser	Asp	Glu	
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Gly	Ile	Val	Ala	Thr	Arg	Leu	Cys	Thr	His	Gln	Asp	Asp	Val	Ala	Leu	
		335				340				345					350	
acc	aac	gag	agg	cgg	ctt	cag	gag	ctg	cca	ggc	aag	gta	cac	aga	ttt	1286
Thr	Asn	Glu	Arg	Arg	Leu	Gln	Glu	Leu	Pro	Gly	Lys	Val	His	Arg	Phe	
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gag	gct	atg	gac	agc	aac	cct	gag	ctg	gcc	agt	acc	ctg	gat	gcc	cag	1334
Glu	Ala	Met	Asp	Ser	Asn	Pro	Glu	Leu	Ala	Ser	Thr	Leu	Asp	Ala	Gln	
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Cys	Pro	Val	Ser	Gln	Leu	Leu	Gln	Leu	Lys	Leu	Gly	Ala	Gln	Val	Met	
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Leu	Val	Lys	Asn	Leu	Ser	Val	Ser	Arg	Gly	Leu	Val	Asn	Gly	Ala	Arg	
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Gly	Val	Val	Val	Gly	Phe	Glu	Ala	Glu	Gly	Arg	Gly	Leu	Pro	Gln	Val	
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Arg	Phe	Leu	Cys	Gly	Val	Thr	Glu	Val	Ile	His	Ala	Asp	Arg	Trp	Thr	
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Val	Gln	Ala	Thr	Gly	Gly	Gln	Leu	Leu	Ser	Arg	Gln	Gln	Leu	Pro	Leu	
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cag	ctg	gcc	tgg	gcg	atg	tcc	atc	cac	aag	agc	caa	ggc	cta	cgt	gtg	1622
Gln	Leu	Ala	Trp	Ala	Met	Ser	Ile	His	Lys	Ser	Gln	Gly	Leu	Arg	Val	
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ctg	gac	ttt	gac	ccc	atg	gcg	gtt	cgc	tgt	gac	ccc	cgt	gtg	ctg	cac	1670
Leu	Asp	Phe	Asp	Pro	Met	Ala	Val	Arg	Cys	Asp	Pro	Arg	Val	Leu	His	
		480				485					490					
ttc	tat	gcc	acc	ctg	cgg	cgg	ggc	agg	agc	ctc	agt	ctg	gag	tcc	cca	1718
Phe	Tyr	Ala	Thr	Leu	Arg	Arg	Gly	Arg	Ser	Leu	Ser	Leu	Glu	Ser	Pro	
		495				500				505				510		
gat	gat	gat	gag	gca	gcc	tca	gac	cag	gag	aac	atg	gac	cca	atc	ctc	1766
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 Asn Tyr Phe Ala Ile Thr Ser Gly Ile Cys Thr Gly Pro Lys Ala Asp
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gca tac cgt gca cag ata tta cgc att cag tat gca tgg gca aac tct 144
 Ala Tyr Arg Ala Gln Ile Leu Arg Ile Gln Tyr Ala Trp Ala Asn Ser
 35 40 45

gag att tcc cag gtc tgt gct acc aaa ctg ttc aaa tat gca gag 192
 Glu Ile Ser Gln Val Cys Ala Thr Lys Leu Phe Lys Lys Tyr Ala Glu
 50 55 60

aaa tat tct gca att att gat tct gac aat gtt gaa tct ggg ttg aat 240
 Lys Tyr Ser Ala Ile Ile Asp Ser Asp Asn Val Glu Ser Gly Leu Asn
 65 70 75 80

aat tat gca gaa aac att tta act ttg gca gga tct caa caa aca gat 288
 Asn Tyr Ala Glu Asn Ile Leu Thr Leu Ala Gly Ser Gln Gln Thr Asp
 85 90 95

agt gac aag tgg cag tct gga ttg tca ata aat aat gtt ttc aaa atg 336
 Ser Asp Lys Trp Gln Ser Gly Leu Ser Ile Asn Asn Val Phe Lys Met
 100 105 110

agt agt gta cag aag atg atg caa gct ggc aaa aaa ttc aaa gac tct 384
 Ser Ser Val Gln Lys Met Met Gln Ala Gly Lys Lys Phe Lys Asp Ser
 115 120 125

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 Leu Leu Glu Pro Ala Leu Ala Ser Val Val Ile His Lys Glu Ala Thr
 130 135 140

gtc ttt gat ctt cct aaa ttt agt gtt tgt ggt agt tct caa gag agt 480
 Val Phe Asp Leu Pro Lys Phe Ser Val Cys Gly Ser Ser Gln Glu Ser
 145 150 155 160

gac tca tta cct aac tca gct cat gat cga gac cgg acc caa gac ttc 528
 Asp Ser Leu Pro Asn Ser Ala His Asp Arg Asp Arg Thr Gln Asp Phe
 165 170 175

ccg gag agc aat cgt ttg aaa ctc ctt cag aat gcc cag cca cct atg 576
 Pro Glu Ser Asn Arg Leu Lys Leu Leu Gln Asn Ala Gln Pro Pro Met
 180 185 190

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Glu	Ser	Ala	Thr	Ala	Lys	Phe	His	Val	Thr	Pro	Leu	Phe	Gly	Asn	Val	
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Lys	Lys	Glu	Asn	His	Ser	Ser	Ala	Lys	Glu	Asn	Ile	Gly	Leu	Asn	Val	
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Phe	Leu	Ser	Asn	Gln	Ser	Cys	Phe	Pro	Ala	Ala	Cys	Glu	Asn	Pro	Gln	
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Arg	Lys	Ser	Phe	Tyr	Gly	Ser	Gly	Thr	Ile	Asp	Ala	Leu	Ser	Asn	Pro	
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Ile	Leu	Asn	Lys	Ala	Cys	Ser	Lys	Thr	Glu	Asp	Asn	Gly	Pro	Lys	Glu	
		275						280					285			
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Asp	Ser	Ser	Leu	Pro	Thr	Phe	Lys	Thr	Ala	Lys	Glu	Gln	Leu	Trp	Val	
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gat	cag	caa	aaa	aag	tac	cac	caa	cct	cag	cgt	gca	tca	ggg	tct	tca	960
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tat	ggg	ggg	gta	aaa	aag	tct	cta	gga	gct	agt	aga	tcc	cga	ggg	ata	1008
Tyr	Gly	Gly	Val	Lys	Lys	Ser	Leu	Gly	Ala	Ser	Arg	Ser	Arg	Gly	Ile	
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Leu	Gly	Lys	Phe	Val	Pro	Pro	Ile	Pro	Lys	Gln	Asp	Gly	Gly	Glu	Gln	
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Asn	Gly	Gly	Met	Gln	Cys	Lys	Pro	Tyr	Gly	Ala	Gly	Pro	Thr	Glu	Pro	
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Ala	His	Pro	Val	Asp	Glu	Arg	Leu	Lys	Asn	Leu	Glu	Pro	Lys	Met	Ile	
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Glu	Asp	Ile	Ala	Gly	Val	Glu	Phe	Ala	Lys	Ala	Thr	Ile	Lys	Glu	Ile	
						405				410					415	
gtt	gtg	tgg	ccc	atg	ttg	agg	cca	gac	atc	ttt	act	ggg	tta	agg	gga	1296
Val	Val	Trp	Pro	Met	Leu	Arg	Pro	Asp	Ile	Phe	Thr	Gly	Leu	Arg	Gly	
						420			425					430		
ccc	cct	aaa	gga	att	ttg	ctc	ttt	ggg	cct	cct	ggg	act	ggg	aaa	act	1344
Pro	Pro	Lys	Gly	Ile	Leu	Leu	Phe	Gly	Pro	Pro	Gly	Thr	Gly	Lys	Thr	

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atg gtc cgt gca ttg ttt gct gtt gca agg tgt cag caa cca gct gtg Met Val Arg Ala Leu Phe Ala Val Ala Arg Cys Gln Gln Pro Ala Val 485 490 495			1488
ata ttt att gac gaa att gat tcc ttg tta tct caa cgg gga gat ggt Ile Phe Ile Asp Glu Ile Asp Ser Leu Leu Ser Gln Arg Gly Asp Gly 500 505 510			1536
gag cat gaa tct tct aga agg ata aaa aca gaa ttt tta gtt caa tta Glu His Glu Ser Ser Arg Arg Ile Lys Thr Glu Phe Leu Val Gln Leu 515 520 525			1584
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aca aat cgg cca caa att gat gag gct gcc cgg aga aga ttg gtg Thr Asn Arg Pro Gln Glu Ile Asp Glu Ala Ala Arg Arg Leu Val 545 550 555 560			1680
aaa agg ctt tat att ccc ctc cca gaa gct tca gcc agg aaa cag ata Lys Arg Leu Tyr Ile Pro Leu Pro Glu Ala Ser Ala Arg Lys Gln Ile 565 570 575			1728
gta att aat cta atg tcc aaa gag cag tgt tgc ctc agt gaa gaa gaa Val Ile Asn Leu Met Ser Lys Glu Gln Cys Cys Leu Ser Glu Glu Glu 580 585 590			1776
att gaa cag att gta cag cag tct gat gcg ttt tca gga gca gac atg Ile Glu Gln Ile Val Gln Gln Ser Asp Ala Phe Ser Gly Ala Asp Met 595 600 605			1824
aca cag ctt tgc agg gag gct tct ctt ggt cct att cgc agt tta caa Thr Gln Leu Cys Arg Glu Ala Ser Leu Gly Pro Ile Arg Ser Leu Gln 610 615 620			1872
act gct gac att gct acc ata aca ccg gat caa gtt cga ccc ata gct Thr Ala Asp Ile Ala Thr Ile Thr Pro Asp Gln Val Arg Pro Ile Ala 625 630 635 640			1920
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cca aaa gat tta gag ctt tat gaa aac tgg aac aaa act ttt ggt tgt Pro Lys Asp Leu Glu Leu Tyr Glu Asn Trp Asn Lys Thr Phe Gly Cys 660 665 670			2016
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tgaaac   atg aat ctt tgc ctc gtc ctg gct gcc ttt tgc ttg gga ata      228
          Met Asn Leu Ser Leu Val Leu Ala Ala Phe Cys Leu Gly Ile
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gcc tcc gct gtt cca aaa ttt gac caa aat ttg gat aca aag tgg tac      276
Ala Ser Ala Val Pro Lys Phe Asp Gln Asn Leu Asp Thr Lys Trp Tyr
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cag tgg aag gca aca cac aga aga tta tat ggc gcg aat gaa gaa gga      324
Gln Trp Lys Ala Thr His Arg Arg Leu Tyr Gly Ala Asn Glu Glu Gly
          35             40             45

tgg agg aga gca gtg tgg gaa aag aat atg aaa atg att gaa ctg cac      372
Trp Arg Arg Ala Val Trp Glu Lys Asn Met Lys Met Ile Glu Leu His
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aat ggg gaa tac agc caa ggg aaa cac agc ttc aca atg gcc atg aat      420
Asn Gly Glu Tyr Ser Gln Gly Lys His Ser Phe Thr Met Ala Met Asn
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gcc ttt gga gac atg acc aat gaa gaa ttc agg cag gtg atg aat ggt      468
Ala Phe Gly Asp Met Thr Asn Glu Glu Phe Arg Gln Val Met Asn Gly
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ttt caa tac cag aag cac agg aag ggg aaa cag ttc cag gaa cgc ctg      516
Phe Gln Tyr Gln Lys His Arg Lys Gly Lys Phe Gln Glu Arg Leu
          95             100             105             110

ctt ctt gag atc ccc aca tct gtg gac tgg aga gag aaa ggc tac atg      564
Leu Leu Glu Ile Pro Thr Ser Val Asp Trp Arg Glu Lys Gly Tyr Met
          115             120             125

act cct gtg aag gat cag ggt cag tgt ggc tct tgt tgg gct ttt agt      612
Thr Pro Val Lys Asp Gln Gly Gln Cys Gly Ser Cys Trp Ala Phe Ser
          130             135             140

gca act ggt gct ctg gaa ggg cag atg ttc tgg aaa aca ggc aaa ctt      660
Ala Thr Gly Ala Leu Glu Gly Gln Met Phe Trp Lys Thr Gly Lys Leu
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cag gag aac gga ggc ctg gac tct gag gaa tcc tat cca tat gag gca Gln Glu Asn Gly Gly Leu Asp Ser Glu Glu Ser Tyr Pro Tyr Glu Ala 195 200 205	804
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agt gaa gac atg gat cat ggt gtg ctg gtg gtt ggc tac gga ttt gaa Ser Glu Asp Met Asp His Gly Val Leu Val Val Gly Tyr Gly Phe Glu 275 280 285	1044
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ggt gaa gaa tgg ggc atg ggt ggc tac gta aag atg gcc aaa gac cgg Gly Glu Glu Trp Gly Met Gly Gly Tyr Val Lys Met Ala Lys Asp Arg 305 310 315	1140
aga aac cat tgt gga att gcc tca gca gcc agc tac ccc act gtg tga Arg Asn His Cys Gly Ile Ala Ser Ala Ala Ser Tyr Pro Thr Val 320 325 330	1188
gctggtggac ggtgatgagg aaggacttga ctggggatgg cgaatgcatg ggaggaattc	1248
atcttcagtc taccagcccc cgctgtgtcg gatacacact cgaatcattg aagatccgag	1308
tgtgatttga attctgtgat attttcacac tggtaaatgt tacctctatt ttaattactg	1368
ctataaatag gtttatatta ttgattcact tactgacttt gcattttcgt ttttaaaagg	1428
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 <213> Homo sapiens

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ccaagcc atg ctg tgc gcc cgc tgg agg cgt tgc cgc cgc cgg ccc gag 169
Met Leu Cys Gly Arg Trp Arg Arg Cys Arg Arg Pro Pro Glu
1 5 10
gag ccc cca gtg gcc gcc cag gtc gca gcc caa gtc gcg gcg ccg gtc 217
Glu Pro Pro Val Ala Ala Gln Val Ala Ala Gln Val Ala Ala Pro Val
15 20 25 30
gct ctc cgg tcc cgg cgg act ccc tcc gat ggc ggc acc aag agg ccc 265
Ala Leu Pro Ser Pro Pro Thr Pro Ser Asp Gly Gly Thr Lys Arg Pro
35 40 45
ggg ctg cgg gcg ctg aag aag atg ggc ctg acg gag gac gag gac gtg 313
Gly Leu Arg Ala Leu Lys Lys Met Gly Leu Thr Glu Asp Glu Asp Val
50 55 60
cgc gcc atg ctg cgg gcc tcc cgg ctc cgc aag atc cgc tgc cgc acg 361
Arg Ala Met Leu Arg Gly Ser Arg Leu Arg Lys Ile Arg Ser Arg Thr
65 70 75
tgg cac aag gag cgg ctg tac cgg ctg cag gag gac ggc ctg agc gtg 409
Trp His Lys Glu Arg Leu Tyr Arg Leu Gln Glu Asp Gly Leu Ser Val
80 85 90
tgg ttc cag cgg cgc atc cgg cgt gcg cca tgc cag cac atc ttc ttc 457
Trp Phe Gln Arg Arg Ile Pro Arg Ala Pro Ser Gln His Ile Phe Phe
95 100 105 110
gtg cag cac atc gag gcg gtc cgc gag ggc cac cag tcc gag ggc ctg 505
Val Gln His Ile Glu Ala Val Arg Glu Gly His Gln Ser Glu Gly Leu
115 120 125
cgg cgc ttc ggg ggt gcc ttc gcg cca gcg cgc tgc ctc acc atc gcc 553
Arg Arg Phe Gly Gly Ala Phe Ala Pro Ala Arg Cys Leu Thr Ile Ala
130 135 140
ttc aag gcc cgc cgc aag aac ctg gac ctg gcg gcg ccc acg gct gag 601
Phe Lys Gly Arg Arg Lys Asn Leu Asp Leu Ala Ala Pro Thr Ala Glu
145 150 155
gaa gcg cag cgc tgg gtg cgc ggt ctg acc aag ctc cgc gcg cgc ctg 649
Glu Ala Gln Arg Trp Val Arg Gly Leu Thr Lys Leu Arg Ala Arg Leu
160 165 170
gac gcc atg agc cag cgc gag cgg cta gac cac tgg atc cac tcc tat 697
Asp Ala Met Ser Gln Arg Glu Arg Leu Asp His Trp Ile His Ser Tyr
175 180 185 190
ctg cac cgg gct gac tcc aac cag gac agc aag atg agc ttc aag gag 745
Leu His Arg Ala Asp Ser Asn Gln Asp Ser Lys Met Ser Phe Lys Glu
195 200 205

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atc aag agc ctg ctg aga atg gtc aac gtg gac atg aac gac atg tac Ile Lys Ser Leu Leu Arg Met Val Asn Val Asp Met Asn Asp Met Tyr 210 215 220	793
gcc tac ctc ctc ttc aag gag tgt gac cac tcc aac aac gac cgt cta Ala Tyr Leu Leu Phe Lys Glu Cys Asp His Ser Asn Asp Arg Arg Leu 225 230 235	841
gag ggg gct gag atc gag gag ttc ctg cgg cgg ctg ctg aag cgg ccg Glu Gly Ala Glu Ile Glu Glu Phe Leu Arg Arg Leu Lys Arg Pro 240 245 250	889
gag ctg gag gag atc ttc cat cag tac tcg ggc gag gac cgc gtg ctg Glu Leu Glu Glu Ile Phe His Gln Tyr Ser Gly Glu Asp Arg Val Leu 255 260 265 270	937
agt gcc cct gag ctg ctg gag ttc ctg gag gac cag ggc gag gag gcc Ser Ala Pro Glu Leu Leu Glu Phe Leu Glu Asp Gln Gly Glu Glu Gly 275 280 285	985
gcc aca ctg gcc cgc gcc cag cag ctc att cag acc tat gag ctc aac Ala Thr Leu Ala Arg Ala Gln Gln Ile Gln Thr Tyr Glu Leu Asn 290 295 300	1033
gag aca gcc aag cag cat gag ctg atg aca ctg gat ggc ttc atg atg Glu Thr Ala Lys Gln His Glu Leu Met Thr Leu Asp Gly Phe Met Met 305 310 315	1081
tac ctg ttg tcg ccg gag ggg gct gcc ttg gac aac acc cac acg tgt Tyr Leu Leu Ser Pro Glu Gly Ala Ala Leu Asp Asn Thr His Thr Cys 320 325 330	1129
gtg ttc cag gac atg aac cag ccc ctt gcc cac tac ttc atc tct tcc Val Phe Gln Asp Met Asn Gln Pro Leu Ala His Tyr Phe Ile Ser Ser 335 340 345 350	1177
tcc cac aac acc tat ctg act gac tcc cag atc ggg ggg ccc agc agc Ser His Asn Thr Tyr Leu Thr Asp Ser Gln Ile Gly Gly Pro Ser Ser 355 360 365	1225
acc gag gcc tat gtt agg tac tgt agc agg ggg gcc ttt gcc cag gga Thr Glu Ala Tyr Val Arg Tyr Cys Ser Arg Gly Ala Phe Ala Gln Gly 370 375 380	1273
tgc cgc tgc gtg gag ctg gac tgc tgg gag ggg cca gga ggg gag ccc Cys Arg Cys Val Glu Leu Asp Cys Trp Glu Gly Pro Gly Gly Glu Pro 385 390 395	1321
gtc atc tat cat ggc cat acc ctc acc tcc aag att ctc ttc cgg gac Val Ile Tyr His Gly His Thr Leu Thr Ser Lys Ile Leu Phe Arg Asp 400 405 410	1369
gtg gtc caa gcc gtg cgc gac cat gcc ttc acg ctg tcc cct tac cct Val Val Gln Ala Val Arg Asp His Ala Phe Thr Leu Ser Pro Tyr Pro 415 420 425 430	1417
gtc atc cta tcc ctg gag aac cac tgc ggg ctg gag cag cag gct gcc Val Ile Leu Ser Leu Glu Asn His Cys Gly Leu Glu Gln Gln Ala Ala 435 440 445	1465

atg gcc cgc cac ctc tgc acc atc ctg ggg gac atg ctg gtg aca cag	1513
Met Ala Arg His Leu Cys Thr Ile Leu Gly Asp Met Leu Val Thr Gln	
450 455 460	
gcg ctg gac tcc cca aat ccc gag gag ctg cca tcc cca gag cag ctg	1561
Ala Leu Asp Ser Pro Asn Pro Glu Glu Leu Pro Ser Pro Glu Gln Leu	
465 470 475	
aag ggc cgg gtc ctg gtg aag gga aag aag ctg ccc gct gct cgg agc	1609
Lys Gly Arg Val Leu Val Lys Gly Lys Leu Pro Ala Ala Arg Ser	
480 485 490	
gag gat ggc cgg gct ctg tgc gat cgg gag gag gag gag gat gac	1657
Glu Asp Gly Arg Ala Leu Ser Asp Arg Glu Glu Glu Glu Glu Asp Asp	
495 500 505 510	
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Glu Glu Glu Glu Glu Glu Val Glu Ala Ala Ala Gln Arg Arg Leu Ala	
515 520 525	
aag cag atc tcc cgg gag ctg tgc gcc ctg gct gtg tac tgc cac gcc	1753
Lys Gln Ile Ser Pro Glu Leu Ser Ala Leu Ala Val Tyr Cys His Ala	
530 535 540	
acc cgc ctg cgg acc ctg cac cct gcc ccc aac gcc cca caa ccc tgc	1801
Thr Arg Leu Arg Thr Leu His Pro Ala Pro Asn Ala Pro Gln Pro Cys	
545 550 555	
cag gtc agc tcc ctc agc gag cgc aaa gcc aag aaa ctc att cgg gag	1849
Gln Val Ser Ser Leu Ser Glu Arg Lys Ala Lys Leu Ile Arg Glu	
560 565 570	
gca ggg aac agc ttt gtc agg cac aat gcc cgc cag ctg acc cgc gtg	1897
Ala Gly Asn Ser Phe Val Arg His Asn Ala Arg Gln Leu Thr Arg Val	
575 580 585 590	
tac ccg ctg ggg ctg cgg atg aac tca gcc aac tac agt ccc cag gag	1945
Tyr Pro Leu Gly Leu Arg Met Asn Ser Ala Asn Tyr Ser Pro Gln Glu	
595 600 605	
atg tgg aac tgc ggc tgt cag ctg gtg gcc ttg aac ttc cag acg cca	1993
Met Trp Asn Ser Gly Cys Gln Leu Val Ala Leu Asn Phe Gln Thr Pro	
610 615 620	
ggc tac gag atg gac ctc aat gcc ggg cgc ttc cta gtc aat ggg cag	2041
Gly Tyr Glu Met Asp Leu Asn Ala Gly Arg Phe Leu Val Asn Gly Gln	
625 630 635	
tgt ggc tac gtc cta aaa cct gcc tgc ctg cgg caa cct gac tgc acc	2089
Cys Gly Tyr Val Leu Lys Pro Ala Cys Leu Arg Gln Pro Asp Ser Thr	
640 645 650	
ttt gac ccc gag tac cca gga cct ccc aga acc act ctc agc atc cag	2137
Phe Asp Pro Glu Tyr Pro Gly Pro Pro Arg Thr Thr Leu Ser Ile Gln	
655 660 665 670	
gtg ctg act gca cag cag ctg ccc aag ctg aat gcc gag aag cca cac	2185
Val Leu Thr Ala Gln Gln Leu Pro Lys Leu Asn Ala Glu Lys Pro His	
675 680 685	
tcc att gtg gac ccc ctg gtg cgc att gag atc cat ggg gtg ccc gca	2233

Ser Ile Val Asp Pro Leu Val Arg Ile Glu Ile His Gly Val Pro Ala	
690 695 700	
gac tgt gcc cgg cag gag act gac tac gtg ctc aac aat ggc ttc aac	2281
Asp Cys Ala Arg Gln Glu Thr Asp Tyr Val Leu Asn Asn Gly Phe Asn	
705 710 715	
ccc cgc tgg ggg cag acc ctg cag ttc cag ctg cgg gct ccg gag ctg	2329
Pro Arg Trp Gly Gln Thr Leu Gln Phe Gln Leu Arg Ala Pro Glu Leu	
720 725 730	
gca ctg gtc cgg ttt gtg gtg gaa gat tat gac gcc acc tcc ccc aat	2377
Ala Leu Val Arg Phe Val Val Glu Asp Tyr Asp Ala Thr Ser Pro Asn	
735 740 745 750	
gac ttt gtg ggc cag ttt aca ctg cct ctt agc agc cta aag caa ggg	2425
Asp Phe Val Gly Gln Phe Thr Leu Pro Leu Ser Ser Leu Lys Gln Gly	
755 760 765	
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Tyr Arg His Ile His Leu Leu Ser Lys Asp Gly Ala Ser Leu Ser Pro	
770 775 780	
gcc acg ctc ttc atc caa atc cgc atc cag cgc tcc tga gggccacct	2522
Ala Thr Leu Phe Ile Gln Ile Arg Ile Gln Arg Ser	
785 790	
cactcgccctt ggggttctgc gagtgccagt ccacatcccc tcagagagccc tctctcctc	2582
tggagtcagg tgggtgggagt accagcccc cagccccacc acctggcccca ctgagcccat	2642
tcaccaggcg ctggtctcac ctgggtgctg agggctgcct gggccccctcc tgaagaacag	2702
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cccctaagcc ctcccttacc ccaggccttc ctggaactct ccctccagct ccggaacctg	3002
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tttacagcaa tcatcaccct ttgcagagga ggtgagctca ccaggactca tctgccattt	180
cagacctttt gctgctacct gccagggtggc cccactgct gacgagag atg gtg gat	237
Met Val Asp	
1	
ctc tca gtc tcc ccg gac tcc ttg aag cca gta tgc ctg acc agc agt	285
Leu Ser Val Ser Pro Asp Ser Leu Lys Pro Val Ser Leu Thr Ser Ser	
5 10 15	
ctt gtc ttc ctc atg cac ctc ctc ctc ctt cag cct ggg gag ccg agc	333
Leu Val Phe Leu Met His Leu Leu Leu Leu 30 Pro Gly Glu Pro Ser 35	
20 25	
tca gag gtc aag gtg cta ggc cct gag tat ccc atc ctg gcc ctc gtc	381
Ser Glu Val Lys Val Leu Gly Pro Glu Tyr Pro Ile Leu Ala Leu Val	
40 45 50	
ggg gag gag gtg gag ttc ccg tgc cac cta tgg cca cag ctg gat gcc	429
Gly Glu Glu Val Glu Phe Pro Cys His Leu Trp Pro Gln Leu Asp Ala	
55 60 65	
cag caa atg gag atc cgc tgg ttc cgg agt cag acc ttc aat gtg gta	477
Gln Gln Met Glu Ile Arg Trp Phe Arg Ser Gln Thr Phe Asn Val Val	
70 75 80	
cac ctg tac cag gag cag cag gag ctc cct ggc agg cag atg ccg gcg	525
His Leu Tyr Gln Glu Gln Gln Glu Leu Pro Gly Arg Gln Met Pro Ala	
85 90 95	
ttc cgg aac agg acc aag ttg gtc aag gac gac atc gcc tat ggc agc	573
Phe Arg Asn Arg Thr Lys Leu Val Lys Asp Asp Ile Ala Tyr Gly Ser	
100 105 110 115	
gtg gtc ctg cag ctt cac agc atc atc ccc tct gac aag ggc aca tat	621
Val Val Leu Gln Leu His Ser Ile Ile Pro Ser Asp Lys Gly Thr Tyr	
120 125 130	
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Gly Cys Arg Phe His Ser Asp Asn Phe Ser Gly Glu Ala Leu Trp Glu	
135 140 145	
ctg gag gta gca ggg ctg ggc tca gac cct cac ctc tcc ctt gag ggc	717
Leu Glu Val Ala Gly Leu Gly Ser Asp Pro His Leu Ser Leu Glu Gly	
150 155 160	
ttc aag gaa gga ggc att cag ctg agg ctc aga tcc agt ggc tgg tac	765
Phe Lys Glu Gly Gly Ile Gln Leu Arg Leu Arg Ser Ser Gly Trp Tyr	
165 170 175	
ccc aag cct aag gtt cag tgg aga gac cac cag gga cag tgc ctg cct	813
Pro Lys Pro Lys Val Gln Trp Arg Asp His Gln Gly Gln Cys Leu Pro	
180 185 190 195	
cca gag ttt gaa gcc atc gtc tgg gat gcc cag gac ctg ttc agt ctg	861
Pro Glu Phe Glu Ala Ile Val Trp Asp Ala Gln Asp Leu Phe Ser Leu	
200 205 210	


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gaa aca tct gtg gtt gtc cga gcg gga gcc ctc agc aat gtg tcc gtc      909
Glu Thr Ser Val Val Val Arg Ala Gly Ala Leu Ser Asn Val Ser Val
      215                                220
tcc atc cag aat ctc ctc ttg agc cag aag aaa gag ttg gtg gtc cag      957
Ser Ile Gln Asn Leu Leu Leu Ser Gln Lys Lys Glu Leu Val Val Gln
      230                                235                                240
ata gca ggt cag tgg ctg tta gct cac acc cat ctt cct agt cct cat      1005
Ile Ala Gly Gln Trp Leu Leu Ala His Thr His Leu Pro Ser Pro His
      245                                250                                255
gtg tac ata cac att ggc cca aag gca gtc tat aaa gag aca atg gta      1053
Val Tyr Ile His Ile Gly Pro Lys Ala Val Tyr Lys Glu Thr Met Val
      260                                265                                270
ctg cgc ctg tct gca tat agg gtg tgt tgg cct tga cacc tgaaaattca      1103
Leu Arg Leu Ser Ala Tyr Arg Val Cys Trp Pro
      280                                285
gcaccttgga tattaggaac acactaagaa cgctactgag aacccaaaca gtcagtgaga      1163
gagggccccag agagcccgcc ttctctgtgcc taaggccata cactaaaacc catcaactct      1223
gctcatcaga ggcacatcgg gagccaatag attcgtaatg ctgtctctca aacagtatgt      1283
attgagtttc cacaacgtga ccccgagtcgc taccctcagg tcccctagcc agtgggggat      1343
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<222> (254) .. (1909)

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acttgaaagg aaccaggga aaagtgtcca ggtgtgagca tgagcgggta gaggtgtgcc      180
cttgtttget tcaggetgtc tgcttttcgc cctgactgt tttttctgtt tctggccatg      240
gaggaagaga aag      atg aca agc cca cag gct gac ttc tgc ctg gcc acc      289
      Met Thr Ser Pro Gln Ala Asp Phe Cys Leu Gly Thr
      1                                5                                10
gcc ctg cac tct tgg gga ctg tgg ttc acg gag gaa ggt tca ccg tcc      337
Ala Leu His Ser Trp Gly Leu Trp Phe Thr Glu Glu Gly Ser Pro Ser
      15                                20                                25

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acc atg ctg acg ggg att gca gtt gga gcc ctc ctg gcc ctg gcc ttg Thr Met Leu Thr Gly Ile Leu Phe Ala Val Gly Ala Leu Leu Ala Leu 30 35 40	385
gtt ggt gtc ctc atc ctt ttc atg ttc aga agg ctt aga caa ttt cga Val Gly Val Leu Ile Leu Phe Met Phe Arg Arg Leu Arg Gln Phe Arg 45 50 55 60	433
caa gca cag ccc act cct cag tac cgg ttc cgg aag aga gac aaa gtg Gln Ala Gln Pro Thr Pro Gln Tyr Arg Phe Arg Lys Arg Asp Lys Val 65 70 75	481
atg ttt tac ggc cgg aag atc atg agg aag gtg acc aca ctc ccc aac Met Phe Tyr Gly Arg Lys Ile Met Arg Lys Val Thr Thr Leu Pro Asn 80 85 90	529
acc ctt gtg gag aac act gcc ctg ccc cgg cag cgg gcc agg aag agg Thr Leu Val Glu Asn Thr Ala Leu Pro Arg Gln Arg Ala Arg Lys Arg 95 100 105	577
acc aag gtg ctg tct ttg gcc aag agg att ctg cgt ttc aag aag gaa Thr Lys Val Leu Ser Leu Ala Lys Arg Ile Leu Arg Phe Lys Lys Glu 110 115 120	625
tac ccg gcc ctg cag ccc aag gag ccc ccg ccc tcc ctg ctg gag gcc Tyr Pro Ala Leu Gln Pro Lys Glu Pro Pro Ser Leu Leu Glu Ala 125 130 135 140	673
gac ctc acg gag ttt gac gtg aag aat tct cac ctg cca tcg gaa gtt Asp Leu Thr Glu Phe Asp Val Lys Asn Ser His Leu Pro Ser Glu Val 145 150 155	721
ctg tac atg ctg aaa aac gtt cgg gtc ctg ggc cac ttt gag aag ccg Leu Tyr Met Leu Lys Asn Val Arg Val Leu Gly His Phe Glu Lys Pro 160 165 170	769
ctg ttc ctg gag ctt tgc aaa cac atc gtc ttt gtg cag ctg cag gaa Leu Phe Leu Glu Lys Cys Lys His Ile Val Phe Val Gln Leu Gln Glu 175 180 185	817
ggg gag cac gtc ttc cag ccc agg gag ccg gac ccc agc atc tgt gtg Gly Glu His Val Phe Gln Pro Arg Glu Pro Asp Pro Ser Ile Cys Val 190 195 200	865
gtg cag gac ggg cgg ctg gag gtc tgc atc cag gac act gac ggc acc Val Gln Asp Gly Arg Leu Glu Val Cys Ile Gln Asp Thr Asp Gly Thr 205 210 215 220	913
gag gtg gtg gtg aaa gag gtt ctg gcg gga gac agc gtc cac agc ctg Glu Val Val Val Lys Glu Val Leu Ala Gly Asp Ser Val His Ser Leu 225 230 235	961
ctc agc atc ctg gac atc atc acc ggc cat gct gca cct tac aaa acg Leu Ser Ile Leu Asp Ile Ile Thr Gly His Ala Ala Pro Tyr Lys Thr 240 245 250	1009
gtc tcc gtc cgc gcg gcc atc ccg tcc acc atc ctc cgg ctt cca gct Val Ser Val Arg Ala Ala Ile Pro Ser Thr Ile Leu Arg Leu Pro Ala 255 260 265	1057
gcg gct ttt cat gga gtt ttt gag aaa tat ccg gaa act ctg gtg agg	1105

Ala	Ala	Phe	His	Gly	Val	Phe	Glu	Lys	Tyr	Pro	Glu	Thr	Leu	Val	Arg	
270						275					280					
gtg	gtg	cag	atc	atc	atg	gtg	cgg	ctg	cag	agg	gtg	acc	ttt	ctg	gct	1153
Val	Val	Gln	Ile	Ile	Met	Val	Arg	Leu	Gln	Arg	Val	Thr	Phe	Leu	Ala	
285					290					295				300		
ctg	cac	aac	tac	ctc	ggc	ctg	acc	aca	gag	ctc	ttc	aac	gct	gag	agc	1201
Leu	His	Asn	Tyr	Leu	Gly	Leu	Thr	Thr	Glu	Leu	Phe	Asn	Ala	Glu	Ser	
				305					310				315			
cag	gcc	atc	cct	ctc	gtg	tct	gta	gcc	agt	gtg	gct	gcc	ggg	aag	gcc	1249
Gln	Ala	Ile	Pro	Leu	Val	Ser	Val	Ala	Ser	Val	Ala	Ala	Gly	Lys	Ala	
			320					325					330			
aag	aag	cag	gtg	ttc	tat	ggc	gaa	gaa	gag	cgg	ctt	aaa	aag	cca	ccg	1297
Lys	Lys	Gln	Val	Phe	Tyr	Gly	Glu	Glu	Glu	Arg	Leu	Lys	Lys	Pro	Pro	
		335					340					345				
cgg	ctc	cag	gag	tcc	tgt	gac	tca	ggt	act	gtc	ctg	cac	caa	gga	ggg	1345
Arg	Leu	Gln	Glu	Ser	Cys	Asp	Ser	Gly	Thr	Val	Leu	His	Gln	Gly	Gly	
		350				355					360					
caa	tgt	cca	gcc	cca	gag	tcc	ggg	gga	tcc	tgc	tcc	cac	tgc	ctc	agg	1393
Gln	Cys	Pro	Ala	Pro	Glu	Ser	Gly	Gly	Ser	Cys	Ser	His	Cys	Leu	Arg	
		365			370				375					380		
tca	ccc	cag	gtc	atc	ttg	cac	atg	cct	gag	gcc	acc	aca	cac	atc	ccc	1441
Ser	Pro	Gln	Val	Ile	Leu	His	Met	Pro	Glu	Ala	Thr	Thr	His	Ile	Pro	
			385					390						395		
ggg	tca	cct	cac	acg	gcc	cag	gtc	acc	cta	caa	gtc	cca	caa	gtc	acc	1489
Gly	Ser	Pro	His	Thr	Ala	Gln	Val	Thr	Leu	Gln	Val	Pro	Gln	Val	Thr	
			400					405					410			
tca	cat	gcc	ccc	cag	gtc	tac	tca	cac	gca	ccc	cag	gtc	ccc	tca	cgt	1537
Ser	His	Ala	Pro	Gln	Val	Tyr	Ser	His	Ala	Pro	Gln	Val	Pro	Ser	Arg	
		415					420					425				
gcc	tca	ggt	ccc	ctc	aca	cgt	gcc	cca	ggt	cac	ctc	aca	tgc	ccc	cca	1585
Ala	Ser	Gly	Pro	Leu	Thr	Arg	Ala	Pro	Gly	His	Leu	Thr	Cys	Pro	Pro	
		430				435					440					
ggt	ctc	atc	aga	tgg	ccc	ccc	agg	tct	cct	cac	gtg	tcc	cca	tct	cct	1633
Gly	Leu	Ile	Arg	Trp	Pro	Pro	Arg	Ser	Pro	His	Val	Ser	Pro	Ser	Pro	
		445			450				455					460		
cac	atg	cgg	gct	gga	tgt	cct	cag	acc	tcc	cca	ggt	ctc	atc	agg	tgt	1681
His	Met	Arg	Ala	Gly	Cys	Pro	Gln	Thr	Ser	Pro	Gly	Leu	Ile	Arg	Cys	
			465					470					475			
gcc	cat	ctc	aca	tgt	ggg	ctg	gat	gtc	ctc	aaa	cct	cca	acg	gtc		1729
Ala	His	Leu	Leu	Thr	Cys	Gly	Leu	Asp	Val	Leu	Lys	Pro	Pro	Thr	Val	
			480					485					490			
tca	tta	cgt	gtg	ccc	gtc	tcc	tca	cat	gag	gcc	cgg	atg	tcc	tca	gac	1777
Ser	Leu	Arg	Val	Pro	Val	Ser	Ser	His	Glu	Ala	Arg	Met	Ser	Ser	Asp	
		495				500						505				
agg	ccc	agg	acc	ctt	cac	cct	cca	ttc	ttc	agt	tgt	tcc	cag	aat	tct	1825
Arg	Pro	Arg	Thr	Leu	His	Pro	Pro	Phe	Ser	Cys	Ser	Gln	Asn	Ser		

510	515	520	
cca ctg ggc cag gtg cct ggt ggg gag tgg gcc tcc cgc gat ggg ctc Pro Leu Gly Gln Val Pro Gly Gly Glu Trp Ala Ser Arg Asp Gly Leu 525 530 535 540			1873
tca ccc gct gtt ctg agt gct aac cgg ggg gcc tga atct gaggaggaag Ser Pro Ala Val Leu Ser Ala Asn Arg Gly Ala 545 550			1923
cggtcgggtg cggcgtgcac tgcattgagtc agccacgac gatctgtgtg atggagttaa cagccaccct acagatgagg tgcgcgcttg gttatttata gcccatcatg ttcccaaaag aattgaagtg actacaaaaa ggat			1983 2043 2067
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ggcaggggaa tcgctgaaat gacctagaag ggccctcttaa actttctggt tggaccgagc			180
agaggaggga gagagagggt tgtctcttgt gaggtgggtg aacgtctttt tattccctcc			240
caatccacca acttcgcccc aagccaggat ctgtcacaac tcgagagggtg gaaattccgg			300
tttccctggc ctatagctcc cagtgtctggc tttggcatga tgggcacctg gagggccgca			360
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tcttctttct cctgaatggc acccccgccc tagaatccag acaccgagtt tcccactgtg			480
gctgggtcaa gggtatgtga gagctccctg gtgacagtct gtggctgagc		atg gcc Met Ala 1	536
ctc cca gcc ctg ggc ctg gac ccc tgg agc ctc ctg ggc ctt ttc ctc Leu Pro Ala Leu Gly Leu Asp Pro Trp Ser Leu Leu Gly Leu Phe Leu 5 10 15			584
ttc caa ctg ctt cag ctg ctg ctg cgg acg acg acc gcg ggg gga ggc Phe Gln Leu Leu Gln Leu Leu Pro Thr Thr Ala Gly Gly Gly 20 25 30			632
ggg cag ggg ccc atg ccc agg gtc aga tac tat gca ggg gat gaa cgt Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Ala Gly Asp Glu Arg 35 40 45 50			680

agg gca ctt agc ttc ttc cac cag aag ggc ctc cag gat ttt gac act	728
Arg Ala Leu Ser Phe His Gln Lys Gly Leu Gln Asp Phe Asp Thr	
55 60 65	
ctg ctc ctg agt ggt gat gga aat act ctc tac gtg ggg gct cga gaa	776
Leu Leu Leu Ser Gly Asp Gly Asn Thr Leu Tyr Val Gly Ala Arg Glu	
70 75 80	
gcc att ctg gcc ttg gat atc cag gat cca ggg gtc ccc agg cta aag	824
Ala Ile Leu Ala Leu Asp Ile Gln Asp Pro Gly Val Pro Arg Leu Lys	
85 90 95	
aac atg ata ccg tgg cca gcc agt gac aga aaa aag agt gaa tgt gcc	872
Asn Met Ile Pro Trp Pro Ala Ser Asp Arg Lys Ser Glu Cys Ala	
100 105 110	
ttt aag aag aag agc aat gag aca cag tgt ttc aac ttc atc cgt gtc	920
Phe Lys Lys Lys Ser Asn Glu Thr Gln Cys Phe Asn Phe Ile Arg Val	
115 120 125 130	
ctg gtt tct tac aat gtc acc cat ctc tac acc tgc ggc acc ttc gcc	968
Leu Val Ser Tyr Asn Val Thr His Leu Tyr Thr Cys Gly Thr Phe Ala	
135 140 145	
ttc agc cct gct tgt acc ttc att gaa ctt caa gat tcc tac ctg ttg	1016
Phe Ser Pro Ala Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr Leu Leu	
150 155 160	
ccc atc tcg gag gac aag gtc atg gag gga aaa ggc caa agc ccc ttt	1064
Pro Ile Ser Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser Pro Phe	
165 170 175	
gac ccc gct cac aag cat acg gct gtc ttg gtg gat ggg atg ctc tat	1112
Asp Pro Ala His Lys His Thr Ala Val Leu Val Asp Gly Met Leu Tyr	
180 185 190	
tct ggt act atg aac aac ttc ctg ggc agt gag ccc atc ctg atg cgc	1160
Ser Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu Met Arg	
195 200 205 210	
aca ctg gga tcc cag cct gtc ctc aag acc gac aac ttc ctc cgc tgg	1208
Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu Arg Trp	
215 220 225	
ctg cat cat gac gcc tcc ttt gtg gca gcc atc cct tcg acc cag gtc	1256
Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr Gln Val	
230 235 240	
gtc tac ttc ttc ttc gag gag aca gcc agc gag ttt gac ttc ttt gag	1304
Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp Phe Phe Glu	
245 250 255	
agg ctc cac aca tcg cgg gtg gct aga gtc tgc aag aat gac gtg ggc	1352
Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys Asn Asp Val Gly	
260 265 270	
ggc gaa aag ctg ctg cag aag aag tgg acc acc ttc ctg aag gcc cag	1400
Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr Phe Leu Lys Ala Gln	
275 280 285 290	
ctg ctc tgc acc cag ccg ggg cag ctg ccc ttc aac gtc atc cgc cac	1448

Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro	Phe	Asn	Val	Ile	Arg	His	
				295					300					305		
gcg	gtc	ctg	ctc	ccc	gcc	gat	tct	ccc	aca	gct	ccc	cac	atc	tac	gca	1496
Ala	Val	Leu	Leu	Pro	Ala	Asp	Ser	Pro	Thr	Ala	Pro	His	Ile	Tyr	Ala	
			310					315					320			
gtc	ttc	acc	tcc	cag	tgg	tga	gc	agcaggggctg	gaccatgggg	gctggacacg						1549
Val	Phe	Thr	Ser	Gln	Trp											
			325													
ggacttgcag	ccagtggaggc	cccagctcgt	gagcggaggc	aggaattgac	atgagccagc											1609
acctaactcag	cactttcaca	taggaaggca	ttaaatacgtc	ccccccctc	agggaaaaaa											1669
aaaaa																1674

<210> 32
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (487) .. (648)

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ccttcttccc	ctcacatgtg
ccccacaacc	tactgatgct
gatagtttct	attcctatgt
gccattaatc	cogtccagtg
ccagcttgag	cctttgggta
tggctagtgg	ggcagtgagc
acgggt	atg atg gag acc atg cag ctg aaa gta aac cgt cac ccc ttc
	Met Met Glu Thr Met Gln Leu Lys Val Asn Arg His Pro Phe
	1 5 10
tgc ttc agt gtg aaa ggc cag gtg aag atg ctg cag ctg atg agg ctg	576
Cys Phe Ser Val Lys Gly Gln Val Lys Met Leu Gln Leu Met Arg Leu	
15 20 25 30	
ggc ctt agg gtg cgg ggg gtg gtg gaa tct gct tgt ggg cgg gag atg	624
Gly Leu Arg Val Arg Gly Val Val Glu Ser Ala Cys Gly Arg Glu Met	
35 40 45	
tgg cta tgt ggc tat aaa gga tga agatgaacgc cctgtttgct tttcagcctc	678
Trp Leu Cys Gly Tyr Lys Gly	
50	

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<211> 1526
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (684)..(1016)
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t t t t a a t t c c c t t t t c g a c g a a t t c g t g o g g g g a g a a t g g t g g e t g c t t t t g a a t t t c e t		120
g a c t c t g g t g g c t t c a c t g t c a c a t c t a t g g g g t g t a a g g g a g g a a g a g t g t c g a g t t t		180
t g t g c c a t g a a c a g a t t c c g t t t e t g c g a g g a c a g c g t g c a g g g g a c a c c e t t c g a g g c		240
t t t g g a g c c a c e t a g g a a g c a g g c t g g c t g c t g c a c a g g c c t c t g c t g g c c t c e t t g c a c		300
a t g t c e t t g g t g g g t g a g g c a g c c a c g t g a g a t g g c t t c c g g c a c t g c t g g c g t g a g t a g		360
c e t t c e t g g c a a t g c c a g c t e t t g c c g t c c t c a c t c e t g g c c c a g a t g g c c g c a t g a c		420
g g c t c t e t g t t e t a c a c a g e c e t c e t g g t c t t c a g t g c c c t g g g a a a c a t c e t t g c c e t t		480
t g c e t t a c c t g t c a a a a g a g c a g g a a g a t c a a c t g c a c a g g c a t c t a c c t g g t g c a c c t g		540
g c t g t g t c t g a c c t g c t g t t c a c c g t g g c c t t a c c g g g a a g g g t g g t g t g t t a t g t g e t g		600
g g c t c c a g e t g g c c t t t c g g c a a g g g g c t c t g c a g g t g a c g g c g t t t g t g c t c t a c a c c		660
g a c a c e t a c g g g g g g t e t a c c t c	atg gcc tgt gtg agc gtg gac cat tac Met Ala Cys Val Ser Val Asp His Tyr	710
	1 5	
c c a g e t g t g g t c t g t g c c c a c t g g g g c c c g t g c c t c c g c a c g g c t g g c		758
Pro Ala Val Val Cys Ala His Trp Gly Pro Cys Leu Arg Thr Ala Gly		
10 15 20 25		
c g c g c c a g g c t g g t c t g c g t g g c c a t c t g g a c c t t g g t g c t g c t g c a g		806
Arg Ala Arg Leu Val Cys Val Ala Ile Trp Thr Leu Val Leu Leu Gln		
30 35 40 45		
a c g a t g c c c t t g c t c t t g a t g c c c a t g a c c a a g c c g c t g g t g g g c a a g		854
Thr Met Pro Leu Leu Leu Met Pro Met Thr Lys Pro Leu Val Gly Lys		
45 50 55		
c t g g c c t g c a t g g a g t a c a g c a g c a t g g a g t c a g t c c t c g g g c t g c c c		902
Leu Ala Cys Met Glu Tyr Ser Ser Met Glu Ser Val Leu Gly Leu Pro		
60 65 70		

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ctc atg gtc ctg gtg gcc ttt gcc att ggc ttc tgt ggg cca gtg ggg      950
Leu Met Val Leu Val Ala Phe Ala Ile Gly Phe Cys Gly Pro Val Gly
      75              80              85

atc atc ctg tcc tgc tat atg aag atc acc tgg aag ctg tgc agc aca      998
Ile Ile Leu Ser Cys Tyr Met Lys Ile Thr Trp Lys Leu Cys Ser Thr
      90              95              100              105

gct ggg aga acc cag tga ccagcg ggaaaggaca ccaccggcgg ggcagcccg      1052
Ala Gly Arg Thr Gln
      110

gaggaccag tgaccagcag gaaaggacgc caccggcggg gcagcccagg aggaccag      1112

gaccagcggg aaaggacacc accagcagga cagcccagaga ggaccagtg accagcggga      1172

aaggatgcc cggcgggac agcccgagg gaccagtgga ccagcaggaa aggacgccac      1232

tggcgaggt gctgcttac gctgctgat ctggtggcgg tgggtggtctg ctcagcccc      1292

taccacctca acatcaagca gttcatggcg agagggatgc tccacctgcc atcctgtgcc      1352

gagcgagggg ctttcttact gtcccttcag gccaccgtgg cctcatgaa catgaactgt      1412

ggcattaccc catcatttac ttctttgcat ccaccatta caggaatagg ctcctgggca      1472

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<210> 34
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<212> DNA
<213> Homo sapiens

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atctactgac taatggatcc tccaattgtt aagcctatgt tacaggacaa aggcgctcgc      180
tttgtaaaag cttgaagtgc agtttctgctc tgagtacaga agacctttgc aaacagagag      240
gggagatttt ctctgtaagg ttgcaaacaa gagcaggtcc tggaagataa gattccccgc      300

c   atg tta tcc tcc gtg gtg ttt tgg gga cta att gcc ctc att ggc      346
Met Leu Ser Ser Val Val Phe Trp Gly Leu Ile Ala Leu Ile Gly
      1              5              10              15

act tcc agg ggc tca tac ccc ttc agt cac tca atg aag cct cac cta      394
Thr Ser Arg Gly Ser Tyr Pro Phe Ser His Ser Met Lys Pro His Leu
      20              25              30

cat cca cgc ctg tac cac ggc tgc tat ggg gac atc atg acc atg aag      442

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His	Pro	Arg	Leu	Tyr	His	Gly	Cys	Tyr	Gly	Asp	Ile	Met	Thr	Met	Lys		
				35					40					45			
acc	tct	ggg	gcc	act	tgt	gat	gca	aac	agt	gtg	atg	aac	tgc	ggg	atc	490	
Thr	Ser	Gly	Ala	Thr	Cys	Asp	Ala	Asn	Ser	Val	Met	Asn	Cys	Gly	Ile		
				50					55					60			
cgt	ggt	tct	gaa	atg	ttt	gct	gag	atg	gat	ttg	agg	gcc	ata	aaa	cct	538	
Arg	Gly	Ser	Glu	Met	Phe	Ala	Glu	Met	Asp	Leu	Arg	Ala	Ile	Lys	Pro		
				65					70					75			
tac	cag	act	ctg	atc	aaa	gaa	gtc	ggg	cag	aga	cat	tgc	gtg	gac	cct	586	
Tyr	Gln	Thr	Leu	Ile	Lys	Glu	Val	Gly	Gln	Arg	His	Cys	Val	Asp	Pro		
				80					85					90			95
gct	gtc	atc	gca	gcc	atc	atc	tcc	agg	gaa	agc	cat	ggc	gga	tct	gtc	634	
Ala	Val	Ile	Ala	Ala	Ile	Ile	Ser	Arg	Glu	Ser	His	Gly	Gly	Ser	Val		
				100					105					110			
ctg	caa	gac	ggc	tgg	gac	cac	agg	gga	ctt	aaa	ttt	ggc	ttg	atg	cag	682	
Leu	Gln	Asp	Gly	Trp	Asp	His	Arg	Gly	Leu	Lys	Phe	Gly	Ileu	Met	Gln		
				115					120					125			
ctt	gat	aaa	caa	acg	tac	cac	cct	gtc	ggt	gcc	tgg	gat	agc	aaa	gag	730	
Leu	Asp	Lys	Gln	Thr	Tyr	His	Pro	Val	Gly	Ala	Trp	Asp	Ser	Lys	Glu		
				130					135					140			
cac	ctt	tca	cag	gct	act	ggg	att	cta	aca	gag	aga	att	aag	gca	atc	778	
His	Leu	Ser	Gln	Ala	Thr	Gly	Ile	Leu	Thr	Glu	Arg	Ile	Lys	Ala	Ile		
				145					150					155			
cag	aaa	aaa	ttc	ccc	acg	tgg	agt	gtt	gct	cag	cac	ctc	aaa	ggt	ggt	826	
Gln	Lys	Lys	Phe	Pro	Thr	Trp	Ser	Val	Ala	Gln	His	Leu	Lys	Gly	Gly		
				160					165					170			175
ctc	tca	gct	ttt	aag	tca	gga	att	gaa	gcg	att	gcc	acc	cca	tcg	gac	874	
Leu	Ser	Ala	Phe	Lys	Ser	Gly	Ile	Glu	Ala	Ile	Ala	Thr	Pro	Ser	Asp		
				180					185					190			
ata	gac	aat	gac	ttc	gtc	aat	gat	atc	att	gct	cga	gct	aag	ttc	tat	922	
Ile	Asp	Asn	Asp	Phe	Val	Asn	Asp	Ile	Ile	Ala	Arg	Ala	Lys	Phe	Tyr		
				195					200					205			
aaa	aga	caa	agc	ttc	tag	gcaaag	ctctgtgggt	gggccagggt	ggcagagtgc							976	
Lys	Arg	Gln	Ser	Phe													
				210													
tcagatggcc	gcctttgaga	gttttacgtg	aatgtgtgtg	atacaacact	ggcacagaaa											1036	
tgattaaaat	catgaaagaa	aattcatttc	ccaattttct	gaatgaaaat	aatcattgaa											1096	
aaaaggaaag	aaaaataaaa	gaaatccatc	cagttocaaa	tatgttctct	aggaaaaggga											1156	
catagacata	tatataacta	ctttgcagta	aatgtgaata	tcattggcaaa	tggtccctag											1216	
gtattccagc	caggcttcat	tttagcctgt	gattccaatg	cccacctact	ccctgtctac											1276	
cagaattgct	aacaagttaa	gtaagcccta	cccgagcctt	tgtctttttt	ccagtatctg											1336	
cccgagagccc	tcaagctttg	cttatgagaa	gttc												1370		

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<210> 35
<211> 1225
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (375)..(1178)

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ttccaacatg caaaggacaa gtacgatcat gtgtgccacc tcctcaactc tccaatgggtg      120
aagttaagga gataagaaaa gaggaatatg gacacaatga agtagtgga tatgattgca      180
atcctaattt tataataaac gggcctaaga aaatacaatg cgtggatgga gaatggacaa      240
ctttaccac ttgtgttgaa caagtgaaaa catgtggata catacctgaa ctcgagtacg      300
gttatgttca gccgtctgtc cctccctatc aacatggagt ttcagtcgag gtgaattgca      360
gaaatgaata tgca atg att gga aat aac atg att acc tgt att aat gga      410
Met Ile Gly Asn Asn Met Ile Thr Cys Ile Asn Gly
      1 5 10
ata tgg aca gag ctt cct atg tgt gtt gca aca cac caa ctt aag agg      458
Ile Trp Thr Glu Leu Pro Met Cys Val Ala Thr His Gln Leu Lys Arg
      15 20 25
tgc aaa ata gca gga gtt aat ata aaa aca tta ctc aag cta tct ggg      506
Cys Lys Ile Ala Gly Val Asn Ile Lys Thr Leu Lys Leu Ser Gly
      30 35 40
aaa gaa ttt aat cat aat tct aga ata cgt tac aga tgt tca gac atc      554
Lys Glu Phe Asn His Asn Ser Arg Ile Arg Tyr Arg Cys Ser Asp Ile
      45 50 55 60
ttc aga tac agg cac tca gtc tgt ata aac ggg aaa tgg aat cct gaa      602
Phe Arg Tyr Arg His Ser Val Cys Ile Asn Gly Lys Trp Asn Pro Glu
      65 70 75
gta gac tgc aca gaa aaa agg gaa caa ttc tgc cca ccg cca cct cag      650
Val Asp Cys Thr Glu Lys Arg Glu Gln Phe Cys Pro Pro Pro Pro Gln
      80 85 90
ata cct aat gct cag aat atg aca acc aca gtg aat tat cag gat gga      698
Ile Pro Asn Ala Gln Asn Met Thr Thr Thr Val Asn Tyr Gln Asp Gly
      95 100 105
gaa aaa gta gct gtt ctc tgt aaa gaa aac tat cta ctt cca gaa gca      746
Glu Lys Val Ala Val Leu Cys Lys Glu Asn Tyr Leu Leu Pro Glu Ala
      110 115 120
aaa gaa att gta tgt aaa gat gga cga tgg caa tca tta cca cgc tgt      794
Lys Glu Ile Val Cys Lys Asp Gly Arg Trp Gln Ser Leu Pro Arg Cys
      125 130 135 140

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gtt gag tct act gca tat tgt ggg ccc cct cca tct att aac aat gga      842
Val Glu Ser Thr Ala Tyr Cys Gly Pro Pro Ser Ile Asn Asn Gly
      145                      150                      155

gat acc acc tca ttc cca tta tca gta tat cct cca ggg tca aca gtg      890
Asp Thr Thr Ser Phe Pro Leu Ser Val Tyr Pro Pro Gly Ser Thr Val
      160                      165                      170

acg tac cgt tgc cag tcc ttc tat aaa ctc cag ggc tct gta act gta      938
Thr Tyr Arg Cys Gln Ser Phe Tyr Lys Leu Gln Gly Ser Val Thr Val
      175                      180                      185

aca tgc aga aat aaa cag tgg tca gaa cca cca aga tgc cta gat cca      986
Thr Cys Arg Asn Lys Gln Trp Ser Glu Pro Pro Arg Cys Leu Asp Pro
      190                      195                      200

tgt gtg gta tct gaa gaa aac atg aac aaa aat aac ata cag tta aaa      1034
Cys Val Val Ser Glu Glu Asn Met Asn Lys Asn Asn Ile Gln Leu Lys
      205                      210                      215                      220

tgg aga aac gat gga aaa ctc tat gca aaa aca ggg gat gct gtt gaa      1082
Trp Arg Asn Asp Gly Lys Leu Tyr Ala Lys Thr Gly Asp Ala Val Glu
      225                      230                      235

ttc cag tgt aaa ttc cca cat aaa gcg atg ata tca tca cca cca ttt      1130
Phe Gln Cys Lys Phe Pro His Lys Ala Met Ile Ser Ser Pro Pro Phe
      240                      245                      250

cga gca atc tgt cag gaa ggg aaa ttt gaa tat cct ata tgt gaa tga      1178
Arg Ala Ile Cys Gln Glu Gly Lys Phe Glu Tyr Pro Ile Cys Glu
      255                      260                      265

agcaagcata attttcctga atatattcct caaacatcca tctatgc      1225

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<210> 36
<211> 4397
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (306)..(4397)

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<400> 36
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actgtgaaga ggtgaactct tcaaacacgc tgagcaaaaca gggccgactc ccagggccgc      120
atccgggatg tctcaatagc tgtggccttg acgtccacct cggaccacct ccccgaccc      180
agcccagttc ccaatgggcc ctctgcccg ggagcgggtc taccggcctg gatgtgaaag      240
agagcttgga gacccagag acctcggaac ctacagcttt ggaagtgaag tcggtggggg      300

tcccc      atg ggg ccg gac gag gcc aca cca ccc gac ctg gtg ctt cct      347
Met Gly Pro Asp Glu Ala Thr Pro Pro Asp Leu Val Leu Pro
      1                      5                      10

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gcc tgg cgt ctg cgc cac gga gca ttc agg acg ctg gtg acc agg gag	395
Ala Trp Arg Leu Arg His Gly Ala Phe Arg Thr Leu Val Thr Arg Glu	
15 20 25 30	
cca gga gcc ccc agg atg ggt gcc cgg agc gcg tgc cgg acg ctg gtg	443
Pro Gly Ala Pro Arg Met Gly Ala Pro Ser Ala Cys Arg Thr Leu Val	
35 40 45	
ttg gct ctg gcg gcc atg ctc gtg gtg ccg cag gca gag acc cag ggc	491
Leu Ala Leu Ala Ala Met Leu Val Val Pro Gln Ala Glu Thr Gln Gly	
50 55 60	
cct gtg gag cgg agc tgg gag aat gca ggg cac acc atg gat ggc ggt	539
Pro Val Glu Pro Ser Trp Glu Asn Ala Gly His Thr Met Asp Gly Gly	
65 70 75	
gcc cgg acg tcc tcg ccc acc cgg cgc gtg agc ttt gtt cca ccc gtc	587
Ala Pro Thr Ser Ser Pro Thr Arg Arg Val Ser Phe Val Pro Pro Val	
80 85 90	
act gtc ttc ccc agc ctg agc ccc ctg aac cgg gcg cac aat ggg cgg	635
Thr Val Phe Pro Ser Leu Ser Pro Leu Asn Pro Ala His Asn Gly Arg	
95 100 105 110	
gtg tgc agc acc tgg ggt gac ttc cac tac aag acc ttc gac ggc gac	683
Val Cys Ser Thr Trp Gly Asp Phe His Tyr Lys Thr Phe Asp Gly Asp	
115 120 125	
gtc ttc cgc ttc cct ggc ctt tgc aac tac gtg ttc tct gag cac tgc	731
Val Phe Arg Phe Pro Gly Leu Cys Asn Tyr Val Phe Ser Glu His Cys	
130 135 140	
cgc gcc gcc tac gag gac ttc aac gtc cag cta cgc cga ggc cta gtg	779
Arg Ala Ala Tyr Glu Asp Phe Asn Val Gln Leu Arg Arg Gly Leu Val	
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Gly Ser Arg Pro Val Val Thr Arg Val Val Ile Lys Ala Gln Gly Leu	
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Val Leu Glu Ala Ser Asn Gly Ser Val Leu Ile Asn Gly Gln Arg Glu	
175 180 185 190	
gag ctg cct tac agc cgc act ggc ctc ctg gtg gag cag agc ggg gac	923
Glu Leu Pro Tyr Ser Arg Thr Gly Leu Leu Val Glu Gln Ser Gly Asp	
195 200 205	
tac atc aag gtc agc atc cgg ctg gtg ctg aca ttc ctg tgg aac gga	971
Tyr Ile Lys Val Ser Ile Arg Leu Val Leu Thr Phe Leu Trp Asn Gly	
210 215 220	
gag gac agt gcc ctg ctg gag ctg gat ccc aaa tac gcc aac cag acc	1019
Glu Asp Ser Ala Leu Leu Glu Leu Asp Pro Lys Tyr Ala Asn Gln Thr	
225 230 235	
tgt ggc ctg tgt ggg gac ttc aac ggc ctc ccg gcc ttc aac gag ttc	1067
Cys Gly Leu Cys Gly Asp Phe Asn Gly Leu Pro Ala Phe Asn Glu Phe	
240 245 250	
tat gcc cac agt gag tgc cac ctg gac gcc agg ctg acc cgg ctc cag	1115

Tyr	Ala	His	Ser	Glu	Cys	His	Leu	Asp	Ala	Arg	Leu	Thr	Pro	Leu	Gln	
255					260					265					270	
ttt	ggg	aac	ctg	cag	aag	ttg	gat	ggg	ccc	acg	gag	cag	tgc	ccg	gac	1163
Phe	Gly	Asn	Leu	Gln	Lys	Leu	Asp	Gly	Pro	Thr	Glu	Gln	Cys	Pro	Asp	
				275					280					285		
ccg	ctg	ccc	ttg	ccg	gcc	ggc	aac	tgc	acg	gac	gag	gag	ggc	atc	tgc	1211
Pro	Leu	Pro	Leu	Pro	Ala	Gly	Asn	Cys	Thr	Asp	Glu	Glu	Gly	Ile	Cys	
			290					295					300			
cac	cgc	acc	ctg	ctg	ggg	ccg	gcc	ttt	gcg	gag	tgc	cac	gca	ctg	gtg	1259
His	Arg	Thr	Leu	Leu	Gly	Pro	Ala	Phe	Ala	Glu	Cys	His	Ala	Leu	Val	
			305					310					315			
gac	agc	act	gcg	tac	ctg	gcc	gcc	tgc	gcc	cag	gac	ctg	tgc	cgc	tgc	1307
Asp	Ser	Thr	Ala	Tyr	Leu	Ala	Ala	Cys	Ala	Gln	Asp	Leu	Cys	Arg	Cys	
			320				325					330				
ccc	acc	tgc	ccg	tgt	gcc	acc	ttt	gtg	gaa	tac	tca	cgc	cag	tgc	gcc	1355
Pro	Thr	Cys	Pro	Cys	Ala	Thr	Phe	Val	Glu	Tyr	Ser	Arg	Gln	Cys	Ala	
					340					345				350		
cac	gcg	ggg	ggc	cag	ccg	cgg	aac	tgg	agg	tgc	cct	gag	ctc	tgc	ccc	1403
His	Ala	Gly	Gly	Gln	Pro	Arg	Asn	Trp	Arg	Cys	Pro	Glu	Leu	Cys	Pro	
				355					360					365		
cgg	acc	tgc	ccc	ctc	aac	atg	cag	cac	cag	gag	tgt	ggc	tca	ccc	tgc	1451
Arg	Thr	Cys	Pro	Leu	Asn	Met	Gln	His	Gln	Glu	Cys	Gly	Ser	Pro	Cys	
				370					375				380			
acg	gac	acc	tgc	tcc	aac	ccc	cag	cgc	gcg	cag	ctc	tgt	gag	gac	cac	1499
Thr	Asp	Thr	Cys	Ser	Asn	Pro	Gln	Arg	Ala	Gln	Leu	Cys	Glu	Asp	His	
				385					390				395			
tgt	gtg	gac	ggc	tgc	ttc	tgc	ccc	cca	ggc	acg	gtg	ctg	gat	gac	atc	1547
Cys	Val	Asp	Gly	Cys	Phe	Cys	Pro	Pro	Gly	Thr	Val	Leu	Asp	Asp	Ile	
				400			405					410				
acg	cac	tct	ggc	tgc	ctg	ccc	ctc	ggg	cag	tgc	ccc	tgc	acc	cac	ggc	1595
Thr	His	Ser	Gly	Cys	Leu	Pro	Leu	Gly	Gln	Cys	Pro	Cys	Thr	His	Gly	
					420					425				430		
ggc	cgc	acc	tac	agc	ccg	ggc	acc	tcc	ttc	aac	acc	acc	tgc	agc	tcc	1643
Gly	Arg	Thr	Tyr	Ser	Pro	Gly	Thr	Ser	Phe	Asn	Thr	Thr	Cys	Ser	Ser	
					435				440					445		
tgc	acc	tgc	tcc	ggg	ggg	cta	tgg	cag	tgc	cag	gac	ctg	ccg	tgc	cct	1691
Cys	Thr	Cys	Ser	Gly	Gly	Leu	Trp	Gln	Cys	Gln	Asp	Leu	Pro	Cys	Pro	
				450					455				460			
ggc	acc	tgc	tct	gtg	cag	ggc	ggg	gcc	cac	atc	tcc	acc	tat	gat	gag	1739
Gly	Thr	Cys	Ser	Val	Gln	Gly	Gly	Ala	His	Ile	Ser	Thr	Tyr	Asp	Glu	
							470					475				
aaa	ctc	tac	gac	ctg	cat	ggc	gac	tgc	agc	tac	gtt	ctg	tcc	aag	aaa	1787
Lys	Leu	Tyr	Asp	Leu	His	Gly	Asp	Cys	Ser	Tyr	Val	Leu	Ser	Lys	Lys	
				480			485					490				
tgt	gcc	gac	agc	agc	ttc	acc	gtg	ctg	gct	gag	ctg	cgg	aag	tgc	ggc	1835
Cys	Ala	Asp	Ser	Ser	Phe	Thr	Val	Leu	Ala	Glu	Leu	Arg	Lys	Cys	Gly	

495	500					505					510					
ctg acg gac aac gag aac tgc ctg aaa gcg gtg acg ctc agc ctg gac	aag gaa gaa gaa gaa					gaa gaa gaa gaa gaa					gaa gaa gaa gaa gaa					1883
Leu Thr Asp Asn Glu Asn Cys Leu Lys Ala Val Thr Leu Ser Leu Asp	515					520					525					
ggc ggg gac acg gcc atc cgg gtc caa gcg gac ggc ggc gtg ttc ctc	gaa gaa gaa gaa gaa					gaa gaa gaa gaa gaa					gaa gaa gaa gaa gaa					1931
Gly Gly Asp Thr Ala Ile Arg Val Gln Ala Asp Gly Gly Val Phe Leu	530					535					540					
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Asn Ser Ile Tyr Thr Gln Leu Pro Leu Ser Ala Ala Asn Ile Thr Leu	545					550					555					
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Phe Thr Pro Ser Ser Phe Phe Ile Val Val Gln Thr Gly Leu Gly Leu	560					565					570					
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Gln Leu Leu Val Gln Leu Val Pro Leu Met Gln Val Phe Val Arg Leu	575					580					585					
gac ccc gcc cac cag ggc cag atg tgc ggc ctg tgt ggg aac ttc aac	aag gaa gaa gaa gaa					gaa gaa gaa gaa gaa					gaa gaa gaa gaa gaa					2123
Asp Pro Ala His Gln Gly Gln Met Cys Gly Leu Cys Gly Asn Phe Asn	595					600					605					
cag aac cag gct gac gac ttc acg gcc ctc agc ggg gtg gtg gag gcc	aag gaa gaa gaa gaa					gaa gaa gaa gaa gaa					gaa gaa gaa gaa gaa					2171
Gln Asn Gln Ala Asp Asp Phe Thr Ala Leu Ser Gly Val Val Glu Ala	610					615					620					
acg ggc gca gcc ttc gcc aac acc tgg aag gcc cag gct gcc tgt gcc	aag gaa gaa gaa gaa					gaa gaa gaa gaa gaa					gaa gaa gaa gaa gaa					2219
Thr Gly Ala Ala Phe Ala Asn Thr Trp Lys Ala Gln Ala Ala Cys Ala	625					630					635					
aat gcc agg aac agc ttt gag gac ccc tgc tcc ctc agt gtg gag aat	aag gaa gaa gaa gaa					gaa gaa gaa gaa gaa					gaa gaa gaa gaa gaa					2267
Asn Ala Arg Asn Ser Phe Glu Asp Pro Cys Ser Leu Ser Val Glu Asn	640					645					650					
gag aac tac gcc cgg cac tgg tgc tgc cgc ctg acc gat ccc aac agt	aag gaa gaa gaa gaa					gaa gaa gaa gaa gaa					gaa gaa gaa gaa gaa					2315
Glu Asn Tyr Ala Arg His Trp Cys Ser Arg Leu Thr Asp Pro Asn Ser	655					660					665					
gcc ttc tog cgc tgc cac tcc atc atc aac ccc aag ccc ttc cac tog	aag gaa gaa gaa gaa					gaa gaa gaa gaa gaa					gaa gaa gaa gaa gaa					2363
Ala Phe Ser Arg Cys His Ser Ile Ile Asn Pro Lys Pro Phe His Ser	675					680					685					
aac tgc atg ttc gac acc tgc aac tgt gag cgg agc gag gac tgc ctg	aag gaa gaa gaa gaa					gaa gaa gaa gaa gaa					gaa gaa gaa gaa gaa					2411
Asn Cys Met Phe Asp Thr Cys Asn Cys Glu Arg Ser Glu Asp Cys Leu	690					695					700					
tgc gcc gcg ctg tcc tcc tat gtg cac gcc tgt gcc gcc aag ggc gta	aag gaa gaa gaa gaa					gaa gaa gaa gaa gaa					gaa gaa gaa gaa gaa					2459
Cys Ala Ala Leu Ser Ser Tyr Val His Ala Cys Ala Ala Lys Gly Val	705					710					715					
cag ctc agc gac tgg agg gac ggc gtc tgc acc aag tac atg cag aac	aag gaa gaa gaa gaa					gaa gaa gaa gaa gaa					gaa gaa gaa gaa gaa					2507
Gln Leu Ser Asp Trp Arg Asp Gly Val Cys Thr Lys Tyr Met Gln Asn	720					725					730					
tgc ccc aag tcc cag cgc tac gcc tac gtg gtg gat gcc tgc cag ccc	aag gaa gaa gaa gaa					gaa gaa gaa gaa gaa					gaa gaa gaa gaa gaa					2555
Cys Pro Lys Ser Gln Arg Tyr Ala Tyr Val Val Asp Ala Cys Gln Pro	735					740					745					

act tgc cgc ggc ctg agt gag gcc gac gtc acc tgc agc gtt tcc ttc Thr Cys Arg Gly Leu Ser Glu Ala Asp Val Thr Cys Ser Val Ser Phe 755 760 765	2603
gtg cct gtg gac ggc tgc acc tgc ccc gcg ggc acc ttc ctc aat gac Val Pro Val Asp Gly Cys Thr Cys Pro Ala Gly Thr Phe Leu Asn Asp 770 775 780	2651
gcg ggc gcc tgt gtg ccc gcc cag aag tgc ccc tgc tac gct cac ggc Ala Gly Ala Cys Val Pro Ala Gln Lys Cys Pro Cys Tyr Ala His Gly 785 790 795	2699
acc gtg ctg gct cct gga gag gtg gtg cac gac gag ggc gcc gtg tgt Thr Val Leu Ala Pro Gly Glu Val Val His Asp Gly Ala Val Cys 800 805 810	2747
tca tgt acg ggt ggg aag cta agc tgc ctg gga gcc tct ctg cag aaa Ser Cys Thr Gly Gly Lys Leu Ser Cys Leu Gly Ala Ser Leu Gln Lys 815 820 825 830	2795
agc aca ggg tgt gca gcc ccc atg gtg tac ctg gac tgc agc aac agc Ser Thr Gly Cys Ala Ala Pro Met Val Tyr Leu Asp Cys Ser Asn Ser 835 840 845	2843
tcg gcg ggc acc cct ggg gcc gag tgc ctc cgg agc tgc cac acg ctg Ser Ala Gly Thr Pro Gly Ala Glu Cys Leu Arg Ser Cys His Thr Leu 850 855 860	2891
gac gtg ggc tgt ttc agc aca cac tgc gtg tcc ggc tgt gtc tgt ccc Asp Val Gly Cys Phe Ser Thr His Cys Val Ser Gly Cys Val Cys Pro 865 870 875	2939
ccg ggg ctg gtg tgc gat ggg agt ggg ggc tgc att gcc gag gag gac Pro Gly Leu Val Ser Asp Gly Ser Gly Gly Cys Ile Ala Glu Glu Asp 880 885 890	2987
tgc ccc tgt gtg cac aac gag gcc acc tac aag cct gga gag acc atc Cys Pro Cys Val His Asn Glu Ala Thr Tyr Lys Pro Gly Glu Thr Ile 895 900 905 910	3035
agg gtc gac tgc aac acc tgc acc tgc agg aac cgg agg tgg gag tgc Arg Val Asp Cys Asn Thr Cys Thr Cys Arg Asn Arg Arg Trp Glu Cys 915 920 925	3083
agc cac cgg ctc tgc ctg ggc acc tgc gtg gcc tac ggg gat ggc cac Ser His Arg Leu Cys Leu Gly Thr Cys Val Ala Tyr Gly Asp Gly His 930 935 940	3131
ttc atc acc ttt gat ggc gat cgc tac agc ttt gaa ggc agc tgc gag Phe Ile Thr Phe Asp Gly Asp Arg Tyr Ser Phe Glu Gly Ser Cys Glu 945 950 955	3179
tac atc ttg gcc cag gac tac tgt ggg gag aac acc acc cac ggc acc Tyr Ile Leu Ala Gln Asp Tyr Cys Gly Asp Asn Thr Thr His Gly Thr 960 965 970	3227
ttc cgc atc gtc acc gag aac atc ccc tgt ggg acc acc ggc acc acc Phe Arg Ile Val Thr Glu Asn Ile Pro Cys Gly Thr Thr Gly Thr Thr 975 980 985 990	3275

tgc tcc aag gcc atc aag ctc ttc gtg gag agc tac gag ctg atc ctc Cys Ser Lys Ala Ile Lys Leu Phe Val Glu Ser Tyr Glu Leu Ile Leu 995 1000 1005	3323
caa gag ggg acc ttt aag gcg gtg gcg aga ggg ccg ggt ggg gac cca Gln Glu Gly Thr Phe Lys Ala Val Ala Arg Gly Pro Gly Gly Asp Pro 1010 1015 1020	3371
ccc tac aag ata cgc tac atg ggg atc ttc ctg gtc atc gag acc cac Pro Tyr Lys Ile Arg Tyr Met Gly Ile Phe Leu Val Ile Glu Thr His 1025 1030 1035	3419
ggg atg gcc gtg tcc tgg gac cgg aag acc agc gtg ttc atc cga ctg Gly Met Ala Val Ser Trp Asp Arg Lys Thr Ser Val Phe Ile Arg Leu 1040 1045 1050	3467
cac cag gac tac aag ggc agg gtc tgc ggc ctg tgc ggg aac ttc gac His Gln Asp Tyr Lys Gly Arg Val Cys Gly Leu Cys Gly Asn Phe Asp 1055 1060 1065 1070	3515
gac aat gcc atc aat gac ttt gcc acg cgt agc cgg tcc gtg gtg ggg Asp Asn Ala Ile Asn Asp Phe Ala Thr Arg Ser Arg Ser Val Val Gly 1075 1080 1085	3563
gac gca ctg gag ttt ggg aac agc tgg aag ctc tcc ccc tcc tgc ccg Asp Ala Leu Glu Phe Gly Asn Ser Trp Lys Leu Ser Pro Ser Cys Pro 1090 1095 1100	3611
gac gcc ctg gca ccc aag gac ccc tgc acg gcc aac ccc ttc cgc aag Asp Ala Leu Ala Pro Lys Asp Pro Cys Thr Ala Asn Pro Phe Arg Lys 1105 1110 1115	3659
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gcc tgc cgc tcc cag gtt gac tcc acc aag tac tac gag gcc tgc gtg Ala Cys Arg Ser Gln Val Asp Ser Thr Lys Tyr Tyr Glu Ala Cys Val 1135 1140 1145 1150	3755
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aac cca cat ggg ggc tgt gag tgg cac tac cag ccc tgc ggg gca ccc Asn Pro His Gly Gly Cys Glu Trp His Tyr Gln Pro Cys Gly Ala Pro 1200 1205 1210	3947
tgc cta aaa acc tgc cgg aac ccc agt ggg cac tgc ctg gtg gac ctg Cys Leu Lys Thr Cys Arg Asn Pro Ser Gly His Cys Leu Val Asp Leu 1215 1220 1225 1230	3995
cct ggc ctg gaa ggc tgc tac ccg aag tgc cca ccc agc cag ccc ttc	4043

Pro Gly Leu Glu Gly Cys Tyr	Pro Lys Cys Pro Pro Ser Gln Pro Phe	
1235	1240	1245
ttc aat gag gac cag atg aag tgc gtg gcc cag tgt ggc tgc tac gac	4091	
Phe Asn Glu Asp Gln Met Lys Cys Val Ala Gln Cys Gly Cys Tyr Asp		
1250	1255	1260
aag gac gga aac tac tat gac gtc ggt gca agg gtc ccc aca gcg gag	4139	
Lys Asp Gly Asn Tyr Tyr Asp Val Gly Ala Arg Val Pro Thr Ala Glu		
1265	1270	1275
aac tgc cag agc tgt aac tgc aca ccc agt ggc atc cag tgc gct cac	4187	
Asn Cys Gln Ser Cys Asn Cys Thr Pro Ser Gly Ile Gln Cys Ala His		
1280	1285	1290
agc ctt gag gcc tgc acc tgc acc tat gag gac agg acc tac agc tac	4235	
Ser Leu Glu Ala Cys Thr Cys Thr Tyr Glu Asp Arg Thr Tyr Ser Tyr		
1295	1300	1305
cag gac gtc atc tac aac acc acc gat ggg ctt ggc gcc tgc ttg atc	4283	
Gln Asp Val Ile Tyr Asn Thr Thr Asp Gly Leu Gly Ala Cys Leu Ile		
1315	1320	1325
gcc atc tgc gga agc aac gcc acc atc atc agg aag gct gtg gca tgt	4331	
Ala Ile Cys Gly Ser Asn Gly Thr Ile Ile Arg Lys Ala Val Ala Cys		
1330	1335	1340
cct gga act cca gcc aca acg cca ttc acc ttc acc acc gcc tgg gtc	4379	
Pro Gly Thr Pro Ala Thr Thr Pro Phe Thr Phe Thr Thr Ala Trp Val		
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cag aat aca gaa acc tca tcc ctt gtc agc atg acc tct gcc acc att	96	
Gln Asn Thr Glu Thr Ser Ser Leu Val Ser Met Thr Ser Ala Thr Ile		
15 20 25		
ccc agt gtg aga cca act ttt aca agt aca cac aac act ctg aca agt	144	
Pro Ser Val Arg Pro Thr Phe Thr Ser Thr His Asn Thr Leu Thr Ser		
30 35 40		

tcc ctc cta acg acg ttc cca ggg acg tat tca ttt tcc tct tcc atg Ser Leu Leu Thr Thr Phe Pro Gly Thr Tyr Ser Phe Ser Ser Ser Met 45 50 55 60	192
tct gcc agc agt gat ggg acc act cac aca gaa act atc acc tca ctt Ser Ala Ser Ser Asp Gly Thr Thr His Thr Glu Thr Ile Thr Ser Leu 65 70 75	240
cca gcc agc acc agt aca ctc cac acc aca gct gaa tcc acc aca gca Pro Ala Ser Thr Ser Thr Leu His Thr Thr Ala Glu Ser Thr Thr Ala 80 85 90	288
cac act acc acc acc tca ttc aca act tcc aca act atg gaa tca cct His Thr Thr Thr Thr Ser Phe Thr Thr Ser Thr Thr Met Glu Ser Pro 95 100 105	336
tca tcc agt gta gca act aca agc aca ggt cag acc acc ttc tcc agc Ser Ser Ser Val Ala Thr Thr Ser Thr Gly Gln Thr Thr Phe Ser Ser 110 115 120	384
tct acg gcc aca ttc act gag acc acc aca ttg act cct acg act gac Ser Thr Ala Thr Phe Thr Glu Thr Thr Thr Leu Thr Pro Thr Thr Asp 125 130 135 140	432
ttt tct gaa gaa act ctc aca aca gcc atg act tct act ccc ccc atc Phe Ser Glu Glu Thr Thr Ala Met Thr Ser Thr Pro Pro Ile 145 150 155	480
act tct tca atc act ccc acc aat aca gtg act tct atg aca act atg Thr Ser Ser Ile Thr Pro Thr Asn Thr Val Thr Ser Met Thr Thr Met 160 165 170	528
acc tcc tgg ccc aca gcc act aat acg ttg tca tcc ctc acc act aac Thr Ser Trp Pro Thr Ala Thr Asn Thr Leu Ser Ser Leu Thr Thr Asn 175 180 185	576
att tta tct tct aca cct gtc ccg agc aca gag agg acc acc agt cat Ile Leu Ser Ser Thr Pro Val Pro Ser Thr Glu Arg Thr Thr Ser His 190 195 200	624
act aca aac atc aat cct gta tcc acc ttg gtg acc aca ctc ccc act Thr Thr Asn Ile Asn Pro Val Ser Thr Leu Val Thr Thr Leu Pro Thr 205 210 215 220	672
acc atc acc agg tct aca cct aca tct gag acc acc tac cct att tct Thr Ile Thr Arg Ser Thr Pro Thr Ser Glu Thr Thr Tyr Pro Ile Ser 225 230 235	720
tcc acc agc act gtc aca gag tcc acg act gaa atc acc tat tcc act Ser Thr Ser Thr Val Thr Glu Ser Thr Thr Thr Glu Ile Thr Tyr Ser Thr 240 245 250	768
act atg aca gag aca tca tcc agt gcc acc tct ctt cca ctc acc tct Thr Met Thr Glu Thr Ser Ser Ser Ala Thr Ser Leu Pro Leu Thr Ser 255 260 265	816
ccc ttg gtc tca acc aca gaa aca gcc aaa act cct acc aca atc ttg Pro Leu Val Ser Thr Thr Glu Thr Ala Lys Thr Pro Thr Thr Ile Leu 270 275 280	864
gta acc acc acc aag acc acc tca cat agt acc acc agc ttc act	912

Val Thr Thr Thr Thr Lys Thr Thr Ser His Ser Thr Thr Ser Phe Thr	285	290	295	300	
tct tca acc gtc tac tcc aca gcc agc aca cac acc act gcc atc act					960
Ser Ser Thr Val Tyr Ser Thr Ala Ser Thr His Thr Thr Ala Ile Thr	305	310	315		
tca gtt ccc act acc ttg ggt acc atg gtg act tct aca tcc agg atc					1008
Ser Val Pro Thr Thr Leu Gly Thr Met Val Thr Ser Thr Ser Arg Ile	320	325	330		
cca tct act gtg agt acg agt atc cct acc tca caa cca aaa acc gtc					1056
Pro Ser Thr Thr Val Ser Thr Ser Ile Pro Thr Ser Gln Pro Lys Thr Val	335	340	345		
aat tcc tca tct ggg ggc atc act ggt tca tta cct atg atg aca gac					1104
Asn Ser Ser Ser Gly Gly Ile Thr Gly Ser Leu Pro Met Met Thr Asp	350	355	360		
ctt acc tca ggg tac acc gtc tcc agt atg tct gca att ccc aca act					1152
Leu Thr Ser Gly Tyr Thr Val Ser Ser Met Ser Ala Ile Pro Thr Thr	365	370	375		
gtc att cct aca tct ctc act gtc cag aat aca gaa acc tca atc ttt					1200
Val Ile Pro Thr Ser Leu Thr Val Gln Asn Thr Glu Thr Ser Ile Phe	385	390	395		
gtc agc atg acc tct gcc acc act ccc agt ggg aga cca act ttc aca					1248
Val Ser Met Thr Ser Ala Thr Thr Pro Ser Gly Arg Pro Thr Phe Thr	400	405	410		
agt act gtg aac act ccc aca agg tcc ctc ctg aca agc ttt cca acg					1296
Ser Thr Val Asn Thr Pro Thr Arg Ser Leu Leu Thr Ser Phe Pro Thr	415	420	425		
aca cat tta ttc tct tct tcc atg tct gaa agc agt gct ggg acc act					1344
Thr His Leu Phe Ser Ser Ser Met Ser Glu Ser Ser Ala Gly Thr Thr	430	435	440		
cac aca gag agt atc tcc tca cct cca gcc acc acc agt aca ctc cac					1392
His Thr Glu Ser Ile Ser Ser Pro Pro Ala Thr Thr Ser Thr Leu His	445	450	455	460	
aca aca gct gaa tcc acc ccg tcg tgc act acc acc acg tca ttc atc					1440
Thr Thr Ala Glu Ser Thr Pro Ser Cys Thr Thr Thr Thr Ser Phe Ile	465	470	475		
aca tcc aca act atg gaa cca ctt tca acc att gta gca acg aca ggc					1488
Thr Ser Thr Thr Met Glu Pro Leu Ser Thr Thr Ile Val Ala Thr Thr Gly	480	485	490		
aca gtt aag acc acc gtc acc agc tcc aca gcc aca ttc cgg gag acc					1536
Thr Val Lys Thr Thr Val Thr Ser Ser Thr Ala Thr Phe Arg Glu Thr	495	500	505		
acc aca ctg act tct aca act gac atc tcc aca gaa tct ctc atg aca					1584
Thr Thr Leu Thr Ser Thr Asp Ile Ser Thr Glu Ser Leu Met Thr	510	515	520		
gca atg act tct act acc cga ctc act tct gca atc act tcc aag act					1632
Ala Met Thr Ser Thr Thr Arg Leu Thr Ser Ala Ile Thr Ser Lys Thr					

525	530	535	540	
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acg tta tca tca ctc acc agt agc att ttg tct tcc aca ctt gtc ccc Thr Leu Ser Ser Leu Thr Ser Ser Ile Leu Ser Ser Thr Leu Val Pro	560	565	570	1728
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atc caa agt aca gaa acc tca tcc ctt gtg ggc acc acc tct ccc acc Ile Gln Ser Thr Glu Thr Ser Ser Ser Leu Val Gly Thr Thr Ser Pro Thr	765	770	775	2352
			780	

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Met Met Gly Gln
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Asp Lys Ile Gln Gly His Ser Val Ile Ser Glu Glu Ser Asp Gly Lys
5 10 15 20

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Leu Ile Glu Asp Ser Leu Ile Gln Leu Arg Cys His Phe Thr Trp Lys

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Ala Val Ser Glu Arg Asp Lys Val Lys Phe Thr Val Gln Thr Lys Ser
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Cys Leu Pro His Phe Ala Gln Thr Glu Phe Ser Val Val Arg Gln His
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cgg gaa gag ttt gcc aag atg aag cag gag ctg gaa gcg gag tac ctg	Arg Glu Glu Phe Ala Lys Met Lys Gln Glu Leu Glu Ala Glu Tyr Leu															800
gcc atc ttt aag aag aca gtt gcg atg cac gaa gtc ttt ctg cag cgc	Ala Ile Phe Lys Lys Thr Val Ala Met His Glu Val Phe Leu Gln Arg															848
ctg gcg gcc cac ccc acc ctg cgt cga gac cac aac ttc ttt gtg ttt	Leu Ala Ala His Pro Thr Leu Arg Arg Asp His Asn Phe Phe Val Phe															896
ttg gaa tat gga cag gat ctg agt gtc cgg ggg aag aac agg aag gag	Leu Glu Tyr Gly Gln Asp Leu Ser Val Arg Gly Lys Asn Arg Lys Glu															944
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Ser Phe Arg Lys Asn Leu Ile Glu Leu Ala Glu Leu Glu Leu Lys His	Arg Lys Asn Leu Ile Glu Leu Ala Glu Leu Glu Leu Lys His	Arg Lys Asn Leu Ile Glu Leu Ala Glu Leu Glu Leu Lys His		
	370	375	380	
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Ala Lys Ala Ser Thr Leu Ile Leu Arg Asn Thr Leu Val Ala Leu Lys	Ala Lys Ala Ser Thr Leu Ile Leu Arg Asn Thr Leu Val Ala Leu Lys	Ala Lys Ala Ser Thr Leu Ile Leu Arg Asn Thr Leu Val Ala Leu Lys		
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Asp Phe Phe Gly Asn Gly Pro Pro Val Asn Tyr Lys Thr Gly Asn Leu	Phe Phe Gly Asn Gly Pro Pro Val Asn Tyr Lys Thr Gly Asn Leu	Phe Phe Gly Asn Gly Pro Pro Val Asn Tyr Lys Thr Gly Asn Leu		
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ogg aga gct cat gga agg cga gtg gga acc cgg ctg cct gcc ttt ttt Arg Arg Ala His Gly Arg Arg Val Gly Thr Arg Leu Pro Ala Phe Phe 260 265 270	993
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gcc gct gcc tcc caa gcc gag gtc gag tcc gag gca gga tgg ggc atg      96
Ala Ala Ala Ser Gln Ala Glu Val Glu Ser Glu Ala Gly Trp Gly Met
20          25          30

gtg acg cct gat ctg ctc ttc gcc gag ggg acc gca gcc tac gcg cgc      144
Val Thr Pro Asp Leu Leu Phe Ala Glu Gly Thr Ala Ala Tyr Ala Arg
35          40          45

ggg gac tgg ccc ggg gtg gtc ctg agc atg gaa cgg gcg ctg cgc tcc      192
Gly Asp Trp Pro Gly Val Val Leu Ser Met Glu Arg Ala Leu Arg Ser
50          55          60

cgg gca gcc ctc cgc gcc ctt cgc ctg cgc tgc cgc acc cag tgt gcc      240
Arg Ala Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala
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gcc gac ttc ccg tgg gag ctg gac ccc gac tgg tcc ccc agc ccg gcc      288
Ala Asp Phe Pro Trp Glu Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala
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cag gcc tcg ggc gcc gcc gcc ctg cgc gac ctg agc ttc ttc ggg ggc      336
Gln Ala Ser Gly Ala Ala Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly
100          105          110

ctt ctg cgt cgc gct gcc tgc ctg cgc cgc tgc ctc ggg ccg ccg gcc      384
Leu Leu Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala
115          120          125

gcc cac tcg ctc agc gaa gag atg gag ctg gag ttc cgc aag cgg agc      432
Ala His Ser Leu Ser Glu Glu Met Glu Leu Glu Phe Arg Lys Arg Ser
130          135          140

ccc tac aac tac ctg cag gtc gcc tac ttc aag gtg cag acc tgc ctg      480
Pro Tyr Asn Tyr Leu Gln Val Ala Tyr Phe Lys Val Gln Thr Cys Leu
145          150          155          160

gaa cca ggc ggc cgg ggt cct tct ggg gag agg agt gtt gca ggg gac      528
Glu Pro Gly Gly Arg Gly Pro Ser Gly Arg Ser Val Ala Gly Asp
165          170          175

ctg agg agc ttg ggg gat cgg gga agt gtc cgc agg gag ggg aaa gtg      576
Leu Arg Ser Leu Gly Asp Arg Gly Ser Val Arg Arg Glu Gly Lys Val
180          185          190

gcc tcc tgg ctg ggg agc tct cct cgg agc cgg gga gag ctg ctc cct      624
Ala Ser Trp Leu Gly Ser Ser Pro Arg Ser Arg Gly Glu Leu Leu Pro
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gcc atc aca gat cat tac atc cag gtc ctc aac tgt aag cag aac tgt Ala Ile Thr Asp His Tyr Ile Gln Val Leu Asn Cys Lys Asn Cys 340 345 350	1056
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gct tat gat gtt ttt gga att ccc ttt gtg gat ccg gat tca tgg act	1392

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cca	gaa	gaa	gtg	att	ccc	aag	aga	ttg	caa	gag	aaa	cag	aag	tca	gaa	1440
Pro	Glu	Glu	Val	Ile	Pro	Lys	Arg	Leu	Gln	Glu	Lys	Gln	Lys	Ser	Glu	
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cgg	gaa	aca	gcc	gta	cgc	atc	tcc	cag	gag	att	ggg	aac	ctt	atg	aag	1488
Arg	Glu	Thr	Ala	Val	Arg	Ile	Ser	Gln	Glu	Ile	Gly	Asn	Leu	Met	Lys	
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Glu	Ile	Glu	Thr	Leu	Val	Glu	Glu	Lys	Thr	Lys	Glu	Ser	Leu	Asp	Val	
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Ser	Arg	Leu	Thr	Arg	Glu	Gly	Gly	Pro	Leu	Leu	Tyr	Glu	Gly	Ile	Ser	
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Leu	Thr	Met	Asn	Ser	Lys	Leu	Leu	Asn	Gly	Ser	Gln	Arg	Val	Val	Met	
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Asn	Val	Ala	Ala	Thr	Ser	Gly	Asp	Gly	Tyr	Arg	Gly	Gln	Thr	Ser	Pro	
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His	Thr	Pro	Asn	Glu	Lys	Phe	Tyr	Gly	Val	Thr	Val	Phe	Lys	Ala	Leu	
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Lys	Leu	Gly	Gln	Glu	Gly	Lys	Val	Pro	Leu	Gln	Ser	Ala	His	Leu	Tyr	
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Tyr	Asn	Val	Thr	Glu	Lys	Val	Arg	Arg	Ile	Met	Glu	Ser	Tyr	Phe	Arg	
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Ala	Ile	Glu	Glu	Val	Gln	Ala	Glu	Arg	Lys	Asp	Asp	Ser	His	Pro	Val	
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Glu	Pro	Pro	Ala	Tyr	Thr	Phe	Arg	Asp	Tyr	Ser	Ala	Ile	Leu	Tyr	Leu	
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Asn	Gly	Asp	Phe	Asp	Gly	Gly	Asn	Phe	Tyr	Phe	Thr	Glu	Leu	Asp	Ala	

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 60 65 70 75

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Phe	Ser	Ile	Leu	Cys	Ile	Ala	His	Pro	Leu	Glu	Lys	Arg	Glu	Ser	Ser		
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Glu	Glu	Pro	Leu	Ala	Pro	Ser	Asp	Pro	Phe	Ser	Leu	Lys	Thr	Ile	Glu		
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Asp	Val	Arg	Glu	Phe	Leu	Gly	Arg	His	Ser	Glu	Arg	Phe	Asp	Arg	Asn		
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Gln	Met	Asn	Leu	Met	Lys	Gln	Ala	Val	Glu	Ile	Tyr	Val	His	His	Glu		
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agg ctg ttc ctt aag cag aga atg agc tta ctc tct cag atg act tcg Arg Leu Phe Leu Lys Gln Arg Met Ser Leu Leu Ser Gln Met Thr Ser 380 385 390 395			1321
tct ccc acc gac tgc ctg ttt aag cac att gca tca ggt aac cag aaa Ser Pro Thr Asp Cys Leu Phe Lys His Ile Ala Ser Gly Asn Gln Lys 400 405 410			1369
gaa gtg gag aga ctt ctg agc caa gag gac cat gat aaa gat acc gtc Glu Val Glu Arg Leu Leu Ser Gln Glu Asp His Asp Lys Asp Thr Val 415 420 425			1417
caa aag atg tgt cac cct ctc tgc ttc tgc gat gac tgt gag aaa ctc Gln Lys Met Cys His Pro Leu Cys Phe Cys Asp Asp Cys Glu Lys Leu 430 435 440			1465
gtc tct ggg agg ttg aat gat ccc tca gtt gtc act cca ttc tcc aga Val Ser Gly Arg Leu Asn Asp Pro Ser Val Val Thr Pro Phe Ser Arg 445 450 455			1513
gac gac agg ggg cac acc cct ctc cat gtg gct gct gtc tgt ggg cag Asp Asp Arg Gly His Thr Pro Leu His Val Ala Ala Val Cys Gly Gln 460 465 470 475			1561
gca tcc ctc atc gac ctc ctg gtt tcc aag ggc gcc atg gta aat gcc Ala Ser Leu Ile Asp Leu Leu Val Ser Lys Gly Ala Met Val Asn Ala 480 485 490			1609
aca gac tac cat gga gcc act ccg ctc cac ctg gcc tgt cag aag ggc Thr Asp Tyr His Gly Ala Thr Pro Leu His Leu Ala Cys Gln Lys Gly 495 500 505			1657
tac cag agc gtg acg ctg ctg ctg ctg cac tac aag gcc agc gcg gaa Tyr Gln Ser Ser Val Thr Leu Leu Leu Leu His Tyr Lys Ala Ser Ala Glu 510 515 520			1705
gtg cag gac aac aat ggg aat acg cca cat gta ttg cgg ccg ctc tag Val Gln Asp Asn Asn Gly Asn Thr Pro His Val Leu Arg Pro Leu 525 530 535			1753
aggatcccg ctaacg			1769

<210> 47
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<221> CDS

<222> (749) .. (1447)

<400> 47

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atggtgtaaa ggctggggagc ttggaggggg tcgtgtgtgg ggctggactc tgaggcggcc      180
agaggcctag gaacgttata ctggggcacac cgtgcgtggt gtgcagtctg agtcatgctc      240
cctgggttagg gcattccagct ccagcctggg gagtgctgag agccaaatcc accgtagagc      300
agggggtgaga gtcagggtcc cacctcctct atctgccggc aatccagtgg tgacctaggg      360
taaaagcttg agagtcccat acacacgggc atcccacgac atacctcaca ggccaggcag      420
ggacacacag cccctctccc tcctcccagg gtaccgtcat agctgctagt gtgactgaag      480
gcagtgtccc tggcccacgc tgaagcacgc tagccagcca gggggctcac gcaccttggc      540
ctggtgtccc tagggctcact tgtgccattc agccaagggg acgaccgtgc ctgctggccc      600
agctgagctc gcgccagtga gccacccccc cattctcctg ccactgactc tcgctcttct      660
gcttttccca gcaggaaggg ccagcctcca cctacgagac ctgcagcccc ccgaccagct      720
gaggctcccc tcttagactt ataagtct      atg gcc act ggc atc cgg ctg cct      772
                                   Met Ala Thr Gly Ile Arg Leu Pro
                                   1                               5

gcc ctc cct gcc tcc ccc agg gtc cct tca gag ggt cct ggg ttt tct      820
Ala Leu Pro Ala Ser Pro Arg Val Pro Ser Glu Gly Pro Gly Phe Ser
    10                               15                               20

gaa cac cca gag ggg cct ccg gcg ctc cct cca gcc atc cct ttt agt      868
Glu His Pro Glu Gly Pro Pro Ala Leu Pro Pro Ala Ile Pro Phe Ser
    25                               30                               35                               40

ttc acc ctc ctg gtt caa gca gtg ttc ttt ctc tat cag gcc tgg tgg      916
Phe Thr Leu Leu Val Gln Ala Val Phe Leu Tyr Gln Ala Trp Trp
    45                               50                               55

ctg ttg cat ggg gct ccc caa ggc aag ggg tgg ccc cag gcc agt ggg      964
Leu Leu His Gly Ala Pro Gln Gly Lys Gly Trp Pro Gln Ala Ser Gly
    60                               65                               70

ttg gaa gac agg gtg acc aga gaa gag gga agc ccg agg ggg ccg agc      1012
Leu Glu Asp Arg Val Thr Arg Glu Glu Gly Ser Pro Arg Gly Pro Ser
    75                               80                               85

atc agc ctg aat tgc ggg tgc cct gcc tgg gtg ccg tgt gag agg cca      1060
Ile Ser Leu Asn Cys Gly Cys Pro Ala Trp Val Pro Cys Glu Arg Pro
    90                               95                               100

gcg tgt gtg ggg tgg gga ggg ccg cca cag ccc cca ggc gct atc tgt      1108
Ala Cys Val Gly Trp Gly Gly Pro Pro Gln Pro Pro Gly Ala Ile Cys
    105                               110                               115                               120

gaa gct acg gct cct ccc tcc atc ttc ctc ccc ttt ccc ttc cag ccc      1156

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Glu Ala Thr Ala Pro Pro Ser Ile Phe Leu Pro Phe Pro Phe Gln Pro	
125 130 135	
ctt ttc cag gaa cct tgc cac acc cac acc tgc agc ctc ccc tcc ccg	1204
Leu Phe Gln Glu Pro Cys His Thr His Thr Cys Ser Leu Pro Ser Pro	
140 145 150	
gcc ctc cca cca ctg ctg cgg cgc ggc cgg ccc cgg ccg tgt gct gcg	1252
Ala Leu Pro Pro Leu Leu Arg Arg Gly Arg Pro Arg Pro Cys Ala Ala	
155 160 165	
ctt gcc tta cca gct ctc tcc tgc ctt ttc tct ccc gtt ttc tct ctg	1300
Leu Ala Leu Pro Ala Leu Ser Ser Leu Phe Ser Pro Val Phe Ser Leu	
170 175 180	
ctt tct ctc caa ctg cca gcc gat cgg gtc agg caa gtc cat ccc gtc	1348
Leu Ser Leu Gln Leu Pro Ala Asp Arg Val Arg Gln Val His Pro Val	
185 190 195 200	
ctg aga gcc cca ggc ccc cct tgc acc tct aaa cag atc cct cct ctt	1396
Leu Arg Ala Pro Gly Pro Pro Ser Thr Ser Lys Gln Ile Pro Pro Leu	
205 210 215	
ctc gga gac ctc cct ttc caa gcc tgc ctg gac gcc tgt tct gtg act	1444
Leu Gly Asp Leu Pro Phe Gln Ala Cys Leu Asp Gly Cys Ser Val Thr	
220 225 230	
tga cagt ggctccccc gccccaaagc cagccccctt catctgtgac ttaatctggt	1501

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 <211> 659
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (250)..(567)

<400> 48	
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cgctgctgac ccagcatcgg cttttctacg tcttgaacct ggattcgctt aggggttggg	120
aagggtgtgtg gacggcgttg ggggaggcct gacgagatta ataaagaact cttcagaatt	180
cctggtgttt catcatatat acgactaaga tatcaactct tctagcttgc tgtctctgga	240
ccaaaaaa atg acg tct att atc aaa tta act acc ctt tct ggg gtc	288
Met Thr Ser Ile Ile Lys Leu Thr Thr Leu Ser Gly Val	
1 5 10	
caa gaa gaa tct gcc ctt tgc tat ctt ctc caa gtt gat gag ttt aga	336
Gln Glu Glu Ser Ala Leu Cys Tyr Leu Leu Gln Val Asp Glu Phe Arg	
15 20 25	

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ttt tta ttg gac tgt ggc tgg gat gag cac ttt tct atg gat att att      384
Phe Leu Leu Asp Cys Gly Trp Asp Glu His Phe Ser Met Asp Ile Ile
30                               35                               40                               45

gat tcc ctg agg aag cat gtt cac cag att gat gca gtg ctg ttg tct      432
Asp Ser Leu Arg Lys His Val His Gln Ile Asp Ala Val Leu Leu Ser
50                               55                               60

cac cct gat cct ctc cac ctt ggt gcc ctc cgg tat gct gtc gga aag      480
His Pro Asp Pro Leu His Leu Gly Ala Leu Pro Tyr Ala Val Gly Lys
65                               70                               75

ttg ggt ctg aac tgt gct atc tat gca act att cct gtt tat aaa atg      528
Leu Gly Leu Asn Cys Ala Ile Tyr Ala Thr Ile Pro Val Tyr Lys Met
80                               85                               90

gga cag atg ttc atg tat gat ctt tat cag gta att taa gcaattaaaa      577
Gly Gln Met Phe Met Tyr Asp Leu Tyr Gln Val Ile
95                               100                               105

aaattttgtt agcactcctt cagtgttgg ttttcacett tatttgtgtt attcttttag      637

tctcgacaca atacagaaga tg                                             659

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<210> 49
 <211> 1486
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (187)..(1188)

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<400> 49
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gaaaggtttt attccaaaag gagaggttgg aagacatagc tcattctcctg ctgtgtatca      120
gccaagaagg tgtgagggtgg tgttccttgg ggaatccgctt gcattctactt ggggtgggttt      180
tgaaac   atg aat ctt tgc ctc gtc ctg gct gcc ttt tgc ttg gga ata      228
Met Asn Leu Ser Leu Val Leu Ala Ala Phe Cys Leu Gly Ile
1                               5                               10

gcc tcc gct gtt cca aaa ttt gac caa aat ttg gat aca aag tgg tac      276
Ala Ser Ala Val Pro Lys Phe Asp Gln Asn Leu Asp Thr Lys Trp Tyr
15                               20                               25                               30

cag tgg aag gca aca cac aga aga tta tat ggc gcg aat gaa gaa gga      324
Gln Trp Lys Ala Thr His Arg Arg Leu Tyr Gly Ala Asn Glu Glu Gly
35                               40                               45

tgg agg aga gca gtg tgg gaa aag aat atg aaa atg att gaa ctg cac      372
Trp Arg Arg Ala Val Trp Glu Lys Asn Met Lys Met Ile Glu Leu His
50                               55                               60

aat ggg gaa tac agc caa ggg aaa cac agc ttc aca atg gcc atg aat      420
Asn Gly Glu Tyr Ser Gln Gly Lys His Ser Phe Thr Met Ala Met Asn

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65	70	75	
gcc ttt gga gac atg acc aat gaa gaa ttc agg cag gtg atg aat ggt Ala Phe Gly Asp Met Thr Asn Glu Glu Phe Arg Gln Val Met Asn Gly 80 85 90			468
ttt caa tac cag aag cac agg aag ggg aaa cag ttc cag gaa cgc ctg Phe Gln Tyr Gln Lys His Arg Lys Gly Lys Gln Phe Gln Glu Arg Leu 95 100 105 110			516
ctt ctt gag atc ccc aca tct gtg gac tgg aga gag aaa ggc tac atg Leu Leu Glu Ile Pro Thr Ser Val Asp Trp Arg Glu Lys Gly Tyr Met 115 120 125			564
act cct gtg aag gat cag ggt cag tgt ggc tct tgt tgg gct ttt agt Thr Pro Val Lys Asp Gln Gly Gln Cys Gly Ser Cys Trp Ala Phe Ser 130 135 140			612
gca act ggt gct ctg gaa ggg cag atg ttc tgg aaa aca ggc aaa ctt Ala Thr Gly Ala Leu Glu Gly Gln Met Phe Trp Lys Thr Gly Lys Leu 145 150 155			660
atc tca ctg aat gag cag aat ctg gta gac tgc tct ggg cct caa ggc Ile Ser Leu Asn Glu Gln Asn Leu Val Asp Cys Ser Gly Pro Gln Gly 160 165 170			708
aat gag ggc tgc aat ggt gac ttc atg gat aat ccc ttc cgg tat gtt Asn Glu Gly Cys Asn Gly Asp Phe Met Asp Asn Pro Phe Arg Tyr Val 175 180 185 190			756
cag gag aac gga ggc ctg gac tct gag gaa tcc tat cca tat gag gca Gln Glu Asn Gly Gly Leu Asp Ser Glu Glu Ser Tyr Pro Tyr Glu Ala 195 200 205			804
aca gaa gaa tcc tgt aag tac aat ccc aag tat tct gtt gct aat gac Thr Glu Glu Ser Cys Lys Tyr Asn Pro Lys Tyr Ser Val Ala Asn Asp 210 215 220			852
acc ggc ttt gtg gac atc cct aag cag gag aag gcc ctg atg aag gca Thr Gly Phe Val Asp Ile Pro Lys Gln Glu Lys Ala Leu Met Lys Ala 225 230 235			900
gtt gca act gtg ggg ccc att tct gtt gct att gat gca ggt cat gag Val Ala Thr Val Gly Pro Ile Ser Val Ala Ile Asp Ala Gly His Glu 240 245 250			948
tcc ttc ctg ttc tat aaa gaa ggc att tat ttt gag cca gac tgt agc Ser Phe Leu Phe Tyr Lys Glu Gly Ile Tyr Phe Glu Pro Asp Cys Ser 255 260 265 270			996
agt gaa gac atg gat cat ggt gtg ctg gtg gtt ggc tac gga ttt gaa Ser Glu Asp Met Asp His Gly Val Leu Val Val Gly Tyr Gly Phe Glu 275 280 285			1044
agc aca gaa tca gat aac aat aaa tat tgg ctg gtg aag aac agc tgg Ser Thr Glu Ser Asp Asn Asn Lys Tyr Trp Leu Val Lys Asn Ser Trp 290 295 300			1092
ggt gaa gaa tgg ggc atg ggt ggc tac gta aag atg gcc aaa gac cgg Gly Glu Glu Trp Gly Met Gly Gly Tyr Val Lys Met Ala Lys Asp Arg 305 310 315			1140


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aga aac cat tgt gga att gcc tca gca gcc agc tac ccc act gtg tga      1188
Arg Asn His Cys Gly Ile Ala Ser Ala Ala Ser Tyr Pro Thr Val
   320               325               330

gctgggtggac ggtgatgagg aaggacttga ctggggatgg cgcattgcattg ggaggaattc 1248
atcttcagtc taccagcccc cgctgtgtcg gatacacact cgaatcattg aagatccgag 1308
tgtgatttga attctgtgat attttcacac tggtaaatgt tacctctatt ttaattactg 1368
ctataaataag gtttatatta ttgattcact tactgacttt gcattttcgt ttttaaaagg 1428
atgtataaat ttttacctgt ttaataaaaa ttaatttca aatgtaaaaa aaaaaaaa 1486

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<220>
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<222> (123)..(749)

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gccactgacc accgtggaga agccccgggg aggagggtg ctttctggct gcacactgac      120

ct   atg ttg ggg tgc cag ggc agg atg tac acg ctg ctg tgg ggc ttg      167
Met Leu Gly Cys Gln Gly Arg Met Tyr Thr Leu Leu Ser Gly Leu
   1               5               10               15

tac aag tac atg ttt cag aag gac gag tac tgc atc ctg atc ctg ggc      215
Tyr Lys Tyr Met Phe Gln Lys Asp Glu Tyr Cys Ile Leu Ile Leu Gly
   20               25               30

ctg gac aat gct ggg aag acg acc ttc ctg gag cag tgg aaa acc cga      263
Leu Asp Asn Ala Gly Lys Thr Thr Phe Leu Glu Gln Ser Lys Thr Arg
   35               40               45

ttt aac aag aac tac aag ggg atg agt cta tcc aaa atc acc acc acc      311
Phe Asn Lys Asn Tyr Lys Gly Met Ser Leu Ser Lys Ile Thr Thr Thr
   50               55               60

gtg ggc cta aac atc ggc act gtg gat gtg gga aag gct cgg ctc atg      359
Val Gly Leu Asn Ile Gly Thr Val Asp Val Gly Lys Ala Arg Leu Met
   65               70               75

ttc tgg gac tta gga ggg cag gaa gag ctg cag tct ttg tgg gac aag      407
Phe Trp Asp Leu Gly Gly Gln Glu Glu Leu Gln Ser Leu Trp Asp Lys
   80               85               90               95

tat tat gcg gag tgt cac ggc gtc atc tac gtc att gac tcc acc gac      455
Tyr Tyr Ala Glu Cys His Gly Val Ile Tyr Val Ile Asp Ser Thr Asp
   100              105              110

gag gag agg ctg gct gag tcc aag cag gcg ttt gag aag gtg gtg acc      503

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Glu	Glu	Arg	Leu	Ala	Glu	Ser	Lys	Gln	Ala	Phe	Glu	Lys	Val	Val	Thr		
			115					120					125				
agc	gag	gcg	ctg	ggc	gtc	ccc	gtc	ttg	gtg	ctg	gcc	aac	aag	cag		551	
Ser	Glu	Ala	Leu	Cys	Gly	Val	Pro	Val	Leu	Val	Leu	Ala	Asn	Lys	Gln		
		130				135					140						
gat	gtg	gag	acg	tgc	ctc	tca	atc	cct	gac	atc	aag	acg	gcc	ttc	agc	599	
Asp	Val	Glu	Thr	Cys	Leu	Ser	Ile	Pro	Asp	Ile	Lys	Thr	Ala	Phe	Ser		
		145				150					155						
gac	tgc	acc	agc	aag	atc	ggc	agg	cga	gat	tgc	ctg	acc	cag	gcc	tgc	647	
Asp	Cys	Thr	Ser	Lys	Ile	Gly	Arg	Arg	Asp	Cys	Leu	Thr	Gln	Ala	Cys		
		160			165					170					175		
tcg	gcc	ctc	aca	ggc	aaa	ggg	gtg	cgc	gag	ggc	atc	gag	tgg	atg	gtg	695	
Ser	Ala	Leu	Thr	Gly	Lys	Gly	Val	Arg	Glu	Gly	Ile	Glu	Trp	Met	Val		
			180					185					190				
aag	tgt	gtc	gtg	cgg	aat	gtg	cac	cgg	ccg	ccg	cgg	cag	agg	gac	atc	743	
Lys	Cys	Val	Val	Arg	Asn	Val	His	Arg	Pro	Pro	Arg	Gln	Arg	Asp	Ile		
			195					200					205				
acg	tag	gcgcagcccg	cgcttgcccg	tccgggacgg	ctgggtccct	gggtctggag										799	
Thr																	

<210> 51
 <211> 1464
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> (166)..(855)

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ggcatcaggg	cctggtaaca	ggcagtgagg	tatcagcagg	tgggaaataa	gttctctagt		120	
gatggtaggg	ttggggaatg	ctcaagaaaa	ttgctaggct	gagaa	atg cta tca		174	
					Met Leu Ser			
					1			
gtg gat att	acc agc agg	tac cgt gca	ccc agt acc	tat ctt ctt	aac		222	
Val Asp Ile	Thr Ser Arg	Tyr Arg Ala	Pro Ser Thr	Tyr Leu Leu	Asn			
	5	10	15					
tcc ctg aaa	gag ggg ctg	gaa ggc ctc	cat ggt gaa	tct tgc tct	tct		270	
Ser Leu Lys	Glu Gly Leu	Glu Gly Leu	His Gly Glu	Ser Cys Ser	Ser			
	20	25	30		35			
ttt ctc ctg	ggg ccc tca	gtg gcc atg	aat atg	cag act gca	ggg ctt		318	
Phe Leu Leu	Gly Pro Ser	Val Ala Met	Asn Met	Gln Thr Ala	Gly Leu			
	40	45			50			

gaa atg gac atc tgt gat ggg cat ttc cgc cag aat ggc ggc tgt ggc Glu Met Asp Ile Cys Asp Gly His Phe Arg Gln Asn Gly Gly Cys Gly	366
55 60 65	
tat gtg ctg aag cca gac ttc ctg cgt gat atc cag agt tct ttc cac Tyr Val Leu Lys Pro Asp Phe Leu Arg Asp Ile Gln Ser Ser Phe His	414
70 75 80	
cct gag aag ccc atc agc cct ttc aaa gcc cag act ctc tta atc cag Pro Glu Lys Pro Ile Ser Pro Phe Lys Ala Gln Thr Leu Leu Ile Gln	462
85 90 95	
gtg atc agc ggt cag caa ctc ccc aaa gtg gac aag acc aaa gag ggg Val Ile Ser Gly Gln Gln Leu Pro Lys Val Asp Lys Thr Lys Glu Gly	510
100 105 110 115	
tcc att gtg gat cca ctg gtg aaa gtg cag atc ttt ggc gtt cgt cta Ser Ile Val Asp Pro Leu Val Lys Val Gln Ile Phe Gly Val Arg Leu	558
120 125 130	
gac aca gca cgg cag gag acc aac tat gtg gag aac aat ggt ttt aat Asp Thr Ala Arg Gln Glu Thr Asn Tyr Val Glu Asn Asn Gly Phe Asn	606
135 140 145	
cca tac tgg ggg cag aca cta tgt ttc cgg gtg ctg gtg cct gaa ctt Pro Tyr Trp Gly Gln Thr Leu Cys Phe Arg Val Leu Val Pro Glu Leu	654
150 155 160	
gcc atg ctg cgt ttt gtg gta atg gat tat gac tgg aaa tcc cga aat Ala Met Leu Arg Phe Val Val Met Asp Tyr Asp Trp Lys Ser Arg Asn	702
165 170 175	
gac ttt att ggt cag tac acc ctg cct tgg acc tgc atg caa caa ggt Asp Phe Ile Gly Gln Tyr Thr Leu Pro Trp Thr Cys Met Gln Gln Gly	750
180 185 190 195	
tac cgc cac att cac ctg ctg tcc aaa gat ggc atc agc ctc cgc cca Tyr Arg His Ile His Leu Leu Ser Lys Asp Gly Ile Ser Leu Arg Pro	798
200 205 210	
gct tcc atc ttt gtg tat atc tgc atc cag gaa ggc ctg gag ggg gat Ala Ser Ile Phe Val Tyr Ile Cys Ile Gln Glu Gly Leu Glu Gly Asp	846
215 220 225	
gag tcc tga ggtgggc atttcacggg aagggttggt gtgctggcct tagacgggga Glu Ser	902
gaaacatctg gaaggatgct cgagagaaca aatggagggtg gtgaaaatca agctttggat	962
tgtgcatctc taggcacaaa attacctcat tcttctaac aagcaatctg ggacctgatt	1022
ttccaccttt ttctctcttt cttcccttcc ttgttttca taagccttgg gtatctttcc	1082
tgcccttttc ctttgtgtac tctatactgg agttcccttc ttccctctgc ttagagctca	1142
atcccatacc gacatctaca actaatcttt cccatcaact ctgtgtgaag gcagggtgca	1202
actagaaatt cagaggggct tggaatagag aaacctaaag aagcatcatc ccctccatcc	1262
ccaacttcct caaagcccaa agccaaggga aggataaatc aaggctcaag gcttccccag	1322

caaagattag ggaaagagac ttgacccag gactgtacta cgactcttaa gagaacactg 1382
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 tctctctcca atttggtctc aa 1464

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 <211> 1232
 <212> DNA
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<220>
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 <222> (344)..(1015)

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 gaggggtgatg ctctgacctc tgcagccccc ctccctgtcc tgagaagget tccagctggg 180
 ccttggagga caggggtccac ccctacctcc tgggtctcctt cctcagcttg gaagccccgg 240
 agcctgccct gctgggaatc ggggaagcac tgcttacctg tctctgtctc ccttttcagg 300
 tgcctgtggc aggcagcacc ttgagccaac aggaaccatt gac atg cga ggc cca 355
 Met Arg Gly Pro
 1
 ggg cag gca gac tgt gca gtg gcc att ggg cgg ccc ctc ggg gag gtg 403
 Gly Gln Ala Asp Cys Ala Val Ala Ile Gly Arg Pro Leu Gly Glu Val
 5 10 15 20
 gtg acc ctc cgc gtc ctt gag agt tct ctc aac tgc agt gcg ggg gac 451
 Val Thr Leu Arg Val Leu Glu Ser Ser Leu Asn Cys Ser Ala Gly Asp
 25 30 35
 atg ttg ctg ctt tgg ggc cgg ctc acc tgg agg aag atg tgc agg aag 499
 Met Leu Leu Leu Trp Gly Arg Leu Thr Trp Arg Lys Met Cys Arg Lys
 40 45 50
 ctg ttg gac atg act ttc agc tcc aag acc aac acg ctg gtg gtg agg 547
 Leu Leu Asp Met Thr Phe Ser Ser Lys Thr Asn Thr Leu Val Val Arg
 55 60 65
 cag cgc tgc ggg cgg cca gga ggt ggg gtg ctg ctg cgg tat ggg agc 595
 Gln Arg Cys Gly Arg Pro Gly Gly Val Leu Leu Arg Tyr Gly Ser
 70 75 80
 cag ctt gct cct gaa acc ttc tac aga gaa tgt gac atg cag ctc ttt 643
 Gln Leu Ala Pro Glu Thr Phe Tyr Arg Glu Cys Asp Met Gln Leu Phe
 85 90 95 100
 ggg ccc tgg ggt gaa atc gtg agc ccc tcg ctg agt cca gcc acg agt 691
 Gly Pro Trp Gly Glu Ile Val Ser Pro Ser Leu Ser Pro Ala Thr Ser
 105 110 115

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aat gca ggg ggc tgc cgg ctc ttc att aat gtg gct ccg cac gca cgg      739
Aen Ala Gly Gly Cys Arg Leu Phe Ile Asn Val Ala Pro His Ala Arg
      120                               125                               130

att gcc atc cat gcc ctg gcc acc aac atg ggc gct ggg acc gag gga      787
Ile Ala Ile His Ala Leu Ala Thr Asn Met Gly Ala Gly Thr Glu Gly
      135                               140                               145

gcc aat gcc agc tac atc ttg atc cgg gac acc cac agc ttg agg acc      835
Ala Asn Ala Ser Tyr Ile Leu Ile Arg Asp Thr His Ser Leu Arg Thr
      150                               155                               160

aca gcg ttc cat ggg cag cag gtg ctc tac tgg gag tca gag agc agc      883
Thr Ala Phe His Gly Gln Gln Val Leu Tyr Trp Glu Ser Glu Ser Ser
      165                               170                               175                               180

cag gct gag atg gag ttc agc gag ggc ttc ctg aag gct cag gcc agc      931
Gln Ala Glu Met Glu Phe Ser Glu Gly Phe Leu Lys Ala Gln Ala Ser
      185                               190                               195

ctg cgg ggc cag tac tgg aca ctc caa tca tgg gta ccg gag atg cag      979
Leu Arg Gly Gln Tyr Trp Thr Leu Gln Ser Trp Val Pro Glu Met Gln
      200                               205                               210

gac cct cag tcc tgg aag gga aag gaa gga acc tga gggc cattgaacat      1029
Asp Pro Gln Ser Trp Lys Gly Lys Glu Gly Thr
      215                               220

tgtttccgtg tctggccagc cctggagggt tgacctctgt tctcaattcg      1089

aactttttcc aatcttaggt atctacttta gagtcttctc caatgtccaa aaggctaggg      1149

ggttgagggt ggggactctg gaaaagcagc cccatttcc tcgggtacca ataaataaaa      1209

catgcaggct gaaaaaaaaa aaa      1232

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<210> 53
<211> 934
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (375)..(596)

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<220>
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<222> (1)...(934)
<223> n = a,t,c or g

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<400> 53
cgctgcggc accggtccgg aattcccggt tcgacgattt cgtgctaaga ccctgcttct      60
ccctggctcg tcctctactc gggcactacc cctggcctga ccctggtag cctccacacg      120
cacgggcaat gccttgggtc ctgacccgtg ggctgggagc cacataaagg tcttgggtac      180

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tcttaggagat aggtgcccgg gggagcacgc ccaggacata tcaggttccc tcaccaagct	240
tagccccctc tgcctctgt tgagtctcct gagtccctt ggagtccctc tcttgctccc	300
atgcagacaa ctggaagcag gagctgacaa aattcatcag ccccgaccag ctgcctgtgg	360
agtttggggg gacc atg act gac ccc gat ggc aac ccc aag tgc ctg acc	410
Met Thr Asp Pro Asp Gly Asn Pro Lys Cys Leu Thr	
1 5 10	
aag atc aac tac ggg ggt gag gtg ccc aag agc tac tac ctg tgc aag	458
Lys Ile Asn Tyr Gly Gly Glu Val Pro Lys Ser Tyr Tyr Leu Cys Lys	
15 20 25	
cag gtg agg ctg cag tat gag cac acg agg tcc gtg ggc cgc ggc tcc	506
Gln Val Arg Leu Gln Tyr Glu His Thr Arg Ser Val Gly Arg Gly Ser	
30 35 40	
tcc ctg cag gtg gag aac gag atc ctg ttc ccg ggc tgt gtg ctc aga	554
Ser Leu Gln Val Glu Asn Glu Ile Leu Phe Pro Gly Cys Val Leu Arg	
45 50 55 60	
tgt cct gag gtt tta caa cac cta cag cct ggt tca ttc taa acgcate	603
Cys Pro Glu Val Leu Gln His Leu Gln Pro Gly Ser Phe	
65 70	
agctacaccg tggagggtact gctccagac caaaccttca tggagaagat ggagaaattc	663
taggtgaacc tcatggctcc caccctcc tctttgatct ctgaatccac aatgagttca	723
cagccttccc tggccagacc ctgttcaacc tctcaggaac agggattcta caacagcagg	783
tcacagccta tgcatacag ctggcccaact cctcaagaac ggctgggaca gtgtcctagt	843
ggtgggccga tggtcacagc annagcacac agacactcca tcccactat gacctgctgt	903
gacctcaagc tcagcaaac cccaggcttt g	934

<210> 54
 <211> 700
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (48)..(656)

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Met Ala Glu	
1	
tat tta gct tcg ata ttc ggg act gag aag gac aag gtt aac tgc tct	104
Tyr Leu Ala Ser Ile Phe Gly Thr Glu Lys Asp Lys Val Asn Cys Ser	
5 10 15	
ttt tac ttt aag atc ggg gtc tgc cgg cac ggg gac cgg tgc tcc cgg	152
Phe Tyr Phe Lys Ile Gly Val Cys Arg His Gly Asp Arg Cys Ser Arg	

20	25	30	35	
ctt cac aac aag cgc aca ttc agc cag gag gtg ttc aca gaa ctg cag				200
Leu His Asn Lys Pro Thr Phe Ser Gln Glu Val Phe Thr Glu Leu Gln				
	40	45	50	
gag aag tat ggg gag att gaa gag atg aat gtg tgc gac aac ctt ggg				248
Glu Lys Tyr Gly Glu Ile Glu Glu Met Asn Val Cys Asp Asn Leu Gly				
	55	60	65	
gac cac ctc gtg ggc aac gtc tat gtc aag ttc cgg agg gag gag gat				296
Asp His Leu Val Gly Asn Val Tyr Val Lys Phe Arg Arg Glu Glu Asp				
	70	75	80	
gga gag cgg gcc gtg gct gaa ctc agt aac cgc tgg ttc aac ggg cag				344
Gly Glu Arg Ala Val Ala Glu Leu Ser Asn Arg Trp Phe Asn Gly Gln				
	85	90	95	
gct gtg cac ggg aat gta ccc gag gtg gct tct gca act tca tgc atc				392
Ala Val His Gly Asn Val Pro Glu Val Ala Ser Ala Thr Ser Cys Ile				
	100	105	110	115
tgc ggc cca ttt ccc aga acc tcc aga ggc agc tct atg ggc ggg gac				440
Cys Gly Pro Phe Pro Arg Thr Ser Arg Gly Ser Ser Met Gly Gly Asp				
	120	125	130	
cca ggc gca ggt cac ccc cga ggt tcc ata ctg gcc acc atc ccc gag				488
Pro Gly Ala Gly His Pro Arg Gly Ser Ile Leu Ala Thr Ile Pro Glu				
	135	140	145	
aga gga acc atc ggt gtt ccc ctg atc act ggc atg gcc gct tct gag				536
Arg Gly Thr Ile Gly Val Pro Leu Ile Thr Gly Met Ala Ala Ser Glu				
	150	155	160	
gcc ctg gcc ccc tta ccc ttc acc ccc aac agg gac aga tgt tcc tgg				584
Ala Leu Ala Pro Leu Pro Phe Thr Pro Asn Arg Asp Arg Cys Ser Trp				
	165	170	175	
cag gac ctc tcc tca aag ccc cct tca ctc tcc tgc ccc atc ctt ccc				632
Gln Asp Leu Ser Ser Lys Pro Pro Ser Leu Ser Cys Pro Ile Leu Pro				
	180	185	190	195
agg ctc cgc ggc tcc ata atg taa tctgttcagc atggagacct tcttctaccg				686
Arg Leu Pro Gly Ser Ile Met				
	200			
ccctgtctt aata				700

<210> 55
 <211> 855
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (48)..(773)

 <400> 55

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	1	
tat tta gct tcg ata ttc ggg act gag aag gac aag gtt aac tgc tct		104
Tyr Leu Ala Ser Ile Phe Gly Thr Glu Lys Asp Lys Val Asn Cys Ser		
5 10 15		
ttt tac ttt aag att ggc gcc tgc cgg cac ggg gac cgg tgc tcc cga		152
Phe Tyr Phe Lys Ile Gly Ala Cys Arg His Gly Asp Arg Cys Ser Arg		
20 25 30 35		
ctt cac aac aaa ccg act ttc agc cag acc ata gtc ctg ctc aac ttg		200
Leu His Asn Lys Pro Thr Phe Ser Gln Thr Ile Val Leu Leu Asn Leu		
40 45 50		
tac cgg aat cca cag aac aca gcc caa act gca gac gga tca cac tgt		248
Tyr Arg Asn Pro Gln Asn Thr Ala Thr Ala Asp Gly Ser His Cys		
55 60 65		
cat gtg agc gac gtg gag gtg cag gag cac tat gat agc ttc gag		296
His Val Ser Asp Val Glu Val Gln Glu His Tyr Asp Ser Phe Phe Glu		
70 75 80		
gag gtg ttc aca gaa ctg cag gag aag tat ggg gag att gaa gag atg		344
Glu Val Phe Thr Glu Leu Gln Glu Lys Tyr Gly Glu Ile Glu Glu Met		
85 90 95		
aat gtg tgc gac aac ctt ggg gac cac ctc gtg ggc aac gtc tat gtc		392
Asn Val Cys Asp Asn Leu Gly Asp His Leu Val Gly Asn Val Tyr Val		
100 105 110 115		
aag ttc cgg agg gag gag gat gga gag cgg gcc gtg gct gaa ctc agt		440
Lys Phe Arg Arg Glu Glu Asp Gly Glu Arg Ala Val Ala Glu Leu Ser		
120 125 130		
aac cgc tgg ttc aac ggg cag gct gtg cac ggg aat gta ccc gag gtg		488
Asn Arg Trp Phe Asn Gly Gln Ala Val His Gly Asn Val Pro Glu Val		
135 140 145		
gct tct gca act tca tgc atc tgc ggc cca ttt ccc aga acc tcc aga		536
Ala Ser Ala Thr Ser Cys Ile Cys Gly Pro Phe Pro Arg Thr Ser Arg		
150 155 160		
ggc agc tct atg ggc ggg gac cca ggc gca ggt cac ccc cga ggt tcc		584
Gly Ser Ser Met Gly Gly Asp Pro Gly Ala Gly His Pro Arg Gly Ser		
165 170 175		
ata ctg gcc acc atc ccc gag aga gga acc atc gtt gtt ccc ctg atc		632
Ile Leu Ala Thr Ile Pro Glu Arg Gly Thr Ile Val Val Pro Leu Ile		
180 185 190 195		
act ggc atg gcc gct tct gag gcc ctg gcc ccc tta ccc ttc acc ccc		680
Thr Gly Met Ala Ala Ser Glu Ala Leu Ala Pro Leu Pro Phe Thr Pro		
200 205 210		
aac agg gac aga tgt tcc tgg cag gac ctc tcc tca aag ccc cct tca		728
Asn Arg Asp Arg Cys Ser Trp Gln Asp Leu Ser Ser Lys Pro Pro Ser		
215 220 225		
ctc tcc tgc ccc atc ctt ccc agg ctc ccg ggc tcc ata atg taa tct		776


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Leu Ser Cys Pro Ile Leu Pro Arg Leu Pro Gly Ser Ile Met
230                235                240

gttcagcatg gagaccttct tctactgccc ctgtcttaat aaagctgcgt gttcacttc 836

ggcatcaaaa aaaaaaaaaa 855

<210> 56
<211> 3068
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (128)..(2512)

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ttcgcgcacg cactctgggt cttgcatata aataaccccg ggcccgccccc cggccccccg 120

ccaagcc   atg ctg tgc gcc cgc tgg agg cgt tgc cgc cgc ccg ccc gag 169
           Met Leu Cys Gly Arg Trp Arg Arg Cys Arg Pro Pro Glu
           1             5             10

gag ccc cca gtg gcc gcc cag gtc gca gcc caa gtc gcg gcg ccg gtc 217
Glu Pro Pro Val Ala Ala Gln Val Ala Ala Gln Val Ala Ala Pro Val
15             20             25             30

gct ctc ccg tcc ccg ccg act ccc tcc gat ggc ggc acc aag agg ccc 265
Ala Leu Pro Ser Pro Pro Thr Pro Ser Asp Gly Gly Thr Lys Arg Pro
35             40             45

ggg ctg ccg gcg ctg aag aag atg ggc ctg acg gag gac gag gac gtg 313
Gly Leu Arg Ala Leu Lys Lys Met Gly Leu Thr Glu Asp Glu Asp Val
50             55             60

cgc gcc atg ctg ccg ggc tcc ccg ctc cgc aag atc cgc tgc cgc acg 361
Arg Ala Met Leu Arg Gly Ser Arg Leu Arg Lys Ile Arg Ser Arg Thr
65             70             75

tgg cac aag gag ccg ctg tac ccg ctg cag gag gac ggc ctg agc gtg 409
Trp His Lys Glu Arg Leu Tyr Arg Leu Gln Glu Asp Gly Leu Ser Val
80             85             90

tgg ttc cag ccg cgc atc ccg cgt gcg cca tgc cag cac atc ttc ttc 457
Trp Phe Gln Arg Arg Ile Pro Arg Ala Pro Ser Gln His Ile Phe Phe
95             100            105            110

gtg cag cac atc gag gcg gtc cgc gag ggc cac cag tcc gag ggc ctg 505
Val Gln His Ile Glu Ala Val Arg Glu Gly His Gln Ser Glu Gly Leu
115            120            125

cgg cgc ttc ggg ggt gcc ttc gcg cca gcg cgc tgc ctc acc atc gcc 553
Arg Arg Phe Gly Gly Ala Phe Ala Pro Ala Arg Cys Leu Thr Ile Ala
130            135            140

ttc aag ggc cgc cgc aag aac ctg gac ctg gcg gcg ccc acg gct gag 601

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Phe	Lys	Gly	Arg	Arg	Lys	Asn	Leu	Asp	Leu	Ala	Ala	Pro	Thr	Ala	Glu	
	145						150					155				
gaa	gcg	cag	cgc	tgg	gtg	cgc	ggg	ctg	acc	aag	ctc	cgc	gcg	cgc	ctg	649
Glu	Ala	Gln	Arg	Trp	Val	Arg	Gly	Leu	Thr	Lys	Leu	Arg	Ala	Arg	Leu	
	160					165					170					
gac	gcc	atg	agc	cag	cgc	gag	cgg	cta	gac	cac	tgg	atc	cac	tcc	tat	697
Asp	Ala	Met	Ser	Gln	Arg	Glu	Arg	Leu	Asp	His	Trp	Ile	His	Ser	Tyr	
	175				180					185					190	
ctg	cac	cgg	gct	gac	tcc	aac	cag	gac	agc	aag	atg	agc	ttc	aag	gag	745
Leu	His	Arg	Ala	Asp	Ser	Asn	Gln	Asp	Ser	Lys	Met	Ser	Phe	Lys	Glu	
					195				200					205		
atc	aag	agc	ctg	ctg	aga	atg	gtc	aac	gtg	gac	atg	aac	gac	atg	tac	793
Ile	Lys	Ser	Leu	Leu	Arg	Met	Val	Asn	Val	Asp	Met	Asn	Asp	Met	Tyr	
					210				215					220		
gcc	tac	ctc	ctc	ttc	aag	gag	tgt	gac	cac	tcc	aac	aac	gac	cgt	cta	841
Ala	Tyr	Leu	Phe	Lys	Glu	Cys	Asp	His	Ser	Asn	Asn	Asp	Arg	Leu		
					225				230				235			
gag	ggg	gct	gag	atc	gag	gag	ttc	ctg	cgg	cgg	ctg	ctg	aag	cgg	cgg	889
Glu	Gly	Ala	Glu	Ile	Glu	Glu	Phe	Leu	Arg	Arg	Leu	Leu	Lys	Arg	Pro	
	240					245						250				
gag	ctg	gag	gag	atc	ttc	cat	cag	tac	tcg	ggc	gag	gac	cgc	gtg	ctg	937
Glu	Leu	Glu	Glu	Ile	Phe	His	Gln	Tyr	Ser	Gly	Glu	Asp	Arg	Val	Leu	
	255				260					265					270	
agt	gcc	cct	gag	ctg	ctg	gag	ttc	ctg	gag	gac	cag	ggc	gag	gag	ggc	985
Ser	Ala	Pro	Glu	Leu	Leu	Glu	Phe	Leu	Glu	Asp	Gln	Gly	Glu	Glu	Gly	
					275					280					285	
gcc	aca	ctg	gcc	cgc	gcc	cag	cag	ctc	att	cag	acc	tat	gag	ctc	aac	1033
Ala	Thr	Leu	Ala	Arg	Ala	Gln	Gln	Leu	Ile	Gln	Thr	Tyr	Glu	Leu	Asn	
					290				295					300		
gag	aca	gcc	aag	cag	cat	gag	ctg	atg	aca	ctg	gat	ggc	ttc	atg	atg	1081
Glu	Thr	Ala	Lys	Gln	His	Glu	Leu	Met	Thr	Leu	Asp	Gly	Phe	Met	Met	
					305				310				315			
tac	ctg	ttg	tcg	ccg	gag	ggg	gct	gcc	ttg	gac	aac	acc	cac	acg	tgt	1129
Tyr	Leu	Leu	Ser	Pro	Glu	Gly	Ala	Ala	Leu	Asp	Asn	Thr	His	Thr	Cys	
	320					325						330				
gtg	ttc	cag	gac	atg	aac	cag	ccc	ett	gcc	cac	tac	ttc	atc	tct	tcc	1177
Val	Phe	Gln	Asp	Met	Asn	Gln	Pro	Leu	Ala	His	Tyr	Phe	Ile	Ser	Ser	
	335				340					345					350	
tcc	cac	aac	acc	tat	ctg	act	gac	tcc	cag	atc	ggg	ggg	ccc	agc	agc	1225
Ser	His	Asn	Thr	Tyr	Leu	Thr	Asp	Ser	Gln	Ile	Gly	Gly	Pro	Ser	Ser	
					355				360					365		
acc	gag	gcc	tat	gtt	agg	tac	tgt	agc	agg	ggg	gcc	ttt	gcc	cag	gga	1273
Thr	Glu	Ala	Tyr	Val	Arg	Tyr	Cys	Ser	Arg	Gly	Ala	Phe	Ala	Gln	Gly	
					370				375					380		
tgc	cgc	tgc	gtg	gag	ctg	gac	tgc	tgg	gag	ggg	cca	gga	ggg	gag	ccc	1321
Cys	Arg	Cys	Val	Glu	Leu	Asp	Cys	Trp	Glu	Gly	Pro	Gly	Gly	Glu	Pro	

385						390						395						
gtc	atc	tat	cat	ggc	cat	acc	ctc	acc	tcc	aag	att	ctc	ttc	cgg	gac	1369		
Val	Ile	Tyr	His	Gly	His	Thr	Leu	Thr	Ser	Lys	Ile	Leu	Phe	Arg	Asp			
400						405					410							
gtg	gtc	caa	gcc	gtg	cgc	gac	cat	gcc	ttc	acg	ctg	tcc	cct	tac	cct	1417		
Val	Val	Gln	Ala	Val	Arg	Asp	His	Ala	Phe	Thr	Leu	Ser	Pro	Tyr	Pro			
415					420					425					430			
gtc	atc	cta	tcc	ctg	gag	aac	cac	tgc	ggg	ctg	gag	cag	cag	gct	gcc	1465		
Val	Ile	Leu	Ser	Leu	Glu	Asn	His	Cys	Gly	Leu	Glu	Gln	Gln	Ala	Ala			
				435					440					445				
atg	gcc	cgc	cac	ctc	tgc	acc	atc	ctg	ggg	gac	atg	ctg	gtg	aca	cag	1513		
Met	Ala	Arg	His	Leu	Cys	Thr	Ile	Leu	Gly	Asp	Met	Leu	Val	Thr	Gln			
			450					455					460					
gcg	ctg	gac	tcc	cca	aat	ccc	gag	gag	ctg	cca	tcc	cca	gag	cag	ctg	1561		
Ala	Leu	Asp	Ser	Pro	Asn	Pro	Glu	Glu	Leu	Pro	Ser	Pro	Glu	Gln	Leu			
465						470					475							
aag	ggc	cgg	gtc	ctg	gtg	aag	gga	aag	aag	ctg	ccc	gct	gct	cgg	agc	1609		
Lys	Gly	Arg	Val	Leu	Val	Lys	Gly	Lys	Lys	Leu	Pro	Ala	Ala	Arg	Ser			
480					485					490								
gag	gat	ggc	cgg	gct	ctg	tgc	gat	cgg	gag	gag	gag	gag	gag	gat	gac	1657		
Glu	Asp	Gly	Arg	Ala	Leu	Ser	Asp	Arg	Glu	Glu	Glu	Glu	Glu	Asp	Asp			
495					500				505					510				
gag	gag	gaa	gaa	gag	gag	gtg	gag	gct	gca	gcg	cag	agg	cgg	ctg	gcc	1705		
Glu	Glu	Glu	Glu	Glu	Glu	Val	Glu	Ala	Ala	Ala	Gln	Arg	Arg	Leu	Ala			
				515					520					525				
aag	cag	atc	tcc	ccg	gag	ctg	tgc	gcc	ctg	gct	gtg	tac	tgc	cac	gcc	1753		
Lys	Gln	Ile	Ser	Pro	Glu	Leu	Ser	Ala	Leu	Ala	Val	Tyr	Cys	His	Ala			
			530					535					540					
acc	cgc	ctg	cgg	acc	ctg	cac	cct	gcc	ccc	aac	gcc	cca	caa	ccc	tgc	1801		
Thr	Arg	Leu	Arg	Thr	Leu	His	Pro	Ala	Pro	Asn	Ala	Pro	Gln	Pro	Cys			
			545				550					555						
cag	gtc	agc	tcc	ctc	agc	gag	cgc	aaa	gcc	aag	aaa	ctc	att	cgg	gag	1849		
Gln	Val	Ser	Ser	Leu	Ser	Glu	Arg	Lys	Ala	Lys	Lys	Leu	Ile	Arg	Glu			
560					565						570							
gca	ggg	aac	agc	ttt	gtc	agg	cac	aat	gcc	cgc	cag	ctg	acc	cgc	gtg	1897		
Ala	Gly	Asn	Ser	Phe	Val	Arg	His	Asn	Ala	Arg	Gln	Leu	Thr	Arg	Val			
575					580				585					590				
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Tyr	Pro	Leu	Gly	Leu	Arg	Met	Asn	Ser	Ala	Asn	Tyr	Ser	Pro	Gln	Glu			
				595					600					605				
atg	tgg	aac	tgc	ggc	tgt	cag	ctg	gtg	gcc	ttg	aac	ttc	cag	acg	cca	1993		
Met	Trp	Asn	Ser	Gly	Cys	Gln	Leu	Val	Ala	Leu	Asn	Phe	Gln	Thr	Pro			
			610					615					620					
ggc	tac	gag	atg	gac	ctc	aat	gcc	ggg	cgc	ttc	cta	gtc	aat	ggg	cag	2041		
Gly	Tyr	Glu	Met	Asp	Leu	Asn	Ala	Gly	Arg	Phe	Leu	Val	Asn	Gly	Gln			
625							630					635						

tgt ggc tac gtc cta aaa cct gcc tgc ctg cgg caa cct gac tgg acc Cys Gly Tyr Val Leu Lys Pro Ala Cys Leu Arg Gln Pro Asp Ser Thr	2089
640 645 650	
ttt gac ccc gag tac cca gga cct ccc aga acc act ctc agc atc cag Phe Asp Pro Glu Tyr Pro Gly Pro Pro Arg Thr Thr Leu Ser Ile Gln	2137
655 660 665 670	
gtg ctg act gca cag cag ctg ccc aag ctg aat gcc gag aag cca cac Val Leu Thr Ala Gln Leu Pro Lys Leu Asn Ala Glu Lys Pro His	2185
675 680 685	
tcc att gtg gac ccc ctg gtg cgc att gag atc cat ggg gtg ccc gca Ser Ile Val Asp Pro Leu Val Arg Ile Glu Ile His Gly Val Pro Ala	2233
690 695 700	
gac tgt gcc cgg cag gag act gac tac gtg ctc aac aat ggc ttc aac Asp Cys Ala Arg Gln Glu Thr Asp Tyr Val Leu Asn Asn Gly Phe Asn	2281
705 710 715	
ccc cgc tgg ggg cag acc ctg cag ttc cag ctg cgg gct ccg gag ctg Pro Arg Trp Gly Gln Thr Leu Gln Phe Gln Leu Arg Ala Pro Glu Leu	2329
720 725 730	
gca ctg gtc cgg ttt gtg gtg gaa gat tat gac gcc acc tcc ccc aat Ala Leu Val Arg Phe Val Val Glu Asp Tyr Asp Ala Thr Ser Pro Asn	2377
735 740 745 750	
gac ttt gtg gcc cag ttt aca ctg cct ctt agc agc cta aag caa ggg Asp Phe Val Gly Gln Phe Thr Leu Pro Leu Ser Ser Leu Lys Gln Gly	2425
755 760 765 770	
tac cgc cac ata cac ctg ctt tcc aag gac ggg gcc tca ctg tca cca Tyr Arg His Ile His Leu Leu Ser Lys Asp Gly Ala Ser Leu Ser Pro	2473
770 775 780	
gcc acg ctc ttc atc caa atc cgc atc cag cgc tcc tga gggccacct Ala Thr Leu Phe Ile Gln Ile Arg Ile Gln Arg Ser	2522
785 790	
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tggcag	3068

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<220>
 <221> CDS
 <222> (343)..(690)

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ctctgatgac aagtggcttt cccaaggagag gtccctgtgc ccagaagagc ttggccccaga      120
gccctgtgcc cagtgacccc actagctttt ccctctactt tccccgcctg gctgtgtctcc      180
ccttgattcg tgcctattgg ccgtgcccac agtctctccc aagctcaaag ttcacctctt      240
tctccagatc cccctggggtc cccaagcctg actcagtgtg tctggggggg tcccttctga      300
gcccacgcac cgacccagct cctcttccct gcagttgtgg cc   atg gcg gct gtg      354
                               Met Ala Ala Val
                               1

ccc atg gtg ctc agt gcc atg ggc ttc act gcg gcg gga atc gcc tgg      402
Pro Met Val Leu Ser Ala Met Gly Phe Thr Ala Ala Gly Ile Ala Ser
   5                10                15                20

tcc tcc ata gca gcc aag atg atg tcc gca gca gcc att gcc aac ggg      450
Ser Ser Ile Ala Ala Lys Met Met Ser Ala Ala Ala Ile Ala Asn Gly
                25                30                35

ggg ggt gtt tct gcg ggg agc ctg gtg gct act ctg cag tcc gtg ggg      498
Gly Gly Val Ser Ala Gly Ser Leu Val Ala Thr Leu Gln Ser Val Gly
   40                45                50

gca gct gga ctc tcc aca tca tcc aac atc ctc ctg gcc tct gtt ggg      546
Ala Ala Gly Leu Ser Thr Ser Ser Asn Ile Leu Leu Ala Ser Val Gly
   55                60                65

tca gtg ttg ggg gcc tgc ttg ggg aat tca cct tct tct tct ctc cca      594
Ser Val Leu Gly Ala Cys Leu Gly Asn Ser Pro Ser Ser Ser Leu Pro
   70                75                80

gct gaa ccc gag gct aaa gaa gat gag gca aga gaa aat gta ccc caa      642
Ala Glu Pro Glu Ala Lys Glu Asp Glu Ala Arg Glu Asn Val Pro Gln
   85                90                95                100

ggg gaa cct cca aaa ccc cca ctc aag tca gag aaa cat gag gaa taa      690
Gly Glu Pro Pro Lys Pro Pro Leu Lys Ser Glu Lys His Glu Glu
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aggtcacatg cagatgcaaa aaaaaaaaaa      719

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<211> 1256

<212> DNA

<213> Homo sapiens

<220>

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<222> (137) ..(1021)

<400> 58

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tcgagctgct	gtcagc	atg gcc cag gct cct gct gac ccg ggc aga gaa	Met Ala Gln Ala Pro Ala Asp Pro Gly Arg Glu	1	5	10
gcc aag agg	ccc cag caa cat	gca gct aca att	cca gag acc cct ggc	217		
Ala Lys Arg	Pro Gln Gln His	Ala Ala Thr Ile	Pro Glu Thr Pro Gly	15	20	25
cct cag ttc	agc caa caa cgg	gag gaa gac atc	tac agg ttt ctc aaa	265		
Pro Gln Phe	Ser Gln Gln Arg	Glu Glu Asp Ile Tyr Arg Phe Leu Lys		30	35	40
gac aat ggt	ccc cag agg gcc	ctg gtc atc gcc	caa gca ctg gga atg	313		
Asp Asn Gly	Pro Gln Arg Ala Leu Val Ile	Ala Gln Ala Leu Gly Met		45	50	55
agg aca gca	aaa gat gtg aac	cga gac ttg tac	agg atg aag agc agg	361		
Arg Thr Ala	Lys Asp Val Asn Arg	Asp Leu Tyr Arg Met Lys Ser Arg		60	65	70
cac ctt ctg	gac atg gat gag	cag tcc aaa gca	tgg acg att tac cgc	409		
His Leu Leu	Asp Met Asp Glu Gln Ser Lys	Ala Trp Thr Ile Tyr Arg		80	85	90
cca gaa gat	tct gga aga aga	gca aag tca gcc	tca att att tac cag	457		
Pro Glu Asp	Ser Gly Arg Arg Ala Lys Ser	Ala Ser Ile Ile Tyr Gln		95	100	105
cac aat cca	atc aac atg atc	tgc cag aat gga	ccc aac agc tgg att	505		
His Asn Pro	Ile Asn Met Ile Cys Gln Asn	Gly Pro Asn Ser Trp Ile		110	115	120
tcc att gca	aac tcc gaa gcc	atc cag att gga	cac ggg aac atc att	553		
Ser Ile Ala	Asn Ser Glu Ala Ile Gln Ile	Gly His Gly Asn Ile Ile		125	130	135
aca aga cag	aca gtc tcc agg	gag gac ggt tcc	gcc ggt cca cgc cac	601		
Thr Arg Gln	Thr Val Ser Arg Glu Asp	Gly Ser Ala Gly Pro Arg His		140	145	150
ctc cct tca	atg gca cca ggt	gat tcc tca act	tgg ggg acc cta gtt	649		
Leu Pro Ser	Met Ala Pro Gly Asp Ser Ser Thr	Trp Gly Thr Leu Val		160	165	170
gat ccc tgg	ggg ccc cag gac	atc cac atg gag	cgg tcc ata ctg aga	697		
Asp Pro Trp	Gly Pro Gln Asp Ile His Met	Glu Arg Ser Ile Leu Arg		175	180	185

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cgg gtg cag ctg gga cac agc aat gag atg agg ctc cac ggc gtc ccg      745
Arg Val Gln Leu Gly His Ser Asn Glu Met Arg Leu His Gly Val Pro
      190                      195                      200

tcc gag ggc cct gcc cac atc ccc cct ggc agc ccc cca gtc tct gcc      793
Ser Glu Gly Pro Ala His Ile Pro Pro Gly Ser Pro Pro Val Ser Ala
      205                      210                      215

act gct gcc ggc cca gaa gct tcg ttt gaa gca aga att ccc agt cca      841
Thr Ala Ala Gly Pro Glu Ala Ser Phe Glu Ala Arg Ile Pro Ser Pro
      220                      225                      230

gga act cac cct gag ggg gaa gcc gcc cag aga atc cac atg aaa tcg      889
Gly Thr His Pro Glu Gly Glu Ala Ala Gln Arg Ile His Met Lys Ser
      240                      245                      250

tgc ttt ctc gag gac gcc acc atc ggc aac agc aac aaa atg tct atc      937
Cys Phe Leu Glu Asp Ala Thr Ile Gly Asn Ser Asn Lys Met Ser Ile
      255                      260                      265

cag ccc agg ggt ggc tgg ccc agg agg agt cgc agg gtc tgg aga ggg      985
Gln Pro Arg Gly Gly Trp Pro Arg Arg Ser Arg Arg Val Trp Arg Gly
      270                      275                      280

gga gcc agg gga gga cgc agt tgc tgc ctt cac tga agtc ttgaaccct      1035
Gly Ala Arg Gly Gly Arg Ser Cys Cys Leu His
      285                      290

caaagtcatt catgaaattt ggaatcaact tcttccagac tctgtgaat gttgatagtt      1095

tgacctcttc ccatgaatca caaatgttct taacggcatg tagattgggt atcttttcca      1155

gaagattttc aacttacttt gcccagatcc atctgaggaa tcactctgtg ttgcacttat      1215

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<213> Homo sapiens

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<221> CDS
<222> (115) .. (1101)

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caccaggtg cattggtgcc agcatcttca ctgaaaggag gtaactctggg ctct      117
                                     atg
                                     Met
                                     1

tca gtc cgt tct aaa ttg cca aat tct cca gca gca tct tct cat ccc      165
Ser Val Arg Ser Lys Leu Pro Asn Ser Pro Ala Ala Ser Ser His Pro
      5                      10                      15

aag ctc aag tct tca aaa ggc ata acg aag aaa ccg cag gct cct tca      213
Lys Leu Lys Ser Ser Lys Gly Ile Thr Lys Lys Pro Gln Ala Pro Ser

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20	25	30	
aac aat gca tca tct tca ctt gct tca tta aat cca gta ggt aaa aac Asn Asn Ala Ser Ser Ser Leu Ala Ser Leu Asn Pro Val Gly Lys Asn 35 40 45			261
act tct tca cca gct tta cca aga act gca cct tgt ata tct gag tca Thr Ser Ser Pro Ala Leu Pro Arg Thr Ala Pro Cys Ile Ser Glu Ser 50 55 60 65			309
ccg aga aaa tgt att tca tcc ccc aat acc ccc aag gcc aag gtt att Pro Arg Lys Cys Ile Ser Ser Pro Asn Thr Pro Lys Ala Lys Val Ile 70 75 80			357
cca gcc cag aat tca gca gat ctg ccc gag tcc aca ctt ttg cca aat Pro Ala Gln Asn Ser Ala Asp Leu Pro Glu Ser Thr Leu Leu Pro Asn 85 90 95			405
aag tgt tca gga aaa act caa cct aag tat ttg aaa cat aac cat att Lys Cys Ser Gly Lys Thr Gln Pro Lys Tyr Leu Lys His Asn His Ile 100 105 110			453
tct tcc aga gat aat gca gta tct cac tta gct gca cat tca aat tca Ser Ser Arg Asp Asn Ala Val Ser His Leu Ala Ala His Ser Asn Ser 115 120 125			501
tcc tca aaa tgt ccc aag ctg cct aaa gca aat ata cct gta aga cct Ser Ser Lys Cys Pro Lys Leu Pro Lys Ala Asn Ile Pro Val Arg Pro 130 135 140 145			549
aaa cct tct ttc cag tcc tct gca aaa atg aca aaa acc agt tcc aaa Lys Pro Ser Phe Gln Ser Ser Ala Lys Met Thr Lys Thr Ser Ser Lys 150 155 160			597
acc ata gcc acg ggt cta gga aca cag tct caa cca tcc gat gga gcc Thr Ile Ala Thr Gly Leu Gly Thr Gln Ser Gln Pro Ser Asp Gly Ala 165 170 175			645
cca caa gca aag cca gtc cca gca cag aaa ctt aaa tcg gcc ttg aat Pro Gln Ala Lys Pro Val Pro Ala Gln Lys Leu Lys Ser Ala Leu Asn 180 185 190			693
tta aat cag cca gtt tct gtg tcc tca gtt tct cct gta aaa gcc aca Leu Asn Gln Pro Val Ser Val Ser Ser Val Ser Pro Val Lys Ala Thr 195 200 205			741
cag aaa tca aaa gat aag aat ata gtt tca gct acc aaa aag cag cct Gln Lys Ser Lys Asp Lys Asn Ile Val Ser Ala Thr Lys Lys Gln Pro 210 215 220 225			789
cag aat aaa agt gca ttt cag aag aca gga ccc agc tcc ttg aag tct Gln Asn Lys Ser Ala Phe Gln Lys Thr Gly Pro Ser Ser Leu Lys Ser 230 235 240			837
cct ggc cgt acc cca ctg tcc atc gtg agc cta ccc cag tct tct acc Pro Gly Arg Thr Pro Leu Ser Ile Val Ser Leu Pro Gln Ser Ser Thr 245 250 255			885
aaa aca caa act gca ccg aag tca gca cag act gtc gct aag agc cag Lys Thr Gln Thr Ala Pro Lys Ser Ala Gln Thr Val Ala Lys Ser Gln 260 265 270			933


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cat tca act aaa ggg cct ccc aga agt ggc aaa acc cca gct tca atc      981
His Ser Thr Lys Gly Pro Pro Arg Ser Gly Lys Thr Pro Ala Ser Ile
275                               280                               285

agg aaa cca ccc tca tct gtt aag gat gca gat agt gga gat aaa aaa      1029
Arg Lys Pro Pro Ser Ser Val Lys Asp Ala Asp Ser Gly Asp Lys Lys
290                               295                               300                               305

cct act gca aag aaa aag gaa gat gat gac cat tat ttt gtc atg act      1077
Pro Thr Ala Lys Lys Lys Glu Asp Asp His Tyr Phe Val Met Thr
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<213> Homo sapiens

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Met Ala Pro Thr Leu Phe Gln Lys Leu Phe Ser Lys Arg
1                               5                               10

acc ggg ctg ggc gcg ccc ggc cgc gac gcc cgg gac cca gat tgc ggg      156
Thr Gly Leu Gly Ala Pro Gly Arg Asp Ala Arg Asp Pro Asp Cys Gly
15                               20                               25

ttc agt tgg cct tta cca gag ttt gat cca agc cag att cga ctg att      204
Phe Ser Trp Pro Leu Pro Glu Phe Asp Pro Ser Gln Ile Arg Leu Ile
30                               35                               40                               45

gta tat caa gac tgt gaa aga cga ggg aga aat gtt ttg ttt gac tcc      252
Val Tyr Gln Asp Cys Glu Arg Arg Gly Arg Asn Val Leu Phe Asp Ser
50                               55                               60

agt gtt aag aga aga aat gag gac ata tca gta tcg gac tta aat act      300
Ser Val Lys Arg Arg Asn Glu Asp Ile Ser Val Ser Asp Leu Asn Thr
65                               70                               75

att tat tct tat ctt cat gga atg gaa ata tta tca aat ctc agg gaa      348
Ile Tyr Ser Tyr Leu His Gly Met Glu Ile Leu Ser Asn Leu Arg Glu
80                               85                               90

cat cag ctt aga tta atg tct gca aga gca cgc tat gag aga tac agt      396
His Gln Leu Arg Leu Met Ser Ala Arg Ala Arg Tyr Glu Arg Tyr Ser
95                               100                               105

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ggc aat cag gtt ctc ttt tgt tca gaa acg att gcc aga tgt tgg tat 444 Gly Asn Gln Val Leu Phe Cys Ser Glu Thr Ile Ala Arg Cys Trp Tyr 110 115 120 125
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cct tgc agt ttt ggt aag cag ttt gga gga aaa aga gga tgt gat tgt 540 Pro Cys Ser Phe Gly Lys Gln Phe Gly Gly Lys Arg Gly Cys Asp Cys 145 150 155
ctt gta tta gag cct tca gaa atg att gtg gta gag aat gcc aaa gat 588 Leu Val Leu Glu Pro Ser Glu Met Ile Val Val Glu Asn Ala Lys Asp 160 165 170
aat gaa gat agt att cta caa aga gaa att cct gcc aga caa tcc cga 636 Asn Glu Asp Ser Ile Leu Gln Arg Glu Ile Pro Ala Arg Gln Ser Arg 175 180 185
aga aga ttt cgg aaa att aac tat aaa gga gag cgc caa acc att act 684 Arg Arg Phe Arg Lys Ile Asn Tyr Lys Gly Glu Arg Gln Thr Ile Thr 190 195 200 205
gat gat gtg gag gtt aac agc tat ctt tct ctt cca gct gat ctt acc 732 Asp Asp Val Glu Val Asn Ser Tyr Leu Ser Leu Pro Ala Asp Leu Thr 210 215 220
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tta tct gat atc tat cag gct acg gag agt gag gta gga gat gta gat 876 Leu Ser Asp Ile Tyr Gln Ala Thr Glu Ser Glu Val Gly Asp Val Asp 255 260 265
ttg aca cgt ctt cca gaa gga cct gtt gat tct gag gat gac gaa gag 924 Leu Thr Arg Leu Pro Glu Gly Pro Val Asp Ser Glu Asp Asp Glu Glu 270 275 280 285
gaa gat gaa gag att gat cga aca gat cca ttg cag ggg cga gat ctt 972 Glu Asp Glu Glu Ile Asp Arg Thr Asp Pro Leu Gln Gly Arg Asp Leu 290 295 300
gtt cga gaa tgt ctt gaa aaa gaa cct gca gac aaa act gat gat gac 1020 Val Arg Glu Cys Leu Glu Lys Glu Pro Ala Asp Lys Thr Asp Asp Asp 305 310 315
att gaa caa ttg ctg gag ttt atg cac cag ctc cct gca ttt gca aac 1068 Ile Glu Gln Leu Leu Glu Phe Met His Gln Leu Pro Ala Phe Ala Asn 320 325 330
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Val	Val	Glu	Gln	Ala	Gly	Ala	Ile	Ile	Leu	Glu	Asp	Gly	Gln	Glu	Leu		
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Asp	Ser	Trp	Tyr	Val	Ile	Leu	Asn	Gly	Thr	Val	Glu	Ile	Ser	His	Pro		
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Asp	Gly	Lys	Val	Glu	Asn	Leu	Phe	Met	Gly	Asn	Ser	Phe	Gly	Ile	Thr		
			385					390					395				
ccc	act	ctg	gat	aag	cag	tac	atg	cat	gga	att	gtc	agg	act	aaa	gta	1308	
Pro	Thr	Leu	Asp	Lys	Gln	Tyr	Met	His	Gly	Ile	Val	Arg	Thr	Lys	Val		
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gat	gat	tgt	cag	ttt	gtc	tcg	ata	gcc	cag	caa	gat	tat	tggt	aga	att	1356	
Asp	Asp	Cys	Gln	Phe	Val	Cys	Ile	Ala	Gln	Gln	Asp	Tyr	Trp	Arg	Ile		
			415			420					425						
tta	aac	cat	gtg	gaa	aaa	aat	acc	cat	aaa	gtt	gag	gaa	gag	gga	gaa	1404	
Leu	Asn	His	Val	Glu	Lys	Asn	Thr	His	Lys	Val	Glu	Glu	Glu	Gly	Glu		
			430		435				440					445			
att	gtt	atg	gta	cat	gag	cat	cgg	gaa	cta	gac	cgg	agt	gga	acc	agg	1452	
Ile	Val	Met	Val	His	Glu	His	Arg	Glu	Leu	Asp	Arg	Ser	Gly	Thr	Arg		
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aaa	gga	cac	att	gtg	atc	aag	gca	aca	cct	gag	cgt	ctc	ata	atg	cat	1500	
Lys	Gly	His	Ile	Val	Ile	Lys	Ala	Thr	Pro	Glu	Arg	Leu	Ile	Met	His		
			465				470					475					
tta	ata	gaa	gaa	cat	tcc	atc	gtg	gat	cca	act	tat	ata	gaa	gat	ttt	1548	
Leu	Ile	Glu	Glu	His	Ser	Ile	Val	Asp	Pro	Thr	Tyr	Ile	Glu	Asp	Phe		
			480			485						490					
cta	tta	act	tac	agg	aca	ttt	ctt	gaa	agt	cct	ttg	gat	gtt	ggg	atc	1596	
Leu	Leu	Thr	Tyr	Arg	Thr	Phe	Leu	Glu	Ser	Pro	Leu	Asp	Val	Gly	Ile		
			495			500					505						
aaa	cta	ttg	gaa	tggt	ttt	aag	atc	gac	agc	tta	aga	gat	aag	gtg	aca	1644	
Lys	Leu	Leu	Glu	Trp	Phe	Lys	Ile	Asp	Ser	Leu	Arg	Asp	Lys	Val	Thr		
			510		515				520				525				
cgg	att	gta	tta	tta	tggt	gta	aat	aat	cat	ttt	aat	gat	ttt	gaa	ggt	1692	
Arg	Ile	Val	Leu	Leu	Trp	Val	Asn	Asn	His	Phe	Asn	Asp	Phe	Glu	Gly		
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gac	cct	gct	atg	act	cga	ttt	cta	gag	gaa	ttt	gaa	aaa	aat	ctg	gaa	1740	
Asp	Pro	Ala	Met	Thr	Arg	Phe	Leu	Glu	Glu	Phe	Glu	Lys	Asn	Leu	Glu		
			545					550				555					
gat	aca	aag	atg	aat	ggt	cat	ctc	cgg	tta	ttg	aat	att	gcc	tgt	gct	1788	
Asp	Thr	Lys	Met	Asn	Gly	His	Leu	Arg	Leu	Leu	Asn	Ile	Ala	Cys	Ala		
			560			565						570					
gca	aag	gct	aag	tggt	aga	cag	gtt	gtg	ctg	caa	aag	gct	tcc	cgc	gag	1836	
Ala	Lys	Ala	Lys	Trp	Arg	Gln	Val	Val	Leu	Gln	Lys	Ala	Ser	Arg	Glu		
			575			580					585						
tcc	cct	cta	caa	ttc	agc	ctt	aat	gga	ggg	agt	gag	aag	gga	ttt	ggt	1884	
Ser	Pro	Leu	Gln	Phe	Ser	Leu	Asn	Gly	Gly	Ser	Glu	Lys	Gly	Phe	Gly		

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caa tca caa gat gac agc att gtg gga aca agg cac tgt agg cat agt Gln Ser Gln Asp Asp Ser Ile Val Gly Thr Arg His Cys Arg His Ser 750 755 760 765				2364
ctg gct ata atg ccc atc cct gga aca ctc tca tcc agc agc cct gat Leu Ala Ile Met Pro Ile Pro Gly Thr Leu Ser Ser Ser Ser Pro Asp 770 775 780				2412
ctc ctg cag cct acc acc agt atg ttg gat ttt tcc aat cct tca gat Leu Leu Gln Pro Thr Thr Ser Met Leu Asp Phe Ser Asn Pro Ser Asp 785 790 795				2460
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tac att atc atc agt aaa gac acc aca gct aaa gaa gta gtt ttt cat Tyr Ile Ile Ile Ser Lys Asp Thr Thr Ala Lys Glu Val Val Phe His 815 820 825				2556
gct gtt cat gaa ttt ggt ttg acc ggt gca tcc gac aca tat tct ctc Ala Val His Glu Phe Gly Leu Thr Gly Ala Ser Asp Thr Tyr Ser Leu 830 835 840 845				2604

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850	860
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865	870 875
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880	885 890
gat gct caa gaa cta gtt aag gaa agc cag cta tcc atg ctg cag ctc Asp Ala Gln Glu Leu Val Lys Glu Ser Gln Leu Ser Met Leu Gln Leu	2796
895	900 905
agt acc att gag gtg gcc acc cag ctg tca atg agg gac ttt gat ttg Ser Thr Ile Glu Val Ala Thr Gln Leu Ser Met Arg Asp Phe Asp Leu	2844
910	915 920 925
ttt cgt aat att gaa ccg act gag tac atc gat gac ctt ttt aag tta Phe Arg Asn Ile Glu Pro Thr Glu Tyr Ile Asp Asp Leu Phe Lys Leu	2892
930	935 940
aat tcc aaa aca gga aat act cat ttg aag agg ttt gag gac att gta Asn Ser Lys Thr Gly Asn Thr His Leu Lys Arg Phe Glu Ile Val	2940
945	950 955
aac caa gag aca ttc tgg gtt gcc tca gaa att tta act gaa gca aat Asn Gln Glu Thr Phe Trp Val Ala Ser Glu Ile Leu Thr Glu Ala Asn	2988
960	965 970
cag ctc aaa cga atg aag att att aag cat ttt att aaa att gca ctt Gln Leu Lys Arg Met Lys Ile Ile Lys His Phe Ile Lys Ile Ala Leu	3036
975	980 985
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990	995 1000 1005
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1010	1015 1020
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1025	1030 1035
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1055	1060 1065
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1070	1075 1080 1085

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Gln Glu Leu	Trp	Lys	Ile	Gln	Ser	Ser	Leu	Leu	Leu	Glu	Ala	Val	Trp	
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His Leu His	Val	Gln	Gly	Ile	Val	Ser	Leu	Gln	Glu	Leu	Leu	Glu	Ser	
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His Pro Asp	Met	His	Ala	Val	Gly	Ser	Trp	Leu	Phe	Arg	Asn	Leu	Cys	
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Cys Leu Cys	Glu	Gln	Met	Glu	Ala	Ser	Cys	Gln	His	Ala	Asp	Glu	Ala	
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Glu Leu Leu Ala Gly Arg Val Lys Arg Glu Lys Tyr Asn Pro Glu Arg
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Gln	Glu	Val	Leu	Glu	Thr	Gln	Glu	Val	His	Trp	Gln	Arg	Val	Leu	Ser	
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Ile Ala Cys Phe Ala Val Ile Val Ser Ala Lys Arg Ala Val Glu Arg	120	125	130	
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	Met Tyr Lys Arg Asn Gly	Leu Met Ala Ser Val Leu Val Thr		

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ata cct gtg ttt aaa gct atc cag ccg gag gaa cta gcc agc tgt gga Ile Pro Val Phe Lys Ala Ile Gln Pro Glu Glu Leu Ala Ser Cys Gly 65 70 75			299
tgg agt aag aag gag aaa cac agt ctt gcc cct aac gtt gtg gcc ttt Trp Ser Lys Lys Glu Lys His Ser Leu Ala Pro Asn Val Val Ala Phe 80 85 90			347
acc cgg agg ttt aac cag gtc agt ttt tgg gtt gta cga gaa att cta Thr Arg Arg Phe Asn Gln Val Ser Phe Trp Val Arg Glu Ile Leu 95 100 105 110			395
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gac tac ctg atg tgc aaa gaa gat aat tac aag cgg aca cgg gaa tat Asp Tyr Leu Met Ser Lys Glu Asp Asn Tyr Lys Arg Thr Arg Glu Tyr 175 180 185 190			635
atc cga agc ctg aag atg gtt cca agt att ccc tat cta gga atc tat Ile Arg Ser Leu Lys Met Val Pro Ser Ile Pro Tyr Leu Gly Ile Tyr 195 200 205			683
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Leu Pro His Val Gln Lys Tyr Leu Lys Ser Val Arg Tyr Ile Glu Glu	
255 260 265 270	
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Leu Gln Lys Phe Val Glu Asp Asp Asn Tyr Lys Leu Ser Leu Arg Ile	
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gaa cca gga agc agc tct cca aga cta gtc tct tcc aag gaa gat ctt	971
Glu Pro Gly Ser Ser Pro Arg Leu Val Ser Ser Lys Glu Asp Leu	
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Ala Gly Pro Ser Ala Gly Ser Gly Ser Ala Arg Phe Ser Arg Arg Pro	
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acc tgt cct gac aca tct gtt gct ggc agc ctc ccc aca cct cca gtc	1067
Thr Cys Pro Asp Thr Ser Val Ala Gly Ser Leu Pro Thr Pro Pro Val	
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Pro Arg His Arg Lys Ser His Ser Leu Gly Asn Asn Arg Gly Arg Leu	
335 340 345 350	
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Tyr Ala Thr Leu Gly Pro Asn Trp Arg Val Pro Val Arg Asn Ser Pro	
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aga acc cgg agc tgt gtc tac agc ccc acc ggc cgg tgc atc tgt tct	1211
Arg Thr Arg Ser Cys Val Tyr Ser Pro Thr Gly Pro Cys Ile Cys Ser	
370 375 380	
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Leu Gly Asn Ser Ala Ala Val Pro Thr Met Glu Gly Pro Leu Arg Arg	
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Lys Thr Leu Leu Lys Glu Gly Arg Lys Pro Ala Leu Ser Ser Trp Thr	
400 405 410	
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Arg Tyr Trp Val Ile Leu Ser Gly Ser Thr Leu Leu Tyr Tyr Gly Ala	
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Lys Ser Leu Arg Gly Thr Asp Arg Lys His Val Ser Ile Val Gly Trp	
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Met Val Gln Leu Pro Asp Asp Pro Glu His Pro Asp Ile Phe Gln Leu	
450 455 460	
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Asn Asn Pro Asp Lys Gly Asn Val Tyr Lys Phe Gln Thr Gly Ser Arg	
465 470 475	
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Phe His Ala Ile Leu Trp His Lys His Leu Asp Ala Cys Lys Ser	
480 485 490	

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Ser His Glu Val Asp His Leu Glu Gly Gly Ala Gly Lys Glu Ala Gly
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Pro Cys Ala

gccctgagta aaacccattg tccctctttg gaggagcggc cagaggatga cagcagcccc      1758

agcaggcagc agtgccctggg caggctgac cagcagagca ctaatgggtc agtttcatgt      1818

attggcagat gtggtgtagc atggcaaggc tacaagtttt aaggattttt gtctgatttt      1878

cagacctgga ggaggggatt tttcttcta ctttccccct tttttatttc taatttactt      1938

tcaaccaaatt attccacta tgtgctatat gtaataataa aaagtggaca acaactgaaa      1998

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                                         Met Ala Glu Glu Gln
                                         1                      5

caa cag cag cca cca cag cag cct gat gcc cat cag cag ctt ccc ccc      162
Gln Gln Pro Pro Pro Gln Gln Pro Asp Ala His Gln Gln Leu Pro Pro
                      10                      15                      20

agc gcc ccc aac tgc ggg gtg gcc ctg cca gcc ctt gtg ccc ggg ctg      210
Ser Ala Pro Asn Ser Gly Val Ala Leu Pro Ala Leu Val Pro Gly Leu
                      25                      30                      35

cca ggg aca gag gcc agc gcg ctg caa cac aag atc aag aac tcc atc      258
Pro Gly Thr Glu Ala Ser Ala Leu Gln His Lys Ile Lys Asn Ser Ile
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tgc aaa act gta caa tct aaa gtg gac tgc att ttg caa gaa gtt gag      306
Cys Lys Thr Val Gln Ser Lys Val Asp Cys Ile Leu Gln Glu Val Glu
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gaa cat ccg gag act tca ctg ccc aaa cag gaa gtc tat gat gag tac Glu His Pro Glu Thr Ser Leu Pro Lys Gln Glu Val Tyr Asp Glu Tyr 120 125 130	498
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ttg ggc aca aga ggc aaa tct aaa tat tgc tac agt gga cta aga aaa Leu Gly Thr Arg Gly Lys Ser Lys Tyr Cys Tyr Ser Gly Leu Arg Lys 170 175 180	642
aaa gct ttt gtt cat atg cca aca ctg ccc aac ctt gac ttt cac aaa Lys Ala Phe Val His Met Pro Thr Leu Pro Asn Leu Asp Phe His Lys 185 190 195	690
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cct tct gct ttt ata cct aca gct gaa agt aat tcc ttt cag cct cag Pro Ser Ala Phe Ile Pro Thr Ala Glu Ser Asn Ser Phe Gln Pro Gln 280 285 290	978
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Lys Ile Gln Lys Lys Gln Gln Glu Gln Lys Leu Gln Ser Pro Leu Pro	
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Gly Glu Ser Ala Ala Lys Lys Ser Glu Ser Ala Thr Ser Asn Gly Val	
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Thr Asn Leu Pro Asn Gly Asn Pro Ser Ile Leu Ser Pro Gln Pro Ile	
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Gly Ile Val Met Ala Ala Val Pro Ser Pro Ile Pro Val Gln Arg Thr	
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Arg His Leu Val Thr Ser Pro Ser Pro Met Ser Ser Ser Asp Gly Lys	
375 380 385	
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Val Leu Pro Leu Asn Val Gln Val Ser Leu Ser Thr Cys Ser Leu	
390 395 400	
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ttccttccgg agcc atg tca gaa gga gtg gac ttg att gat ata tat gct 170
Met Ser Glu Gly Val Asp Leu Ile Asp Ile Tyr Ala
1 5 10

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Asp Glu Glu Phe Asn Gln Asp Pro Glu Phe Asn Asn Thr Asp Gln Ile
15 20 25

gac ctg tat gat gat gtg ctg aca gcc acc tca cag ccc tca gat gac 266
Asp Leu Tyr Asp Asp Val Leu Thr Ala Thr Ser Gln Pro Ser Asp Asp
30 35 40

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Arg Ser Ser Ser Thr Glu Pro Pro Pro Val Arg Gln Glu Pro Ser
45 50 55 60

ccc aag ccc aac aac aag acc cct gca att ctg tat acc tac agt ggc 362
Pro Lys Pro Asn Asn Lys Thr Pro Ala Ile Leu Tyr Thr Tyr Ser Gly
65 70 75

ctg cgt aat aga cga gct gcc gtt tat gtg ggc agc ttc tcc tgg tgg 410
Leu Arg Asn Arg Arg Ala Ala Val Tyr Val Gly Ser Phe Ser Trp Trp
80 85 90

acc aca gac cag cag ctg atc cag gtt att cgc tct ata gga gtc tat 458
Thr Thr Asp Gln Gln Leu Ile Gln Val Ile Arg Ser Ile Gly Val Tyr
95 100 105

gat gtg gtg gag ttg aaa ttt gca gag aat cga gca aat ggc cag tcc 506
Asp Val Val Glu Leu Lys Phe Ala Glu Asn Arg Ala Asn Gly Gln Ser
110 115 120

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Lys Gly Tyr Ala Glu Val Val Val Ala Ser Glu Asn Ser Val His Lys
125 130 135 140

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Leu Leu Glu Leu Leu Pro Gly Lys Val Leu Asn Trp Gln Lys Lys Trp
145 150 155

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Thr

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Leu Ala Leu Leu Gly Ala Met Ser Gly Gly Glu Ala Leu His Leu Ile																				
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ctc tta cct gct aca ggc atg gtg gca gag aat tct cca cct ggg act																				147
Leu Leu Pro Ala Thr Gly Asn Val Ala Glu Asn Ser Pro Pro Gly Thr																				
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tca gtg cac aag ttt tct gtg aag tta tca gca tca ttg tca cct gtg																				195
Ser Val His Lys Phe Ser Val Lys Leu Ser Ala Ser Leu Ser Pro Val																				
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atc cca gga ttt ccc cag ata gtc aac tca aat ccc ctc act gaa gct																				243
Ile Pro Gly Phe Pro Gln Ile Val Asn Ser Asn Pro Leu Thr Glu Ala																				
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Phe Arg Val Asn Trp Leu Ser Gly Thr Tyr Phe Glu Val Val Thr Thr																				
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ggg atg gaa caa cta gat ttt gaa aca gga cca aac ata ttt gat ttg																				339
Gly Met Glu Gln Leu Asp Phe Glu Thr Gly Pro Asn Ile Phe Asp Leu																				
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cag att tat gtg aag gat gag gtt ggt gtc aca gac ctt caa gtc ctg																				387
Gln Ile Tyr Val Lys Asp Glu Val Gly Val Thr Asp Leu Gln Val Leu																				
					105					110					115					
act gtc cag gta aca gat gtg aac gag cca cct cag ttt caa ggc aac																				435
Thr Val Gln Val Thr Asp Val Asn Glu Pro Pro Gln Phe Gln Gly Asn																				
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Phe Ile Tyr Gln Val Glu Ala Phe Asp Pro Glu Asp Thr Ser Arg Asn																				
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Ile Pro Leu Ser Tyr Phe Leu Ile Ser Pro Pro Lys Ser Phe Arg Met																				
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Ser Ala Asn Gly Thr Leu Phe Ser Thr Thr Glu Leu Asp Phe Glu Ala																				
					185					190					195					

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	Met Lys Leu Cys Pro Arg Tyr	
	1 5	
aat tcc caa gaa gaa act tta gag ttt gta gca gat tac agt gga caa		161
Asn Ser Gln Glu Glu Thr Leu Glu Phe Val Ala Asp Tyr Ser Gly Gln		
10 15 20		
gat aat ttc tta caa cga gtg gga caa aat ggc tta aag aat tcg gag		209
Asp Asn Phe Leu Gln Arg Val Gly Gln Asn Gly Leu Lys Asn Ser Glu		
25 30 35		
aag gag tcc act gtc aac agc atc ttt cag gtc atc ccg agc tgc aat		257
Lys Glu Ser Thr Val Asn Ser Ile Phe Gln Val Ile Arg Ser Cys Asn		
40 45 50 55		
cga agt ctg gag aca gac gag gag gac agc ccc agt gaa gga aac agc		305
Arg Ser Leu Glu Thr Asp Glu Glu Asp Ser Pro Ser Glu Gly Asn Ser		
60 65 70		
tcc agg aaa agc tcc ttg aag gat aaa agc cga tgg cag ttt ata att		353
Ser Arg Lys Ser Ser Leu Lys Asp Lys Ser Arg Trp Gln Phe Ile Ile		
75 80 85		
gga gat ttg ttg gat tca gac aat gac atc ttt gag caa tcc aaa gaa		401
Gly Asp Leu Leu Asp Ser Asp Asn Asp Ile Phe Glu Gln Ser Lys Glu		
90 95 100		
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Tyr Asp Ser His Gly Ser Glu Asp Ser Gln Lys Ala Phe Asp His Gly		
105 110 115		
acg gag ctc atc cct tgg tac gtg ctg tcc atc caa gcc gat gtg cac		497
Thr Glu Leu Ile Pro Trp Tyr Val Leu Ser Ile Gln Ala Asp Val His		
120 125 130 135		
cag ttc ctg ctg cag ggg gcc acg gtc atc cac tac gac cag gac aca		545
Gln Phe Leu Leu Gln Gly Ala Thr Val Ile His Tyr Asp Gln Asp Thr		
140 145 150		
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His Leu Ser Ala Arg Cys Phe Leu Gln Leu Gln Pro Asp Asn Ser Thr		
155 160 165		
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Leu Thr Trp Val Lys Phe Thr Ala Ser Pro Ala Ser Ser Lys Ala		
170 175 180		
aaa ctt ggt gta ctt aat aac aca gct gag cct gga aaa ttc cca cta		689
Lys Leu Gly Val Leu Asn Asn Thr Ala Glu Pro Gly Lys Phe Pro Leu		
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Leu Gly Asn Ala Gly Leu Ser Ser Leu Thr Glu Gly Val Leu Asp Leu		
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Phe Ala Val Lys Ala Val Tyr Met Gly His Pro Gly Ile Asp Ile His		
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Gly	Val	Thr	Leu	Leu	Tyr	Gly	Leu	Gln	Thr	Thr	Asp	Asn	Arg	Leu	Leu	
		250					255					260				
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Gly	Arg	Arg	Trp	Ser	Ala	Arg	Asn	Pro	Ser	Pro	Gly	Thr	Ser	Ala	Lys	
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gctctgggac cttcgtgctt caaggcctgg ggagcctgtc cttccatgcc cttgtcgagg 1854
gaaagagacc cagaaggac acaaccgctc agagacctgg gagcaggggc aatgaccgtt 1914
tgactgtttg tggcttgggc ctctgacatg acttatgtgt gtgtgtgttt ttgggggtggg 1974
gagggaggga gagaagaggg ggctaaattt gatgctttaa ctgatctcca acagttgaca 2034
ggtcatcctt gccagttgta taactgaaaa aggacttttc taccaggtat gaccttttaa 2094
gtgaaaaatc gaattgttct aaatggaaag aaaaaagtt gcaatctgtg cccttcattg 2154
gggacattcc tctaggactg gtttggggac ggggtgggaat gacctctagg caaggggatg 2214
agaccgcagg aggaaatggc ggggaggagg cattcttgaa ctgctgagga tgggggggtgt 2274
ccctcagcgg gaggccagg gaggggagca gcctagtgg tcttgagag atgggggaag 2334
ctttcagctg atttgcagaa gttgcccatg tggggcccg ccacagggc tggccgtgga 2394
cgtggccctt gccactcac ctgccgcct gccgcccgc ccgcatagca cttgcagacc 2454
tgccctgaacg cacatgacat agcacttgcc gatctgctg tgtccagaag tggcccttgg 2514
ccgagcgccg aactcgctcg cctctagat gtccaagtgc cactgaaat atgcaattta 2574
aagggttgac ccacactaga cgaaactgga ctgcacgac tctttttata ttttttatac 2634
ttgaaatgaa atccttttct tcttttttaa gcgaatgatt gcttttaagt tttgactgta 2694
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aaaaaaaaaaa aaa 2767

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<210> 72
<211> 1494
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (70)..(1293)

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<220>
<221> misc_feature
<222> (1)...(1494)
<223> n = a,t,c or g

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<400> 72
tctctgatt tacggggcgg accgacgcgt cggggcctcc gatggctccg gattcggtac 60

tggcgagcc atg gcg ctg ggg gtg ggg cgc gca agg ccg ggc ctt tcc 108
Met Ala Leu Gly Val Gly Arg Ala Arg Pro Gly Leu Ser
1 5 10

tgt gga gtc atc tca ccg ccg tgc gca ccc act cgt aac tcg cac ccg 156
Cys Gly Val Ile Ser Pro Pro Cys Ala Pro Thr Arg Asn Ser His Pro
15 20 25

```

ggt cct ggc tgc acc gca tcc cct cct gca ccc cct gga tgg ccc ttc Gly Pro Gly Cys Thr Ala Ser Pro Pro Ala Pro Gly Trp Pro Phe 30 35 40 45	204
agc caa cgg ggg cct ggg cga tgg tgc acc acg gag ctg cgc aag gaa Ser Gln Arg Gly Pro Gly Arg Trp Ser Thr Thr Glu Leu Arg Lys Glu 50 55 60	252
aag tcc cgg gat gcg gcc cgc agc cgg cgc agc cag gag acc gag gtg Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Gln Glu Thr Glu Val 65 70 75	300
ctg tac cag ctg gct cac acg ctg ccc ttc gcc cgc ggc gtc agc gcc Leu Tyr Gln Leu Ala His Thr Leu Pro Phe Ala Arg Gly Val Ser Ala 80 85 90	348
cac ctg gac aag gcc tct atc atg cgc ctc acc atc agc tac ctg cgc His Leu Asp Lys Ala Ser Ile Met Arg Leu Thr Ile Ser Tyr Leu Arg 95 100 105	396
atg cac cgc ctc tgc gcc gca ggg gag tgg aac cag gtg gga gca ggg Met His Arg Leu Cys Ala Ala Gly Glu Trp Asn Gln Val Gly Ala Gly 110 115 120 125	444
gga gaa cca ctg gat gcc tgc tac ctg aag gcc ctg gag ggc ttc gtc Gly Glu Pro Leu Asp Ala Cys Tyr Leu Lys Ala Leu Glu Gly Phe Val 130 135 140	492
atg gtg ctc acc gcc gag gga gac atg gct tac ctg tgc gag aat gtc Met Val Leu Thr Ala Glu Gly Asp Met Ala Tyr Leu Ser Glu Asn Val 145 150 155	540
agc aaa cac ctg ggc ctc agt cag ctg gag ctc att gga cac agc atc Ser Lys His Leu Gly Leu Ser Gln Leu Glu Leu Ile Gly His Ser Ile 160 165 170	588
ttt gat ttc atc cac ccc tgt gac caa gag gag ctt cag gac gcc ctg Phe Asp Phe Ile His Pro Cys Asp Gln Glu Glu Leu Gln Asp Ala Leu 175 180 185	636
acc ccc cag cag acc ctg tcc agg agg aag gtg gag gcc ccc acg gag Thr Pro Gln Gln Thr Leu Ser Arg Arg Lys Val Glu Ala Pro Thr Glu 190 195 200 205	684
cgg tgc ttc tcc ttg cgc atg aag agt acg ctc acc agc cgc ggg cgc Arg Cys Phe Ser Leu Arg Met Lys Ser Thr Leu Thr Ser Arg Thr Arg 210 215 220	732
acc ctc aac ctc aag gcg gcc acc tgg aag gtg ctg aac tgc tct gga Thr Leu Asn Leu Lys Ala Ala Thr Trp Lys Val Leu Asn Cys Ser Gly 225 230 235	780
cat atg agg gcc tac aag cca cct gcg cag act tct cca gct ggg agc His Met Arg Ala Tyr Lys Pro Pro Ala Gln Thr Ser Pro Ala Gly Ser 240 245 250	828
cct gac tca gag ccc ccg ctg cag tgc ctg gtg ctc atc tgc gaa gcc Pro Asp Ser Glu Pro Pro Leu Gln Cys Leu Val Leu Ile Cys Glu Ala 255 260 265	876

atc ccc cac cca ggc agc ctg gag ccc cca ctg ggc cga ggg gcc ttc Ile Pro His Pro Gly Ser Leu Glu Pro Pro Leu Gly Arg Gly Ala Phe 270 275 280 285	924
ctc agc cgc cac agc ctg gac atg aag ttc acc tac tgt gac gac agg Leu Ser Arg His Ser Leu Asp Met Lys Phe Thr Tyr Cys Asp Asp Arg 290 295 300	972
att gca gaa gtg gct ggc tat agt ccc gat gac ctg atc ggc tgt tcc Ile Ala Glu Val Ala Gly Tyr Ser Pro Asp Asp Leu Ile Gly Cys Ser 305 310 315	1020
gcc tac gag tac atc cac gcg ctg gac tcc gac gcg gtc agc aag agc Ala Tyr Glu Tyr Ile His Ala Leu Asp Ser Asp Ala Val Ser Lys Ser 320 325 330	1068
atc cac acc tgt atg tat ccc att tcc cca ggt gcg aag cca gct gcc Ile His Thr Cys Met Tyr Pro Ile Ser Pro Gly Ala Lys Pro Ala Ala 335 340 345	1116
aca tgg ccc cca gct gac acc agg acc ccc cag ctg ccc ata ccc cag Thr Trp Pro Pro Ala Asp Thr Arg Thr Pro Gln Leu Pro Ile Pro Gln 350 355 360 365	1164
gat gca ctg cct ccc cac ctg aac acc agc tcc ctg ctg ccc aag ccc Asp Ala Leu Pro Pro His Leu Asn Thr Ser Ser Leu Leu Pro Lys Pro 370 375 380	1212
caa gga act gtc tcc ttc ctt gcc ccc tca tac cca gtc ccc aga tct Gln Gly Thr Val Ser Phe Leu Ala Pro Ser Tyr Pro Val Pro Arg Ser 385 390 395	1260
ttc tct ccc cat ttg ccc cct tgg tgg ccc tga tccctccc gatccccctc Phe Ser Pro His Leu Pro Pro Trp Trp Pro 400 405	1311
ctcagtctg agcaagggcc aggcagtaac agggcagtat cgcttcctgg ccgggagtgg	1371
tggctacctg tggaccacaga ccagggccac agtggtgtca gggggacggg gccccagtc	1431
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tgt	1494

<210> 73
 <211> 1388
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (131) .. (1387)

<400> 73 cgggacctgg ggcggagagc ggttcgcgcg cttcggggcct agtcgggact cggcccgcc gccgccatat tccctgtgga tcttccttac ttgtgcatc ctcgggactc gcatcttcc	60 120
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ttccggagcc	atg	tca	gaa	gga	gtg	gac	ttg	att	gat	ata	tat	gct	gac	169		
	Met	Ser	Glu	Gly	Val	Asp	Leu	Ile	Asp	Ile	Tyr	Ala	Asp			
	1				5					10						
gag	gag	ttc	aac	cag	gac	cca	gag	ttc	aac	aat	aca	gat	cag	att	gac	217
Glu	Glu	Phe	Asn	Gln	Asp	Pro	Glu	Phe	Asn	Asn	Thr	Asp	Gln	Ile	Asp	
	15					20					25					
ctg	tat	gat	gat	gtg	ctg	aca	gcc	acc	tca	cag	ccc	tca	gat	gac	aga	265
Leu	Tyr	Asp	Asp	Val	Leu	Thr	Ala	Thr	Ser	Gln	Pro	Ser	Asp	Asp	Arg	45
	30				35					40						
agc	agc	agc	act	gaa	cca	cct	cct	cct	gtt	cgc	cag	gag	cca	tct	ccc	313
Ser	Ser	Ser	Thr	Glu	Pro	Pro	Pro	Pro	Val	Arg	Gln	Glu	Pro	Ser	Pro	
				50					55					60		
aag	ccc	aac	aac	aag	acc	cct	gca	att	ctg	tat	acc	tac	agt	ggc	ctg	361
Lys	Pro	Asn	Asn	Lys	Thr	Pro	Ala	Ile	Leu	Tyr	Thr	Tyr	Ser	Gly	Leu	
			65					70					75			
cgt	aat	aga	cga	gct	gcc	gtt	tat	gtg	ggc	agc	ttc	tcc	tgg	acc		409
Arg	Asn	Arg	Arg	Ala	Ala	Val	Tyr	Val	Gly	Ser	Phe	Ser	Trp	Trp	Thr	
				80			85					90				
aca	gac	cag	cag	ctg	atc	cag	gtt	att	cgc	tct	ata	gga	gtc	tat	gat	457
Thr	Asp	Gln	Gln	Leu	Ile	Gln	Val	Ile	Arg	Ser	Ile	Gly	Val	Tyr	Asp	
	95					100					105					
gtg	gtg	gag	ttg	aaa	ttt	gca	gag	aat	cga	gca	aat	ggc	cag	tcc	aaa	505
Val	Val	Glu	Leu	Lys	Phe	Ala	Glu	Asn	Arg	Ala	Asn	Gly	Gln	Ser	Lys	
110				115					120					125		
ggg	tat	gct	gag	gtg	gtg	gta	gcc	tct	gaa	aac	tct	gtc	cac	aaa	ttg	553
Gly	Tyr	Ala	Glu	Val	Val	Val	Ala	Ser	Glu	Asn	Ser	Val	His	Lys	Leu	
				130				135						140		
ttg	gaa	ctc	cta	cca	ggg	aaa	gtt	ctt	aat	gga	gaa	aaa	gtg	gac	gtg	601
Leu	Glu	Leu	Leu	Pro	Gly	Lys	Val	Leu	Asn	Gly	Glu	Lys	Val	Asp	Val	
			145				150						155			
agg	ccg	gcc	acc	cgg	cag	aac	ctg	tca	cag	ttt	gag	gca	cag	gct	cgg	649
Arg	Pro	Ala	Thr	Arg	Gln	Asn	Leu	Ser	Gln	Phe	Glu	Ala	Gln	Ala	Arg	
		160				165					170					
aaa	cgt	gag	tgt	gtc	cga	gtc	cca	aga	ggg	gga	ata	cct	cca	cgg	gcc	697
Lys	Arg	Glu	Cys	Val	Arg	Val	Pro	Arg	Gly	Gly	Ile	Pro	Pro	Arg	Ala	
	175					180					185					
cat	tcc	cga	gat	tct	agt	gat	tct	gct	gat	gga	cgg	gcc	aca	ccc	tct	745
His	Ser	Arg	Asp	Ser	Ser	Ser	Ser	Ser	Ala	Asp	Gly	Arg	Ala	Thr	Ser	
190					195					200				205		
gag	aac	ctt	gta	ccc	tca	tct	gct	cgt	gtg	gat	aag	ccc	ccc	agt	gtg	793
Glu	Asn	Leu	Val	Pro	Ser	Ser	Ala	Arg	Val	Asp	Lys	Pro	Pro	Ser	Val	
				210				215						220		
ctg	ccc	tac	ttc	aat	cgt	cct	cct	tcg	gcc	ctt	ccc	ctg	atg	ggg	ctg	841
Leu	Pro	Tyr	Phe	Asn	Arg	Pro	Pro	Ser	Ala	Leu	Pro	Leu	Met	Gly	Leu	
			225					230					235			
ccc	cca	cca	cca	att	cca	ccc	cca	cca	cct	ctc	tcc	tca	agc	ttt	ggg	889

Pro	Pro	Pro	Pro	Ile	Pro	Pro	Pro	Pro	Pro	Leu	Ser	Ser	Ser	Phe	Gly		
		240					245					250					
gtc	cct	cct	cct	cct	cct	ggt	atc	cac	tac	cag	cat	ctc	atg	ccc	cca	937	
Val	Pro	Pro	Pro	Pro	Pro	Gly	Ile	His	Tyr	Gln	His	Leu	Met	Pro	Pro		
	255					260				265							
cct	cct	cga	tta	cct	cct	cat	ctt	gct	gta	cct	ccc	cct	ggg	gcc	atc	985	
Pro	Pro	Arg	Leu	Pro	Pro	His	Leu	Ala	Val	Pro	Pro	Pro	Gly	Ala	Ile		
	270				275					280				285			
cca	cct	gcc	ctt	cac	ctc	aat	cca	gcc	ttc	ctt	ccg	ccg	cca	aac	gct	1033	
Pro	Pro	Ala	Leu	His	Leu	Asn	Pro	Ala	Phe	Leu	Pro	Pro	Pro	Asn	Ala		
				290					295					300			
aca	gtg	ggg	cct	cca	cca	gat	act	tac	atg	aag	gcc	tct	gcc	ccc	tat	1081	
Thr	Val	Gly	Pro	Pro	Pro	Asp	Thr	Tyr	Met	Lys	Ala	Ser	Ala	Pro	Tyr		
			305					310					315				
aac	cac	cat	ggc	agc	cga	gat	tcg	ggc	cct	cca	ccc	tct	aca	gtg	agt	1129	
Asn	His	His	Gly	Ser	Arg	Asp	Ser	Gly	Pro	Pro	Pro	Ser	Thr	Val	Ser		
		320				325						330					
gaa	gcc	gaa	ttt	gaa	gat	atc	atg	aag	cga	aac	aga	gca	att	tcc	agc	1177	
Glu	Ala	Glu	Phe	Glu	Asp	Ile	Met	Lys	Arg	Asn	Arg	Ala	Ile	Ser	Ser		
	335				340					345							
agt	gcc	att	tcc	aaa	gca	gta	tct	gga	gcc	agt	gca	ggg	gat	tac	agt	1225	
Ser	Ala	Ile	Ser	Lys	Ala	Val	Ser	Gly	Ala	Ser	Ala	Gly	Asp	Tyr	Ser		
	350			355				360						365			
gac	gca	att	gag	acg	ctg	ctc	aca	gcc	att	gcg	gtt	atc	aaa	cag	tcc	1273	
Asp	Ala	Ile	Glu	Thr	Leu	Leu	Thr	Ala	Ile	Ala	Val	Ile	Lys	Gln	Ser		
				370				375					380				
cgg	gtt	gcc	aat	gat	gag	cgt	tgc	cgt	gtc	ctc	atc	tcc	tct	ctt	aag	1321	
Arg	Val	Ala	Asn	Asp	Glu	Arg	Cys	Arg	Val	Leu	Ile	Ser	Ser	Leu	Lys		
		385					390					395					
gac	tgt	ctt	cat	ggc	atc	gaa	gcc	aag	tcc	tac	agt	gtg	ggt	gcc	agt	1369	
Asp	Cys	Leu	His	Gly	Ile	Glu	Ala	Lys	Ser	Tyr	Ser	Val	Gly	Ala	Ser		
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ggg	agc	tct	tcc	agg	tga	g										1388	
Gly	Ser	Ser	Ser	Arg													
	415																

<210> 74
 <211> 2184
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (40) .. (2124)

<400> 74

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				Met Gly Ala Pro Ala	
				1 5	
tgc gcc ctc gcg ctc tgc gtg gcc gtg gcc atc gtg gcc ggc gcc tcc	102				
Cys Ala Leu Ala Leu Cys Val Ala Val Ala Ile Val Ala Gly Ala Ser					
	10		15	20	
tgc gag tcc ttg ggg acg gag cag cgc gtc gtg ggg cga gcg gca gaa	150				
Ser Glu Ser Leu Gly Thr Glu Gln Arg Val Val Gly Arg Ala Ala Glu					
	25		30	35	
gtc ccg ggc cca gag ccc ggc cag cag gag cag ttg gtc ttc ggc agc	198				
Val Pro Gly Pro Glu Pro Gly Gln Gln Glu Gln Leu Val Phe Gly Ser					
	40		45	50	
ggg gat gct gtg gag ctg agc tgt ccc ccg ccc ggg ggt ggt ccc atg	246				
Gly Asp Ala Val Glu Leu Ser Cys Pro Pro Pro Gly Gly Gly Pro Met					
	55		60	65	
ggg ccc act gtc tgg gtc aag gat ggc aca ggg ctg gtg ccc tcg gag	294				
Gly Pro Thr Val Trp Val Lys Asp Gly Thr Gly Leu Val Pro Ser Glu					
	70		75	80	85
cgt gtc ctg gtg ggg ccc cag ccg ctg cag gtg ctg aat gcc tcc cac	342				
Arg Val Leu Val Gly Pro Gln Arg Leu Gln Val Leu Asn Ala Ser His					
	90		95	100	
gag gac tcc ggg gcc tac agc tgc ccg cag ccg ctg acg cag cgc gta	390				
Glu Asp Ser Gly Ala Tyr Ser Cys Arg Gln Arg Leu Thr Arg Val					
	105		110	115	
ctg tgc cac ttc agt gtg ccg gtg aca gac gct cca tcc tcg gga gat	438				
Leu Cys His Phe Ser Val Arg Val Thr Asp Ala Pro Ser Ser Gly Asp					
	120		125	130	
gac gaa gac ggg gag gac gag gct gag gac aca ggt gtg gac aca ggg	486				
Asp Glu Asp Gly Glu Asp Glu Ala Glu Asp Thr Gly Val Asp Thr Gly					
	135		140	145	
gcc cct tac tgg aca ccg ccc gag ccg atg gac aag aag ctg ctg gcc	534				
Ala Pro Tyr Trp Thr Arg Pro Glu Arg Met Asp Lys Lys Leu Leu Ala					
	150		155	160	165
gtg ccg gcc gcc aac acc gtc cgc ttc cgc tgc cca gcc gct ggc aac	582				
Val Pro Ala Ala Asn Thr Val Arg Phe Arg Cys Pro Ala Ala Gly Asn					
	170		175	180	
ccc act ccc tcc atc tcc tgg ctg aag aac ggc agg gag ttc cgc ggc	630				
Pro Thr Pro Ser Ile Ser Trp Leu Lys Asn Gly Arg Glu Phe Arg Gly					
	185		190	195	
gag cac cgc att gga ggc atc aag ctg ccg cat cag cag tgg agc ctg	678				
Glu His Arg Ile Gly Gly Ile Lys Leu Arg His Gln Gln Trp Ser Leu					
	200		205	210	
gtc atg gaa agc gtg gtg ccc tcg gac cgc ggc aac tac acc tgc gtc	726				
Val Met Glu Ser Val Val Pro Ser Asp Arg Gly Asn Tyr Thr Cys Val					
	215		220	225	
gtg gag aac aag ttt ggc agc atc ccg cag acg tac acg ctg gac gtg	774				

Val	Glu	Asn	Lys	Phe	Gly	Ser	Ile	Arg	Gln	Thr	Tyr	Thr	Leu	Asp	Val	
230					235					240					245	
ctg	gag	cgc	tcc	cgc	cac	cgg	ccc	atc	ctg	cag	gcg	ggg	ctg	cgc	gcc	822
Leu	Glu	Arg	Ser	Pro	His	Arg	Pro	Ile	Leu	Gln	Ala	Gly	Leu	Pro	Ala	
			250						255					260		
aac	cag	acg	gcg	gtg	ctg	ggc	agc	gac	gtg	gag	ttc	cac	tgc	aag	gtg	870
Asn	Gln	Thr	Ala	Val	Leu	Gly	Ser	Asp	Val	Glu	Phe	His	Cys	Lys	Val	
			265					270					275			
tac	agt	gac	gca	cag	ccc	cac	atc	cag	tgg	ctc	aag	cac	gtg	gag	gtg	918
Tyr	Ser	Asp	Ala	Gln	Pro	His	Ile	Gln	Trp	Leu	Lys	His	Val	Glu	Val	
		280					285						290			
aac	ggc	agc	aag	gtg	ggc	ccg	gac	ggc	aca	ccc	tac	gtt	acc	gtg	ctc	966
Asn	Gly	Ser	Lys	Val	Gly	Pro	Asp	Gly	Thr	Pro	Tyr	Val	Thr	Val	Leu	
	295					300					305					
aag	gtg	tcc	ctg	gag	tcc	aac	gcg	tcc	atg	agc	tcc	aac	aca	cca	ctg	1014
Lys	Val	Ser	Leu	Glu	Ser	Asn	Ala	Ser	Met	Ser	Ser	Asn	Thr	Pro	Leu	
310					315					320				325		
gtg	cgc	atc	gca	agg	ctg	tcc	tca	ggg	gag	ggc	ccc	acg	ctg	gcc	aat	1062
Val	Arg	Ile	Ala	Arg	Leu	Ser	Ser	Gly	Glu	Gly	Pro	Thr	Leu	Ala	Asn	
				330				335						340		
gtc	tcc	gag	ctc	gag	ctg	cct	gcc	gac	ccc	aaa	tgg	gag	ctg	tct	cgg	1110
Val	Ser	Glu	Leu	Glu	Leu	Pro	Ala	Asp	Pro	Lys	Trp	Glu	Leu	Ser	Arg	
			345					350					355			
gcc	cgg	ctg	acc	ctg	ggc	aag	ccc	ctt	ggg	gag	ggc	tgc	ttc	ggc	cag	1158
Ala	Arg	Leu	Thr	Leu	Gly	Lys	Pro	Leu	Gly	Glu	Gly	Cys	Phe	Gly	Gln	
		360					365					370				
gtg	gtc	atg	gcg	gag	gcc	atc	ggc	att	gac	aag	gac	cgg	gcc	gcc	aag	1206
Val	Val	Met	Ala	Glu	Ala	Ile	Gly	Ile	Asp	Lys	Asp	Arg	Ala	Ala	Lys	
	375					380					385					
cct	gtc	acc	gta	gcc	gtg	aag	atg	ctg	aaa	gac	gat	gcc	act	gac	aag	1254
Pro	Val	Thr	Val	Ala	Val	Lys	Met	Leu	Lys	Asp	Asp	Ala	Thr	Asp	Lys	
390					395					400				405		
gac	ctg	tgc	gac	ctg	gtg	tct	gag	atg	gag	atg	atg	aag	atg	atc	ggg	1302
Asp	Leu	Ser	Asp	Leu	Val	Ser	Glu	Met	Glu	Met	Met	Lys	Met	Ile	Gly	
				410					415					420		
aaa	cac	aaa	aac	atc	atc	aac	ctg	ctg	ggc	gcc	tgc	acg	cag	ggc	ggg	1350
Lys	His	Lys	Asn	Ile	Ile	Asn	Leu	Leu	Gly	Ala	Cys	Thr	Gln	Gly	Gly	
			425					430					435			
ccc	ctg	tac	gtg	ctg	gtg	gag	tac	gcg	gcc	aag	ggt	aac	ctg	cgg	gag	1398
Pro	Leu	Tyr	Val	Leu	Val	Glu	Tyr	Ala	Ala	Lys	Gly	Asn	Leu	Arg	Glu	
			440				445						450			
ttt	ctg	cgg	gcg	cgg	cgg	ccc	ccg	ggc	ctg	gac	tac	tcc	ttc	gac	acc	1446
Phe	Leu	Arg	Ala	Arg	Arg	Pro	Pro	Gly	Leu	Asp	Tyr	Ser	Phe	Asp	Thr	
	455					460					465					
tgc	aag	ccg	ccc	gag	gag	cag	ctc	acc	ttc	aag	gac	ctg	gtg	tcc	tgt	1494
Cys	Lys	Pro	Pro	Glu	Glu	Gln	Leu	Thr	Phe	Lys	Asp	Leu	Val	Ser	Cys	

470	475	480	485	
gcc tac cag gtg gcc cgg gcc atg gag tac ttg gcc tcc cag aag tgc Ala Tyr Gln Val Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys	490	495	500	1542
atc cac agg gac ctg gct gcc cgc aat gtg ctg gtg acc gag gac aac Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn	505	510	515	1590
gtg atg aag atc gca gac ttc ggg ctg gcc cgg gac gtg cac aac ctg Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Val His Asn Leu	520	525	530	1638
gac tac tac aag aag aca acc aac gcc cgg ctg ccc gtg aag tgg atg Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met	535	540	545	1686
gcg cct gag gcc ttg ttt gac cga gtc tac act cac cag agt gac gtc Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val	550	555	560	1734
tgg tcc ttt ggg gtc ctg ctc tgg gag atc ttc acg ctg ggg gcc tcc Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser	570	575	580	1782
ccg tac ccc gcc atc cct gtg gag gag ctc ttc aag ctg ctg aag gag Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu	585	590	595	1830
ggc cac cgc atg gac aag ccc gcc aac tgc aca cac gac ctg tac atg Gly His Arg Met Asp Lys Pro Ala Asn Cys Thr His Asp Leu Tyr Met	600	605	610	1878
atc atg cgg gag tgc tgg cat gcc gcg ccc tcc cag agg ccc acc ttc Ile Met Arg Glu Cys Trp His Ala Ala Pro Ser Gln Arg Pro Thr Phe	615	620	625	1926
aag cag ctg gtg gag gac ctg gac cgt gtc ctt acc gtg acg tcc acc Lys Gln Leu Val Glu Asp Leu Asp Arg Val Leu Thr Val Thr Ser Thr	630	635	640	1974
gac gag tac ctg gac ctg tgg gcg cct ttc gag cag tac tcc ccg ggt Asp Glu Tyr Leu Asp Leu Ser Ala Pro Phe Glu Gln Tyr Ser Pro Gly	650	655	660	2022
ggc cag gac acc ccc agc tcc agc tcc tca ggg gac gac tcc gtg ttt Gly Gln Asp Thr Pro Ser Ser Ser Ser Ser Gly Asp Asp Ser Val Phe	665	670	675	2070
gcc cac gac ctg ctg ccc ccg gcc cca ccc agc agt ggg ggc tgg cgg Ala His Asp Leu Leu Pro Pro Ala Pro Pro Ser Ser Gly Gly Ser Arg	680	685	690	2118
acg tga agggccactg gtcaccaaca atgtgagggg tcctctagcag ccctccctgc Thr				2174
tgctggtgca				2184

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<210> 75
<211> 806
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (487) .. (648)

<400> 75
ctctgacttc tggcttgcat tgtttccagt gagaaatctg ctactatttt tatcttagtg      60
tctctgtagt gtgtcttggt tgcttttagg attttctctt ttcattggcc ttgagtcctt      120
ccttcttccc ctcacatgtg gggactttta attccatgta tattaggctg catgaagcct      180
ccccacaacc tactgatgct cttttcatta gaaacatttc ttactctgog tttcattttg      240
gatagtttct attcctatgt tttoaaaccc accaataaaa gattctgcaa catctgacct      300
gccattaatc cgtccagtg tatttttcat ctctgtatt gtagttttca tctctacaat      360
ccagcttgag cctttgggta tatcttccat gttgctcctg cactgtttga acatgcagaa      420
tggctagtggt ggcagtgagc tgaggagaag ggacagaggg gaagctcggc tggtgggtct      480

acgggt      atg atg gag acc atg cag ctg aaa gta aac cgt cac ccc ttc      528
              Met Met Glu Thr Met Gln Leu Lys Val Asn Arg His Pro Phe
              1              5              10

tgc ttc agt gtg aaa ggc cag gtg aag atg ctg cag ctg atg agg ctg      576
Cys Phe Ser Val Lys Gly Gln Val Lys Met Leu Gln Leu Met Arg Leu
15              20              25              30

ggc ctt agg gtg cgg ggg gtg gtg gaa tct gct tgt.ggg cgg gag atg      624
Gly Leu Arg Val Arg Gly Val Val Glu Ser Ala Cys Gly Arg Glu Met
35              40              45

tgg cta tgt ggc tat aaa gga tga agatgaacgc cctgtttgct tttagcctc      678
Trp Leu Cys Gly Tyr Lys Gly
50

gcttgatca aggtataaag gccggttggt gccttcttgg tgggaagaaag agagagataa      738
ggcactgtcc tccccttcgg aggggtctggg gatacactaa tccatcaaaa ccaactgaggg      798
ctgggcgt      806

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<210> 76
<211> 357
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (80) .. (208)

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<400> 76
gcaagagagg ggaaccagag aggaccagag ggggagagac agagcagcaa gcagtggatt 60
gctccttgac gacgccagc atg agc tcc ttc tcc acc acc acc gtg agc ttc 112
Met Ser Ser Phe Ser Thr Thr Val Ser Phe
1 5 10
ctc ctt tta ctg gca ttc cag ctc cta ggt cag acc aga gct aat ccc 160
Leu Leu Leu Leu Ala Phe Gln Leu Leu Gly Gln Thr Arg Ala Asn Pro
15 20 25
atg tac aat gcc gtg tcc aac gca gac ctg tta ctg aaa gtg gtt tga 208
Met Tyr Asn Ala Val Ser Asn Ala Asp Leu Leu Leu Lys Val Val
30 35 40
aagtgaataa acttcagcac catggacaga agacaaatgc ctgcgttggt gtgctttctt 268
tcttcttggg aagagaatc aggcgatat tccttgctgt tttactcttt gtcagaggaa 328
agaatgctga gttttcttc ttcttttca 357

<210> 77
<211> 1297
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (80) .. (949)

<400> 77
cgcccggaat tccgggtcag aggcacgcgt tcgatttaga atcctgcagc accccaccat 60
ctaagagcaa gagccaaag atg ttt gtc ttg ctc tat gtt aca agt ttt gcc 112
Met Phe Val Leu Leu Tyr Val Thr Ser Phe Ala
1 5 10
att tgt gcc agt gga caa ccc cgg ggt aat cag ttg aaa gga gag aac 160
Ile Cys Ala Ser Gly Gln Pro Arg Gly Asn Gln Leu Lys Gly Glu Asn
15 20 25
tac tcc ccc agg tat atc tgc agc att cct ggc ttg cct gga cct cca 208
Tyr Ser Pro Arg Tyr Ile Cys Ser Ile Pro Gly Leu Pro Gly Pro Pro
30 35 40
ggg ccc cct gga gca aat ggt tcc cct ggg ccc cat ggt cgc atc ggc 256
Gly Pro Pro Gly Ala Asn Gly Ser Pro Gly Pro His Gly Arg Ile Gly
45 50 55
ctt cca gga aga gat ggt aga gac ggc agg aaa gga gag aaa ggt gaa 304
Leu Pro Gly Arg Asp Gly Arg Asp Gly Arg Lys Gly Glu Lys Gly Glu
60 65 70 75
aag gga act gca ggt ttg aga ggt aag act gga cgc cta ggt ctt gcc 352
Lys Gly Thr Ala Gly Leu Arg Gly Lys Thr Gly Pro Leu Gly Leu Ala
80 85 90

ggt gag aaa ggg gac caa gga gag act ggg aag aaa gga ccc ata gga Gly Glu Lys Gly Asp Gln Gly Glu Thr Gly Lys Lys Gly Pro Ile Gly	400
95 100 105	
cca gag gga gag aaa gga gaa gta ggt cca att ggt cct cct gga cca Pro Glu Gly Glu Lys Gly Glu Val Gly Pro Ile Gly Pro Gly Pro	448
110 115 120	
aag gga gac aga gga gaa caa ggg gac cgg ggg ctg cct gga gtt tgc Lys Gly Asp Arg Gly Glu Gln Gly Asp Pro Gly Leu Pro Gly Val Cys	496
125 130 135	
aga tgt gga agc atc gtg ctc aaa tcc gcc ttt tct gtt ggc atc aca Arg Cys Gly Ser Ile Val Leu Lys Ser Ala Phe Ser Val Gly Ile Thr	544
140 145 150 155	
acc agc tac cca gaa gaa aga cta cct att ata ttt aac aag gtc ctc Thr Ser Tyr Pro Glu Glu Arg Leu Pro Ile Ile Phe Asn Lys Val Leu	592
160 165 170	
ttc aac gag gga gag cac tac aac cct gcc aca ggg aag ttc atc tgt Phe Asn Glu Gly Glu His Tyr Asn Pro Ala Thr Gly Lys Phe Ile Cys	640
175 180 185	
gct ttc cca ggg atc tat tac ttt tct tat gat atc aca ttg gct aat Ala Phe Pro Gly Ile Tyr Tyr Phe Ser Tyr Asp Ile Thr Leu Ala Asn	688
190 195 200	
aag cat ctg gca atc gga ctg gta cac aat ggg caa tac cgg ata aag Lys His Leu Ala Ile Gly Leu Val His Asn Gly Gln Tyr Arg Ile Lys	736
205 210 215	
acc ttc gac gcc aac aca gga aac cat gat gtg gct tgg ggg tcc aca Thr Phe Asp Ala Asn Thr Gly Asn His Asp Val Ala Ser Gly Ser Thr	784
220 225 230 235	
gtc atc tat ctg cag cca gaa gat gaa gtc tgg ctg gag att ttc ttc Val Ile Tyr Leu Gln Pro Glu Asp Glu Val Trp Leu Glu Ile Phe Phe	832
240 245 250	
aca gac cag aat ggc ctc ttc tca gac cca ggt tgg gca gac agc tta Thr Asp Gln Asn Gly Leu Phe Ser Asp Pro Gly Trp Ala Asp Ser Leu	880
255 260 265	
ttc tcc ggg ttt ctc tta tac gtt gac aca gat tac cta gat tcc ata Phe Ser Gly Phe Leu Leu Tyr Val Asp Thr Asp Tyr Leu Asp Ser Ile	928
270 275 280	
tca gaa gat gat gaa ttg tga tc aggaccaaga tcctgtgggt aaacactctg Ser Glu Asp Asp Glu Leu	981
285	
attgaatctg ggggtccaga aggtggaaca agcaggaatg ggatccaaag agactccac	1041
tcagattcta aagcatttaa agacaattct agcagaattt atcaaaacaa gatgaaacac	1101
agaaaagtgtg aaaccacaac aaaatgaatt ctattaaaga atagccccag atataaattc	1161
tcttgaaagc aatgttcata aatatttaag caaattaaag acaattgttaa caaattttct	1221
attaaatgcc ctgagtgata aaaccagttg gcaataatat tgccttatta aatcttcaaa	1281

aaataaaaaa aaaaaa

1297

<210> 78
 <211> 943
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (189)..(701)

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 gactcgcgcc gccctcccat tcaactgggaa ctaacaccgc gcgccgctca gacatctota 120
 ttccgcctc tcgcaccgcg tctcaactcg ctctgggca gctgcgcgga gaactggggc 180
 tcaccgtc atg gat gct cta tca gaa gca aat ggc aca ttt gca tta aac 230
 Met Asp Ala Leu Ser Glu Ala Asn Gly Thr Phe Ala Leu Asn
 1 5 10
 ctt ttg aaa aag cta ggg gaa aac aac tca aac aac tta ttt ttt tcc 278
 Leu Leu Lys Lys Leu Gly Glu Asn Asn Ser Asn Asn Leu Phe Phe Ser
 15 20 25 30
 cca ctg agc ata tca tca gcc ttg gcc atg gtt ttc atg ggg gca aag 326
 Pro Leu Ser Ile Ser Ser Ala Leu Ala Met Val Phe Met Gly Ala Lys
 35 40 45
 gga aac act gca gct cag atg tct cag gca ctt tgt ttt agt aaa atc 374
 Gly Asn Thr Ala Ala Gln Met Ser Gln Ala Leu Cys Phe Ser Lys Ile
 50 55 60
 gga ggt gaa gat gga gat att cat cga ggt ttt cag tca ctt ctt gtt 422
 Gly Gly Glu Asp Gly Asp Ile His Arg Gly Phe Gln Ser Leu Leu Val
 65 70 75
 gca att aac aga act gac act gaa tat gtg ctt aga act gcc aac ggg 470
 Ala Ile Asn Arg Thr Asp Thr Glu Tyr Val Leu Arg Thr Ala Asn Gly
 80 85 90
 ctc ttt gga gaa aag tct tat gat ttc ctc aca ggt ttt aca gat tcc 518
 Leu Phe Gly Glu Lys Ser Tyr Asp Phe Leu Thr Gly Phe Thr Asp Ser
 95 100 105 110
 tgt ggc aaa ttt tac caa gca acg ata aaa cag cta gac ttt gtg aat 566
 Cys Gly Lys Phe Tyr Gln Ala Thr Ile Lys Gln Leu Asp Phe Val Asn
 115 120 125
 gat aca gag aag tcc aca aca cgt gta aac tcc tgg gtt gct gat aaa 614
 Asp Thr Glu Lys Ser Thr Thr Arg Val Asn Ser Trp Val Ala Asp Lys
 130 135 140
 act aaa ggt gaa aat ata ttg tta ttc tat ttc gat aat att tta aac 662
 Thr Lys Gly Glu Asn Ile Leu Leu Phe Tyr Phe Asp Asn Ile Leu Asn
 145 150 155


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agt ttt ata gtc agt tct tta caa aac tgt caa ata taa aaaggagtcc      711
Ser Phe Ile Val Ser Ser Leu Gln Asn Cys Gln Ile
    160              165              170

ttttttctct aaacaactat gcaaacatta aaacctttct ttggaatat agccaactcg    771
agtccttttc tctagtata gcttttcct tatcaagtat ctgtgatgtc tctctagatg    831
aaataatctc ttgcagggtt ttcacttggt aatattaggt agtacttctc atcacaaata    891
gcggtgaaga taggaagtta acgaatcggt gacagcgaag tcgacccggg aa          943


<210> 79
<211> 1370
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (302)..(940)

<400> 79
tcgggtctat ccacgcatcc gaacacaagc caggtgagtc ttcatgctgg tgtttaaaag    60
tttctccac atcagtatag ccacgctgat gtctactctg ttgaagccag gtgcgcagtg    120
atctactgac taatggattc tccaattggt aagcctatgt tacaggacaa aggcgcgtgc    180
ttgttaaaag cttgaagtgc agtttgctgc tgagtacaga agacctttgc aaacagagag    240
gggagatttt ctctgtaagg ttgcaacaa gagcagggtcc tggaagataa gattccccgc    300

c   atg tta tcc tcc gtg gtg ttt tgg gga cta att gcc ctc att ggc      346
    Met Leu Ser Ser Val Val Phe Trp Gly Leu Ile Ala Leu Ile Gly
      1              5              10              15

act tcc agg ggc tca tac ccc ttc agt cac tca atg aag cct cac cta      394
Thr Ser Arg Gly Ser Tyr Pro Phe Ser His Ser Met Lys Pro His Leu
      20              25              30

cat cca cgc ctg tac cac ggc tgc tat ggg gac atc atg acc atg aag      442
His Pro Arg Leu Tyr His Gly Cys Tyr Gly Asp Ile Met Thr Met Lys
      35              40              45

acc tct ggg gcc act tgt gat gca aac agt gtg atg aac tgc ggg atc      490
Thr Ser Gly Ala Thr Cys Asp Ala Asn Ser Val Met Asn Cys Gly Ile
      50              55              60

cgt ggt tct gaa atg ttt gct gag atg gat ttg agg gcc ata aaa cct      538
Arg Gly Ser Glu Met Phe Ala Glu Met Asp Leu Arg Ala Ile Lys Pro
      65              70              75

tac cag act ctg atc aaa gaa gtc ggg cag aga cat tgc gtg gac cct      586
Tyr Gln Thr Leu Ile Lys Glu Val Gly Gln Arg His Cys Val Asp Pro
      80              85              90              95

gct gtc atc gca gcc atc atc tcc agg gaa agc cat ggc gga tct gtc      634

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Ala Val Ile Ala Ala Ile Ile Ser Arg Glu Ser His Gly Gly Ser Val	
100 105 110	
ctg caa gac ggc tgg gac cac agg gga ctt aaa ttt ggc ttg atg cag	682
Leu Gln Asp Gly Trp Asp His Arg Gly Leu Lys Phe Gly Leu Met Gln	
115 120 125	
ctt gat aaa caa acg tac cac cct gtc ggt gcc tgg gat agc aaa gag	730
Leu Asp Lys Gln Thr Tyr His Pro Val Gly Ala Trp Asp Ser Lys Glu	
130 135 140	
cac ctt tca cag gct act ggg att cta aca gag aga att aag gca atc	778
His Leu Ser Gln Ala Thr Gly Ile Leu Thr Glu Arg Ile Lys Ala Ile	
145 150 155	
cag aaa aaa ttc ccc acg tgg agt gtt gct cag cac ctc aaa ggt ggt	826
Gln Lys Lys Phe Pro Thr Trp Ser Val Ala Gln His Leu Lys Gly Gly	
160 165 170 175	
ctc tca gct ttt aag tca gga att gaa gcg att gcc acc cca tgg gac	874
Leu Ser Ala Phe Lys Ser Gly Ile Glu Ala Ile Ala Thr Pro Ser Asp	
180 185 190	
ata gac aat gac ttc gtc aat gat atc att gct cga gct aag ttc tat	922
Ile Asp Asn Asp Phe Val Asn Asp Ile Ile Ala Arg Ala Lys Phe Tyr	
195 200 205	
aaa aga caa agc ttc tag gcaaag ctctgtgggt gggccagggt ggcagagtgc	976
Lys Arg Gln Ser Phe	
210	
tcagatggcc gcctttgaga gttttacgtg aatgtgtgtg atacaacact ggcacagaaa	1036
tgattaaaat catgaaagaa aattcatttc ccaattttct gaatgaaat aatcattgaa	1096
aaaaggaaag aaaaataaaa gaaatccatc cagttcacaa tatgtttctc aggaaacgga	1156
catagacata tatataacta ctttcagta aatgtgaata tcatggcaca tggcccttag	1216
gtattccagc caggcttcat tttagcctgt gattccaatg cccacctact cctgtctac	1276
cagaattgct aacaagttaa gtaagcctta ccgagcctt tgtctttttt ccagtatctg	1336
cccgagagccc tcaagctttg cttatgagaa gttc	1370

<210> 80
 <211> 1960
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> (161)..(1906)

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 ccccgagcca ggcctctcgc caccgcccc gggccatggc ccccgccgc cacccttctc 120

cgcgcgggccc	ggccccgggg	gctccccggcc	gccgcagctg	atg	gtg	ttc	cgc	aac	175
				Met	Val	Phe	Arg	Asn	
				1				5	
gtg	ggc	cgg	cgc	cgc	gag	gag	gag	gac	223
Val	Gly	Arg	Pro	Pro	Glu	Glu	Glu	Asp	
			10					15	
gga	ccc	tgc	gaa	ctg	ctg	tgt	ccc	cgg	271
Gly	Pro	Ser	Glu	Leu	Leu	Cys	Pro	Arg	
			25				30		
aag	gcc	ctg	cgc	cgc	ggc	ttg	gcg	ctc	319
Lys	Ala	Leu	Pro	Pro	Gly	Leu	Ala	Leu	
			40				45		
gct	gga	cta	gag	gcg	cag	ttg	gcg	gct	367
Ala	Gly	Leu	Glu	Ala	Gln	Leu	Ala	Ala	
			55				60		
ggg	cgc	ggg	gtc	aag	aca	gtc	ggc	ggg	415
Gly	Pro	Gly	Val	Lys	Thr	Val	Gly	Gly	
			70				75		
ccc	cct	cag	cgc	ccc	cct	cgc	cag	ccc	463
Pro	Pro	Gln	Pro	Pro	Pro	Gln	Pro	Gln	
				90			95		
cag	gcc	ggg	gag	gac	ccc	acg	gaa	acg	511
Gln	Ala	Gly	Glu	Asp	Pro	Thr	Glu	Thr	
			105				110		
gag	ggc	ttg	gaa	tgc	gag	gcc	gag	agc	559
Glu	Gly	Leu	Glu	Ser	Glu	Ala	Glu	Ser	
			120				125		
gaa	gag	gag	ctc	agc	agc	cgc	ggc	gga	607
Glu	Glu	Glu	Leu	Ser	Ser	Pro	Gly	Arg	
			135				140		
ctt	ctg	ctg	cag	ccc	cca	ggc	cct	gaa	655
Leu	Leu	Leu	Gln	Pro	Pro	Gly	Pro	Glu	
			150				155		
ctg	cag	gac	ttg	gtc	cct	ctg	ggg	cgc	703
Leu	Gln	Asp	Leu	Val	Pro	Leu	Gly	Arg	
			170				175		
cag	cag	cag	cag	cag	caa	cct	ccc	cgc	751
Gln	Gln	Gln	Gln	Gln	Gln	Pro	Pro	Pro	
			185				190		
ctc	egg	cca	ctc	gcg	ggc	cct	tct	cgg	799
Leu	Arg	Pro	Leu	Ala	Gly	Pro	Ser	Arg	
			200				205		
ctc	agt	cgc	ctc	ttt	cgc	acc	aag	agc	847
Leu	Ser	Arg	Leu	Phe	Arg	Thr	Lys	Ser	
			215				220		
								225	

ggg gat ggg acc ggc aag agg cct tct gga gag ctg gct gct tca gct Gly Asp Gly Thr Gly Lys Arg Pro Ser Gly Glu Leu Ala Ala Ser Ala 230 235 240 245	895
gcg agc ctg aca gac atg gga ggc tct gcg ggc cgg gag ctg gac gcg Ala Ser Leu Thr Asp Met Gly Gly Ser Ala Gly Arg Glu Leu Asp Ala 250 255 260	943
ggg agg aaa ccc aag ttg aca aga act caa agt gcc ttt tct ccg gtc Gly Arg Lys Pro Lys Leu Thr Arg Thr Gln Ser Ala Phe Ser Pro Val 265 270 275	991
tcc ttc agc ccc ctg ttc aca ggt gaa act gtg tgg ctt gtg gat gtg Ser Phe Ser Pro Leu Phe Thr Gly Glu Thr Val Ser Leu Val Asp Val 280 285 290	1039
gac att tct cag cgg ggc ctg acc tct cca cac cct cca act ccc cct Asp Ile Ser Gln Arg Gly Leu Thr Ser Pro His Pro Pro Thr Pro Pro 295 300 305	1087
cct cct ccg aga aga agc ctc agc ctc cta gat gat atc agt ggg acg Pro Pro Pro Arg Arg Ser Leu Ser Leu Leu Asp Asp Ile Ser Gly Thr 310 315 320 325	1135
ctg cct aca tct gtc ctt gtg gct ccg atg ggg tct tcc ttg cag tct Leu Pro Thr Ser Val Leu Val Ala Pro Met Gly Ser Ser Leu Gln Ser 330 335 340	1183
ttc ccc cta cct ccg cct cct cca ccc cat gcc cca gat gca ttt ccc Phe Pro Leu Pro Pro Pro Pro Pro His Ala Pro Asp Ala Phe Pro 345 350 355	1231
cgg att gct ccc atc cga gca gct gaa tcc ctg cac agc caa ccc cca Arg Ile Ala Pro Ile Arg Ala Ala Glu Ser Leu His Ser Gln Pro Pro 360 365 370	1279
cag cac ctc cag tgt ccc ctc tac cgg cct gac tgg agc agc ttt gca Gln His Leu Gln Cys Pro Leu Tyr Arg Pro Asp Ser Ser Ser Phe Ala 375 380 385	1327
gcc agc ctt cga gag ttg gag aag tgt ggt tgg tat tgg ggg cca atg Ala Ser Leu Arg Glu Leu Glu Lys Cys Gly Trp Tyr Trp Gly Pro Met 390 395 400 405	1375
aat tgg gaa gat gca gag atg aag ctg aaa ggg aaa cca gat ggt tct Asn Trp Glu Asp Ala Glu Met Lys Leu Lys Gly Lys Pro Asp Gly Ser 410 415 420	1423
ttc ctg gta cga gac agt tct gat cct cgt tac atc ctg agc ctc agt Phe Leu Val Arg Asp Ser Ser Asp Pro Arg Tyr Ile Leu Ser Leu Ser 425 430 435	1471
ttc cga tca cag ggt atc acc cac cac act aga atg gag cac tac aga Phe Arg Ser Gln Gly Ile Thr His His Thr Arg Met Glu His Tyr Arg 440 445 450	1519
gga acc ttc agc ctg tgg tgt cat ccc aag ttt gag gac cgc tgt caa Gly Thr Phe Ser Leu Trp Cys His Pro Lys Phe Glu Asp Arg Cys Gln 455 460 465	1567
tct gtt gta gag ttt att aag aga gcc att atg cac tcc aag aat gga	1615

Ser Val Val Glu Phe Ile Lys Arg Ala Ile Met His Ser Lys Asn Gly	
470 475 480 485	
aag ttt ctc tat ttc tta aga tcc agg gtt cca gga ctg cca cca act	1663
Lys Phe Leu Tyr Phe Leu Arg Ser Arg Val Pro Gly Leu Pro Pro Thr	
490 495 500	
cct gtc cag ctg ctc tat cca gtg tcc cga ttc agc aat gtc aaa tcc	1711
Pro Val Gln Leu Leu Tyr Pro Val Ser Arg Phe Ser Asn Val Lys Ser	
505 510 515	
ctc cag cac ctt tgc aga ttc cgg ata cga cag ctc gtc agg ata gat	1759
Leu Gln His Leu Cys Arg Phe Arg Ile Arg Gln Leu Val Arg Ile Asp	
520 525 530	
cac atc cca gat ctc cca ctg cct aaa cct ctg atc tct tat atc cga	1807
His Ile Pro Asp Leu Pro Lys Pro Lys Pro Tyr Ile Arg	
535 540 545	
aag ttc tac tac tat gat cct cag gaa gag gta tac ctg tct cta aag	1855
Lys Phe Tyr Tyr Tyr Asp Pro Gln Glu Glu Val Tyr Leu Ser Leu Lys	
550 555 560 565	
gaa gcg cag ctc att tcc aaa cag aag caa gag gtg gaa ccc tcc acg	1903
Glu Ala Gln Leu Ile Ser Lys Gln Lys Gln Glu Val Glu Pro Ser Thr	
570 575 580	
tag cgag gggtccctcg ctggtcacca ccaagggcat ttggttgcca agctccagct	1960

<210> 81
 <211> 1774
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (313)..(576)

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 gtatatataa tgcttatgta atatagaatg gatctccaat gatttttttg tgtgtttttc 120
 acatatattgg catatgtgtg tgatactgct cagtgcacgg catctcttac acacagtagt 180
 caagaatctt ttttggcctc tgcctaacca gattcctcct gcctccagggt agattttata 240
 cttatttcaa ggcagaaact tgggtggaagg aggtaatctg tcgttaattgt gtattttatc 300
 cttcatgcat gt atg cat tca tac cct ggg att ttt ttc ttc oot tta 348
 Met His Ser Tyr Pro Gly Ile Phe Phe Phe Pro Leu
 1 5 10
 gct gtg ttc cag atc atc tcc ctg gta att tac ccc gtg aag tac acc 396
 Ala Val Phe Gln Ile Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr Thr

15	20	25	
cag acc ttc acc ctt cac gat aac cct gct gtt aat tac atc tat aac Gln Thr Phe Thr Leu His Asp Asn Pro Ala Val Asn Tyr Ile Tyr Asn 30 35 40			444
tgg gcc tat ggc ttc gga tgg gcg gcc acc atc atc ttg att ggt tgt Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly Cys 45 50 55 60			492
tcc ttc ttc ttc tgc tgc etc ccc aac tac gag gat gac ctt ttg ggg Ser Phe Phe Phe Cys Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly 65 70 75			540
gcc gcc aag ccc agg tac ttc tat ccc cca gcc taa tgtg ggaggaagag Ala Ala Lys Pro Arg Tyr Phe Tyr Pro Pro Ala 80 85			590
cttgagaaaa gcctgctgca agatggatct gaggaggaaa ctgttctcca aggcacaagg			650
aacctacgtt tgggcaatgt tcatatgatac agaaatgcta gaataaatgc taaagaaaat			710
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gttaaagaat atgcctgtga aacttgataa ggtagaaatg tagcagcctc tcatttaata			890
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<210> 82
 <211> 1870
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (91)..(672)

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<400> 82
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                                         Met Leu Arg Cys Gly Leu Ala
                                         1             5

tgc gag cgc tgc agg tgg atc ctg ccc ctg ctg ctc ctc agc gcc atc      159
Cys Glu Arg Cys Arg Trp Ile Leu Pro Leu Leu Leu Leu Ser Ala Ile
                        10             15             20

gcc ttc gac atc atc gcg ctg gcc ggc cgc ggc tgg ctg cag tct agc      207
Ala Phe Asp Ile Ile Ala Leu Ala Gly Arg Gly Trp Leu Gln Ser Ser
                        25             30             35

aac cac atc cag aca tcg tcg ctt tgg tgg agg tgt ttc gac gag gcc      255
Asn His Ile Gln Thr Ser Ser Leu Trp Trp Arg Cys Phe Asp Glu Gly
                        40             45             50             55

ggc ggc agc ggc tcc tac gac gat ggc tgc cag agc ctc atg gag tac      303
Gly Gly Ser Gly Ser Tyr Asp Asp Gly Cys Gln Ser Leu Met Glu Tyr
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gca tgg gga cga gca gct gca gcc acg ctt ttc tgt ggc ttt atc atc      351
Ala Trp Gly Arg Ala Ala Ala Thr Leu Phe Cys Gly Phe Ile Ile
                        75             80             85

ctg tgc atc tgc ttc att ctc tcg ttc ttc gcc ctg tgt gga ccc cag      399
Leu Cys Ile Cys Phe Ile Leu Ser Phe Phe Ala Leu Cys Gly Pro Gln
                        90             95             100

atg ctt gtt ttc ctg aga gtc att gga ggc ctc ctc gca ctg gct gcc      447
Met Leu Val Phe Leu Arg Val Ile Gly Gly Leu Leu Ala Leu Ala Ala
                        105             110             115

ata ttc cag atc atc tcc ctg gta att tac ccc gtg aag tac acc cag      495
Ile Phe Gln Ile Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr Thr Gln
                        120             125             130             135

acc ttc acc ctt cac gat aac cct gct gtt aat tac atc tat aac tgg      543
Thr Phe Thr Leu His Asp Asn Pro Ala Val Asn Tyr Ile Tyr Asn Trp
                        140             145             150

gcc tat ggc ttc gga tgg gcg gcc acc atc atc ttg att ggt tgt tcc      591
Ala Tyr Gly Phe Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly Cys Ser
                        155             160             165

ttc ttc ttc tgc tgc ctc ccc aac tac gag gat gac ctt ttg ggg gcc      639
Phe Phe Phe Cys Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly Ala
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gcc aag ccc agg tac ttc tat ccc cca gcc taa tgtgggag gaagagcctg      690

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Ala	Lys	Pro	Arg	Tyr	Phe	Tyr	Pro	Pro	Ala	
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cataattagt	gttaagtttc	atgtatgtcg	tgtggagtta	aaaagacttg	aattctgttt					870
gctaagtata	tgctaatttt	tccttatgtc	aattctatac	catttaagct	tcattttgta					930
aagaatatgc	ctgtgaaact	tgataaggtg	gaaatgtagc	agcctctcat	ttaataatct					990
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acataccgga	agggtactta	ttaccttttc	cttaccattt	atacttaact	aatggaaacg					1770
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<210> 83
 <211> 1294
 <212> DNA
 <213> *Homo sapiens*

<220>
 <221> CDS
 <222> (647) .. (910)

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taggaacac	taagctaaaa taagtaacca agagagaatt actcatccta ttcagtctca 180


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cccctacctc atcaaaatact tttatcggtc ctacctctcc ttttaagcca aatattaaaa 240
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atltgcagta ggactatata ctgtagcacc ctccagggtaa aatatcagac acagaatctc 360
aattaccata gcatttcgct taattattat cctcatagcg ggaataatgg ttactaacag 420
aaaataaac atgggccttt ccaaaccagc acctctgcct ctatttagga aaggaatgtt 480
gtttctatat cagccaatca gacctagtaa aaagcgctat taaaaaaac aagctaaaaa 540
gctaaggagt accaaaaaca acaaacagat tcttggtttg ggaacaaaat catagatagc 600
atgggtcctc ccattctctg gccctctctc aataatatac ctaatt atg gga cta 655
Met Gly Leu
1

atg ttc tta ccc tgc cta att aac ctt ttt cag aga ttt ttt aaa ctg 703
Met Phe Leu Pro Cys Leu Ile Asn Leu Phe Gln Arg Phe Phe Lys Leu
5 10 15

aca gga tca tgg cca ttt cac aga caa cta ccc aaa aat atc tac aga 751
Thr Gly Ser Trp Pro Phe His Arg Gln Leu Pro Lys Asn Ile Tyr Arg
20 25 30 35

cgg cac tgc tcc tac caa cac gat acc aga gaa ctc tct gtc ccc tgg 799
Arg His Cys Ser Tyr Gln His Asp Thr Arg Glu Leu Ser Val Pro Ser
40 45 50

tca gca gga agt agc cag aaa gaa cat gcc gcc cct cgt cct ttt tat 847
Ser Ala Gly Ser Ser Gln Lys Glu His Ala Ala Pro Arg Pro Phe Tyr
55 60 65

aac tat gag gtc tgg att gac aga gca gaa gca tca cca ttg tgg ata 895
Asn Tyr Glu Val Trp Ile Asp Arg Ala Glu Ala Ser Pro Leu Trp Ile
70 75 80

agc gcc tca ttt taa aattcacctt aatcaaaaaa tgcctaaatc caaagggcat 950
Ser Ala Ser Phe
85

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<210> 84
 <211> 633
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (148) .. (399)

<400> 84

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cttgttaagaa gtaaatgaag cttcctt      atg agt ctg tta aga ctc cat aga      171
                                   Met Ser Leu Leu Arg Leu His Arg
                                   1                               5
ttg tca ata ata tgg aaa aat ttg ata ttt cat cag gaa tat gaa cat      219
Leu Ser Ile Ile Trp Lys Asn Leu Ile Phe His Gln Glu Tyr Glu His
10                               15                               20
gtg ttt cag gta gag aat gcc aaa gat aat gaa gat agt att cta caa      267
Val Phe Gln Val Glu Asn Ala Lys Asp Asn Glu Asp Ser Ile Leu Gln
25                               30                               35                               40
aga gaa att cct gcc aga caa tcc cga aga aga ttt cgg aaa att aac      315
Arg Glu Ile Pro Ala Arg Gln Ser Arg Arg Arg Phe Arg Lys Ile Asn
45                               50                               55
tat aaa gga gag cgc caa acc att act gat gat gtg gag gtt aac agc      363
Tyr Lys Gly Glu Arg Gln Thr Ile Thr Asp Asp Val Glu Val Asn Ser
60                               65                               70
tat ctt tct gtg agt ata ttt agg aac act tca tga atct tccttaattt      413
Tyr Leu Ser Val Ser Ile Phe Arg Asn Thr Ser
75                               80
tcatatctag tatctttaat ttacatgtat ctttggtaat atcaacatgc tgggctctgt      473
atgtgaaaat ttggggcagg taaatatata atctttttaa atgcttctgt ttggttgaat      533
tgggttaggaa tgctcttacc agtgggaggt ctggttttgc ttttttgttg gtggcctaaac      593
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<210> 85

<211> 2437

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (184) .. (2172)

<400> 85

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aggagtcggg tttgtcttgc caatggaagt tggagtggag ccactccga ctgtgtgcct      120
gtcagatgtg ccaaccgcc acaactggcc aatgggggtga cggaaggcct ggactatggc      180

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Met Lys Glu Val Thr Phe His Cys His Glu Gly Tyr Ile Leu His	
1 5 10 15	
ggt gct cca aaa ctc acc tgt cag tca gat ggc aac tgg gat gca gag	276
Gly Ala Pro Lys Leu Thr Cys Gln Ser Asp Gly Asn Trp Asp Ala Glu	
20 25 30	
att cct ctc tgt aaa cca gtc aac tgt gga cct cct gaa gat ctt gcc	324
Ile Pro Leu Cys Lys Pro Val Asn Cys Gly Pro Pro Glu Asp Leu Ala	
35 40 45	
cat ggt ttc cct aat ggt ttt tcc ttt att cat ggg ggc cat ata cag	372
His Gly Phe Pro Asn Gly Phe Ser Phe Ile His Gly His Ile Gln	
50 55 60	
tat cag tgc ttt cct ggt tat aag ctc cat gga aat tca tca aga agg	420
Tyr Gln Cys Phe Pro Gly Tyr Lys Leu His Gly Asn Ser Ser Arg Arg	
65 70 75	
tgc ctc tcc aat ggc tcc tgg agt ggc agc tca cct tcc tgc ctg cct	468
Cys Leu Ser Asn Gly Ser Trp Ser Gly Ser Pro Pro Ser Cys Leu Pro	
80 85 90 95	
tgc aga tgt tcc aca cca gta att gaa tat gga act gtc aat ggg aca	516
Cys Arg Cys Ser Thr Pro Val Ile Glu Tyr Gly Thr Val Asn Gly Thr	
100 105 110	
gat ttt gac tgt gga aag gca gcc cgg att cag tgc ttc aaa ggc ttc	564
Asp Phe Asp Cys Gly Lys Ala Ala Arg Ile Gln Cys Phe Lys Gly Phe	
115 120 125	
aag ctc cta gga ctt tct gaa atc acc tgt gaa gcc gat ggc cag tgg	612
Lys Leu Leu Gly Leu Ser Glu Ile Thr Cys Glu Ala Asp Gly Gln Trp	
130 135 140	
agc tct ggg ttc cac cac ttt gaa cac act tct tgt ggt tct ctt cca	660
Ser Ser Gly Phe His His Phe Glu His Thr Ser Cys Gly Ser Leu Pro	
145 150 155	
atg ata cca aat gcg ttc atc agt gag acc agc tct tgg aag gaa aat	708
Met Ile Pro Asn Ala Phe Ile Ser Glu Thr Ser Ser Trp Lys Glu Asn	
160 165 170 175	
gtg ata act tac agc tgc agg tct gga tat gtc ata caa ggc agt tca	756
Val Ile Thr Tyr Ser Cys Arg Ser Gly Tyr Val Ile Gln Gly Ser Ser	
180 185 190	
gat ctg att tgt aca gag aaa ggg gta tgg agc cag cct tat cca gtc	804
Asp Leu Ile Cys Thr Glu Lys Gly Val Trp Ser Gln Pro Tyr Pro Val	
195 200 205	
tgt gag ccc ttg tcc tgt ggg tcc cca ccg tct gtc gcc aat gca gtg	852
Cys Glu Pro Leu Ser Cys Gly Ser Pro Pro Ser Val Ala Asn Ala Val	
210 215 220	
gca act gga gag gca cac acc tat gaa agt gaa gtg aaa ctc aga tgt	900
Ala Thr Gly Glu Ala His Thr Tyr Glu Ser Glu Val Lys Leu Arg Cys	
225 230 235	

ctg gaa ggt tat acg atg gat aca gat acc aga tca atc acc tgt cag Leu Glu Gly Tyr Thr Met Asp Thr Asp Thr Arg Ser Ile Thr Cys Gln 240 245 250 255	948
aaa gat ggt cgc tgg ttc cct gag aga atc tcc tgc agt cct aaa aaa Lys Asp Gly Arg Trp Phe Pro Glu Arg Ile Ser Cys Ser Pro Lys Lys 260 265 270	996
tgt cct ctc cgg gaa aac ata aca cat ata ctt gta cat ggg gac gat Cys Pro Leu Pro Glu Asn Ile Thr His Ile Leu Val His Gly Asp Asp 275 280 285	1044
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cca cca ttc tcc gat gaa tct tgc agt cca gtt tct tgt ggg aaa cct Pro Pro Phe Ser Asp Glu Ser Cys Ser Pro Val Ser Cys Gly Lys Pro 320 325 330 335	1188
gaa agt cca gaa cat gga ttt gtg gtt ggc agt aaa tac acc ttt gaa Glu Ser Pro Glu His Gly Phe Val Val Val Gly Ser Lys Tyr Thr Phe Glu 340 345 350	1236
agc aca att att tat cag tgt gag cct ggc tat gaa cta gag ggg aac Ser Thr Ile Ile Tyr Gln Cys Glu Pro Gly Tyr Glu Leu Gly Gly Asn 355 360 365	1284
agg gaa cgt gtc tgc cag gag aac aga cag tgg agt gga ggg gtg gca Arg Glu Arg Val Cys Gln Glu Asn Arg Gln Trp Ser Gly Gly Val Ala 370 375 380	1332
ata tgc aaa gag acc agg tgt gaa act cca ctt gaa ttt ctc aat ggg Ile Cys Lys Glu Thr Arg Cys Glu Thr Pro Leu Glu Phe Leu Asn Gly 385 390 395	1380
aaa gct gac att gaa aac agg acg act gga ccc aac gtg gta tat tcc Lys Ala Asp Ile Glu Asn Arg Thr Thr Gly Pro Asn Val Val Tyr Ser 400 405 410 415	1428
tgc aac aga ggc tac agt ctt gaa ggg cca tct gag gca cac tgc aca Cys Asn Arg Gly Tyr Ser Leu Glu Gly Pro Ser Glu Ala His Cys Thr 420 425 430	1476
gaa aat gga acc tgg agc cac cca gtc cct ctc tgc aaa cca aat cca Glu Asn Gly Thr Trp Ser His Pro Val Pro Leu Cys Lys Pro Asn Pro 435 440 445	1524
tgc cct gtt cct ttt gtg att ccc gag aat gct ctg ctg tct gaa aag Cys Pro Val Pro Phe Val Ile Pro Glu Asn Ala Leu Leu Ser Glu Lys 450 455 460	1572
gag ttt tat gtt gat cag aat gtg tcc atc aaa tgt agg gaa ggt ttt Glu Phe Tyr Val Asp Gln Asn Val Ser Ile Lys Cys Arg Glu Gly Phe 465 470 475	1620
ctg ctg cag ggc cac ggc atc att acc tgc aac ccc gac gag acg tgg	1668

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Thr	Gln	Thr	Ser	Ala	Lys	Cys	Glu	Lys	Ile	Ser	Cys	Gly	Pro	Pro	Ala	
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cac	gta	gaa	aat	gca	att	gct	cga	ggc	gta	cat	tat	caa	tat	gga	gac	1764
His	Val	Glu	Asn	Ala	Ile	Ala	Arg	Gly	Val	His	Tyr	Gln	Tyr	Gly	Asp	
				515				520					525			
atg	atc	acc	tac	tca	tgt	tac	agt	gga	tac	atg	ttg	gag	ggc	ttc	ctg	1812
Met	Ile	Thr	Tyr	Ser	Cys	Tyr	Ser	Gly	Tyr	Met	Leu	Glu	Gly	Phe	Leu	
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Arg	Ser	Val	Cys	Leu	Glu	Asn	Gly	Thr	Trp	Thr	Ser	Pro	Pro	Ile	Cys	
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Arg	Ala	Val	Cys	Arg	Phe	Pro	Cys	Gln	Asn	Gly	Gly	Ile	Cys	Gln	Arg	
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Pro	Asn	Ala	Cys	Ser	Cys	Pro	Glu	Gly	Trp	Met	Gly	Arg	Leu	Cys	Glu	
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gaa	tta	atc	tgc	att	ctt	ccc	tgt	ctg	aac	gga	ggc	cgc	tgt	gtg	gcc	2004
Glu	Leu	Ile	Cys	Ile	Leu	Pro	Cys	Leu	Asn	Gly	Gly	Arg	Cys	Val	Ala	
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Pro	Tyr	Gln	Cys	Asp	Cys	Pro	Pro	Gly	Trp	Thr	Gly	Ser	Arg	Cys	His	
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Thr	Ala	Val	Cys	Gln	Ser	Pro	Cys	Leu	Asn	Gly	Gly	Lys	Cys	Val	Arg	
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cca	aac	cga	tgt	cac	tgt	ctt	tct	tct	tgg	acg	gga	cat	aac	tgt	tcc	2148
Pro	Asn	Arg	Cys	His	Cys	Leu	Ser	Ser	Trp	Thr	Gly	His	Asn	Cys	Ser	
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agg	aaa	agg	agg	act	ggg	ttt	taa	ccactgcacg	acccatctctggc	tctcccaaaa						2202
Arg	Lys	Arg	Arg	Thr	Gly	Phe										
				660												
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 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (19)..(5622)

<400> 86

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		1				5					10		
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Ala	Phe	Gly	Pro	His	Pro	Arg	Gly	Ser	Gly	Glu	Gly	Gln	
		15				20					25		
ctg	cag	cgc	ttc	cca	gag	aag	gac	tgg	gag	gac	aac	cca	147
Leu	Gln	Arg	Phe	Pro	Glu	Lys	Asp	Trp	Glu	Asp	Asn	Pro	
		30				35					40		
ggc	atc	gag	ctg	ttt	tgc	cag	ccc	agc	ggg	tgg	cag	ctg	195
Gly	Ile	Glu	Leu	Phe	Cys	Gln	Pro	Ser	Gly	Trp	Gln	Cys	
	45				50						55		
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Pro Trp Ile Gly Asp Glu Arg Gly Phe Leu Gly Leu Ala Phe His Pro	
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Lys Phe Arg His Asn Arg Lys Phe Tyr Ile Tyr Tyr Ser Cys Leu Asp	
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Lys Lys Lys Val Glu Lys Ile Arg Ile Ser Glu Met Lys Val Ser Arg	
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Ile Glu Glu Pro Ala Ser Asn His Asn Gly Gly Gln Leu Leu Phe Gly	
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Leu Asp Gly Tyr Met Tyr Ile Phe Thr Gly Asp Gly Gly Gln Ala Gly	
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Asp Pro Phe Gly Leu Phe Gly Asn Ala Gln Asn Lys Ser Ser Leu Leu	
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Gly Lys Val Leu Arg Ile Asp Val Asn Arg Ala Gly Ser His Gly Lys	
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His Pro Ala Ile Tyr Ala Tyr Gly Ile Arg Asn Met Trp Arg Cys Ala	
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Val Asp Arg Gly Asp Pro Ile Thr Arg Gln Gly Arg Gly Arg Ile Phe	
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Cys Gly Asp Val Gly Gln Asn Arg Phe Glu Glu Val Asp Leu Ile Leu	
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Lys Gly Gly Asn Tyr Gly Trp Arg Ala Lys Glu Gly Phe Ala Cys Tyr	
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Asp Gly Arg Leu Lys Pro Gly Asp Gln Leu Val Ser Val Asn Lys Glu	
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Ser Met Ile Gly Val Ser Phe Glu Glu Ala Lys Ser Ile Ile Thr Arg	
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aca aat aat gac att tta tct tct tgt gag ata aaa act gga tac aac Thr Asn Asn Asp Ile Leu Ser Ser Cys Glu Ile Lys Thr Gly Tyr Asn 140 145 150			544
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Thr Glu Phe Ile Ile Leu Val Val Asp Ser Ile Asp Arg Glu Arg Leu	
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His	Arg	Thr	Leu	Leu	Gly	Pro	Ala	Phe	Ala	Glu	Cys	His	Ala	Leu	Val															
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Cys	Val	Asp	Gly	Cys	Phe	Cys	Pro	Pro	Gly	Thr	Val	Leu	Asp	Asp	Ile															
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Gln Leu Ser Asp Trp Arg Asp Gly Val Cys Thr Lys Tyr Met Gln Asn	
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Cys Ser Lys Ala Ile Lys Leu Phe Val Glu Ser Tyr Glu Leu Ile Leu		
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Gln Glu Gly Thr Phe Lys Ala Val Ala Arg Gly Pro Gly Asp Pro		
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Pro Tyr Lys Ile Arg Tyr Met Gly Ile Phe Leu Val Ile Glu Thr His		
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 Gln Asn Thr Glu Thr Ser Ser Leu Val Ser Met Thr Ser Ala Thr Ile
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Asn	Ser	Ser	Ser	Gly	Gly	Ile	Thr	Gly	Ser	Leu	Pro	Met	Met	Thr	Asp														
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Thr Thr Leu Thr Ser Thr Thr Asp Ile Ser Thr Glu Ser Leu Met Thr	
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Ala Met Thr Ser Thr Thr Arg Leu Thr Ser Ala Ile Thr Thr Lys Thr	
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545 550 555	
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Ser Thr Asp Met Ile Thr Ser His Thr Thr Asn Leu Thr Arg Ser Ser	
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Pro Leu Leu Ala Thr Leu Pro Thr Thr Ile Thr Arg Ser Thr Pro Thr	
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Ser Glu Thr Thr Tyr Pro Thr Ser Pro Thr Ser Thr Val Lys Gly Ser	
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Ile	Pro	Thr	Thr	Ser	Leu	Arg	Thr	Leu	Thr	Pro	Ser	Ser	Val	Gly	Thr	
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Ser	Thr	Ser	Leu	Thr	Thr	Thr	Arg	Thr	Asp	Phe	Pro	Ser	Ile	Pro	Thr	Asp
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Ile	Ser	Thr	Leu	Pro	Thr	Arg	Thr	His	Ile	Ile	Ser	Ser	Ser	Pro	Ser	
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Ile	Gln	Ser	Thr	Glu	Thr	Ser	Ser	Leu	Val	Gly	Thr	Thr	Ser	Pro	Thr	
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Glu Met Asp Pro Ser Thr Glu Ala Thr Ser Pro Pro Thr Thr Pro Leu				
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Thr Val Phe Pro Phe Thr Thr Glu Met Val Thr Cys Pro Thr Ser Ile				
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Ser Ile Gln Thr Thr Leu Thr Thr Tyr Met Asp Thr Ser Ser Met Met				
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Thr Ser Glu Thr Trp Leu Ser Asn Ser Ser Val Ile Pro Leu Pro Leu				
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ttctatgtgg ccttggaaga cgtgacacca ctatgaaggt gcacatcaag agacccgaga			4543
tgacctgctc ctacgtgtga gcctgcgggg ccccttcacc accccctccg ccttgcctcg			4603
gacacaaggg tctgcattgc gtccatttca agaggtgacc ccaggacgcg ggcagcccag			4663
gctcctgctg ttcttgggga agatgagact gttcccccaa atccccatct tctccttcca			4723
acttggctga aaeccaacctg gagacgcagt tcacgtccag gctcttccac tgtggaatct			4783
tgggcaagtc agtaacgagc ctacgtttcc tcacctgcaa aacgggtaca gcattctctgt			4843
atgatacgtc acgcccgtgt tgtgaaaacc acatagactt ggtaaatctc cggtcctact			4903
ctgccctccc gtctcagccc tcgtgttgcc attgctctc tcggatcctc caatcctcac			4963
gtccttcacc tgggtctctgg ccctggttct tattttctct caattcccta ctgcctgttt			5023

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cttactttga acctggaggc agcctgcagc cccatcccat ctccctgccct ctccctgatct 5083
aactccctgc tgcattctct gctcccatc cttagacgtc ctccctcttt gaccccggtc 5143
cttcatccat cctgcacccc agtcccccag ccctaaatcc tccctcctct cctcacatcc 5203
tggccctcag caaggatag atagcctctg tgtcttagga taccccggtt gctgttccct 5263
cggtcctcct gttgcccggt tcccctgttc tcttgcctc attcctgtat ccttccctcc 5323
tttgagcccg tccattcctc ggttctgccc ccgactcccc cagccctaaa taccccagct 5383
gctgttcccc ccatcaccct gctgcccatt tctttattct ccaccccttt ctctcaccct 5443
tggagccctg cgggtggggg cagggcatga gttccccagt cccaaggaa aggcagcccc 5503
ctcagtctcc ctccctcctc tcccttcca tctccctccc ctctgccttt taaaccctc 5563
ccctcagatt cccctcctcc cccctctctc cctggtgtca cctggattcc tgcagtaatt 5623
ctgagccctt gaaatcctc gtgccttgg cggggaagat tggcttggg gacaggaggt 5683
cggcacatct ccagggtctc atgtgcgcaa tatagagttt attgtaaaaa gc 5735

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<210> 92
<211> 748
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (202)..(456)

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<400> 92
tggaagatga ggctcacct ctgcacagcc aataggtcat tgtcatggga aactgacca 60
ccagacacaa cctccatccc ccgcggggg caegtgcctt tatcacccat ttcctaggtt 120
ttgttgggt tccaggcgg tgccttcag actggctcag cctccatctt cgatgggtcc 180
tccctggctg cctatgagga c atg ctg gtt gtg atc gtc cag tac cgg ctg 231
Met Leu Val Val Ile Val Gln Tyr Arg Leu
1 5 10

gga ata ttt ggc ttc ttc acc aca tgg gat cag cac gct ccc ggg aac 279
Gly Ile Phe Gly Phe Phe Thr Thr Trp Asp Gln His Ala Pro Gly Asn
15 20 25

tgg gcc ttc aag gac cag gtg gct gct cta tcc tgg gtc cag aag aac 327
Trp Ala Phe Lys Asp Gln Val Ala Ala Leu Ser Trp Val Gln Lys Asn
30 35 40

atc gag ttc ttc ggt ggg gac ccc agc tct gtg acc atc ttt gat tct 375
Ile Glu Phe Phe Gly Gly Asp Pro Ser Ser Val Thr Ile Phe Asp Ser
45 50 55

gtc tcc cat ggc cga agg ctt att cca caa agc cgt cat gga gag tgg 423

```

Val	Ser	His	Gly	Arg	Arg	Leu	Ile	Pro	Gln	Ser	Arg	His	Gly	Glu	Trp	
60						65					70					
ggt ggc cat cat cct tta cct gaa ggc cca tga ttatgaga agagtgagga 474 Gly Gly His His Pro Leu Pro Glu Gly Pro 75 80																
cgtacgaata ctgttaaacac cttgccagct tctctctctc agttagggga gaatgtgttc 534																
aggcaccttc tcaccatgtg ccattctatcc caagatattt gtcattctgtc tcttaattat 594																
ctactacaga gtgaggccct agagaccagg atctctctgt ccttcaggcc ccacagcataa 654																
taagtgttat atatcaggca gctataaatg ttctggatga atgagctaat gaatgagctg 714																
tttcattcaa tgcattattaa ttaaaaaaaaaaaaa 748																

<210> 93
 <211> 1947
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (901)..(1524)

<400> 93	
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cggggaccac ttectacccc agaactcccc ccgccagcc cccactgccc ccacccacc	180
cctcaaacg ccagacttcc cactctcccc gcatcagtgc acggcccccg aggactccac	240
atttcttggg ggggtcccg gagacgggca aagatgatcc ctagggtgtgc tccggtgggg	300
gggtcccaa gatcttctt ccaggagcac accaggaggt caggctactc gtgggggcat	360
gtctgtctcag ctaccggcca tctccaatgt ggccaaactc ctctctcact ctggctgggc	420
caacacacag taagtaaggt gtatcgggaa tgggtggggg atggggagca tcgtggctca	480
cgctcgggg gccgtgggga caggcgccaa ggaggccagc ctacacaggg catctctgtc	540
atggtgga aa gatggaatta ggcctgggac acaccccgcc cactacaggg tgtatccaa	600
atgccgcgg ccgcacactc aggcgcacc atctgagccc cctcctctga gaggcagggc	660
acagacaggg ccgaggggga gtggagatgg gaacaggagg ggggctcaga ccatgaaaac	720
attggagaat cttagcggga ctttgacctg atccatacag atactgtagt tgcttagata	780
tgcttattgt ttctcatcaa ttttggggg gtgtgcgtgt gtgtgcgcgt gtgtgtgtgc	840
aggtgggtgc ttgcgtgtgc aacgtgtgtg ctgcgtgttt gtgtgctgtg agctgtgttc	900
atg tat gtg ctg cgc atg agt gtg tgt gct gtg tgt gca tgt gtg tgc	948

Met	Tyr	Val	Leu	Arg	Met	Ser	Val	Cys	Ala	Val	Cys	Ala	Cys	Val	Cys	
1				5					10					15		
tgt	gtg	ttt	gtg	tgt	gct	gtg	ttc	atg	tgt	gct	gtg	cat	gcg	tgt	gtg	996
Cys	Val	Phe	Val	Cys	Ala	Val	Phe	Met	Cys	Ala	Val	His	Ala	Cys	Val	
		20						25				30				
ctg	tgt	gca	tgt	gtg	tgc	tgt	gtg	ctg	tgt	tca	tgt	gtg	tgc	tgt	gtg	1044
Leu	Cys	Ala	Cys	Val	Cys	Cys	Val	Leu	Cys	Ser	Cys	Val	Cys	Cys	Val	
		35					40					45				
tgc	atg	tgc	tgt	gtg	cat	gtg	tgt	gct	gtg	ttt	gtg	tgt	gtg	ctg	tgt	1092
Cys	Met	Cys	Cys	Val	His	Val	Cys	Ala	Val	Phe	Val	Cys	Val	Leu	Cys	
	50					55				60						
gtg	ctg	tgt	tgc	tgt	gtg	ctg	tgt	tgc	cgt	gtg	tgt	gct	gtg	tgt	gca	1140
Val	Leu	Cys	Ser	Cys	Val	Leu	Cys	Ser	Arg	Val	Cys	Ala	Val	Cys	Ala	
	65				70				75						80	
tgt	gtg	tgc	tgt	gtc	ttt	gtg	tgt	gtg	ctg	tgt	gct	agt	gtg	ctg	tgt	1188
Cys	Val	Cys	Cys	Val	Phe	Val	Cys	Val	Leu	Cys	Ala	Ser	Val	Leu	Cys	
				85				90						95		
gtg	cat	gtg	tgt	gcg	tgt	gct	gtg	cgt	ttg	tgt	gct	gtg	tgc	tgc	tgt	1236
Val	His	Val	Cys	Ala	Cys	Ala	Val	Arg	Leu	Cys	Ala	Val	Cys	Ser	Cys	
			100					105					110			
gtg	tgc	tgt	gtg	tgc	gtg	tgt	gct	gtg	cgt	ttg	tgt	gtg	cgt	gtg	cgt	1284
Val	Cys	Cys	Val	Cys	Val	Cys	Ala	Val	Arg	Leu	Cys	Val	Arg	Val	Arg	
		115					120						125			
ttg	cgt	gtg	tgc	tgt	gtg	tgc	atg	tgt	gtg	cgt	gtg	tgt	gcc	gtg	cgt	1332
Leu	Arg	Val	Cys	Cys	Val	Cys	Met	Cys	Val	Arg	Val	Cys	Ala	Val	Arg	
	130					135						140				
ttg	tgt	gct	gtg	tgt	gca	tgt	gtg	tgc	gtg	tgt	gtg	ctg	tgc	gtt	tgt	1380
Leu	Cys	Ala	Val	Cys	Ala	Cys	Val	Cys	Val	Cys	Val	Leu	Cys	Val	Cys	
	145				150				155					160		
gtg	tgt	gct	gtg	tgc	tca	tct	gtg	tgc	tgt	gtg	tgc	tgt	gcg	ttt	gtg	1428
Val	Cys	Ala	Val	Cys	Ser	Ser	Val	Cys	Cys	Val	Cys	Cys	Ala	Phe	Val	
			165					170						175		
tgt	gtg	ctg	tat	gct	cgt	gtg	tgt	gct	gtg	ctc	gtg	tgt	gtg	ctg	tgt	1476
Cys	Val	Leu	Tyr	Ala	Arg	Val	Cys	Ala	Val	Leu	Val	Cys	Val	Leu	Cys	
			180					185					190			
tca	tgc	gtg	tgc	tgt	gtg	ttg	tgt	gtg	tgt	agc	tgc	ggg	gat	gca	taa	1524
Ser	Cys	Val	Cys	Cys	Val	Leu	Cys	Val	Cys	Ser	Cys	Gly	Asp	Ala		
		195				200						205				
agtatgagtg	cttttttagga	tggaattga	gatgtaagat	ttgggggtga	gggtcgtgcc											1584
aattacatatt	catttgcattg	gattttgggtt	ttcatgctct	gtcctccctct	ccttttggtct											1644
tactgggtgc	ctctgactgc	tctgtgattt	ttagtgtatgg	aaaggaggat	gaggaggcag											1704
tctgggttgt	tgtctatttct	ggatggccag	tttaccctga	aaattcccgat	gagaaggagg											1764
atggcgtag	cagcgacgtg	cccacctgtg	atttctgggg	tcctctcttt	ctcttttgcgt											1824

gttcaggagac tcaagtccag gccaatattga ctcaaagtcc aaggagagaag agaaagaggg 1884
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 tac 1947

<210> 94
 <211> 254
 <212> PRT
 <213> Homo sapiens

<400> 94
 Met Lys Arg Ala Ser Ala Gly Gly Ser Arg Leu Leu Ala Trp Val Leu
 1 5 10 15
 Trp Leu Gln Ala Trp Gln Val Ala Ala Pro Cys Pro Gly Ala Cys Val
 20 25 30
 Cys Tyr Asn Glu Pro Lys Val Thr Ser Cys Pro Gln Gln Gly Leu
 35 40 45
 Gln Ala Val Pro Val Gly Ile Pro Ala Ala Ser Gln Arg Ile Phe Leu
 50 55 60
 His Gly Asn Arg Ile Ser His Val Pro Ala Ala Ser Phe Arg Ala Cys
 65 70 75 80
 Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Val Leu Ala Arg Ile
 85 90 95
 Asp Ala Ala Ala Phe Thr Gly Leu Ala Leu Leu Glu Gln Leu Asp Leu
 100 105 110
 Ser Asp Asn Ala Gln Leu Arg Ser Val Asp Pro Ala Thr Phe His Gly
 115 120 125
 Leu Gly Arg Leu His Thr Leu His Leu Asp Arg Cys Gly Leu Gln Glu
 130 135 140
 Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr
 145 150 155 160
 Leu Gln Asp Asn Ala Leu Gln Ala Leu Pro Asp Asp Thr Phe Arg Asp
 165 170 175
 Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile Ser Ser
 180 185 190
 Val Pro Glu Arg Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu
 195 200 205
 Leu His Gln Asn Arg Val Ala His Val His Pro His Ala Phe Arg Asp
 210 215 220
 Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Ala
 225 230 235 240
 Leu Pro Thr Glu Ala Leu Ala Pro Cys Val Pro Cys Ser Thr
 245 250

<210> 95
 <211> 353
 <212> PRT
 <213> Homo sapiens

<400> 95
 Met Ala Ala Thr Lys Arg Lys Arg Arg Gly Gly Phe Ala Val Gln Ala
 1 5 10 15
 Lys Lys Pro Lys Arg Asn Glu Ile Asp Ala Glu Pro Pro Ala Lys Arg
 20 25 30
 His Ala Thr Ala Glu Glu Val Glu Glu Glu Arg Asp Arg Ile Pro

[illegible]

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<210> 96
<211> 410
<212> PRT
<213> Homo sapiens
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<400> 96																
Met	Cys	Ser	Thr	Met	Ser	Ala	Pro	Thr	Cys	Leu	Ala	His	Leu	Pro	Pro	
1				5					10					15		
Cys	Phe	Leu	Leu	Leu	Ala	Leu	Val	Leu	Val	Pro	Ser	Asp	Ala	Ser	Gly	
				20				25					30			
Gln	Ser	Ser	Arg	Asn	Asp	Trp	Gln	Val	Leu	Gln	Pro	Glu	Gly	Pro	Met	
		35					40					45				
Leu	Val	Ala	Glu	Gly	Glu	Thr	Leu	Leu	Leu	Arg	Cys	Met	Val	Val	Gly	
	50					55					60					
Ser	Cys	Thr	Asp	Gly	Met	Ile	Lys	Trp	Val	Lys	Ile	Ala	Leu	Ala	Ser	
65					70					75					80	

Phe Tyr Glu Asp Gly Asp Glu Asp Ile Val Thr Ile Ser Gln Ala
 85 90 95
 Thr Pro Ser Ser Val Ser Arg Gly Thr Ala Pro Ser Asp Asn Arg Val
 100 105 110
 Thr Ser Phe Arg Asp Leu Ile His Asp Gln Asp Glu Asp Glu Glu
 115 120 125
 Glu Glu Gly Gln Arg Phe Tyr Ala Gly Gly Ser Glu Arg Ser Gly Gln
 130 135 140
 Gln Ile Val Gly Pro Pro Arg Lys Lys Ser Pro Asn Glu Leu Val Asp
 145 150 155 160
 Asp Leu Phe Lys Gly Ala Lys Glu His Gly Ala Val Ala Val Glu Arg
 165 170 175
 Val Thr Lys Ser Pro Gly Glu Thr Ser Lys Pro Arg Pro Phe Ala Gly
 180 185 190
 Gly Gly Tyr Arg Leu Gly Ala Ala Pro Glu Glu Glu Ser Ala Tyr Val
 195 200 205
 Ala Gly Glu Lys Arg Gln His Ser Ser Gln Asp Val His Val Val Leu
 210 215 220
 Lys Leu Trp Lys Ser Gly Phe Ser Leu Asp Asn Gly Glu Leu Arg Ser
 225 230 235 240
 Tyr Gln Asp Pro Ser Asn Ala Gln Phe Leu Glu Ser Ile Arg Arg Gly
 245 250 255
 Glu Val Pro Ala Glu Leu Arg Arg Leu Ala His Gly Gly Gln Val Asn
 260 265 270
 Leu Asp Met Glu Asp His Arg Asp Glu Asp Phe Val Lys Pro Lys Gly
 275 280 285
 Ala Leu Gln Ala Phe Thr Gly Glu Gly Gln Lys Leu Gly Ser Thr Ala
 290 295 300
 Pro Gln Val Leu Ser Thr Ser Ser Pro Ala Gln Gln Ala Glu Asn Glu
 305 310 315 320
 Ala Lys Ala Ser Ser Ser Ile Leu Ile Asn Glu Ser Glu Pro Thr Thr
 325 330 335
 Asn Ile Gln Ile Arg Leu Ala Asp Gly Gly Arg Leu Val Gln Lys Phe
 340 345 350
 Asn His Ser His Arg Ile Ser Asp Ile Arg Leu Phe Ile Val Asp Ala
 355 360 365
 Arg Pro Ala Met Ala Ala Thr Ser Phe Ile Leu Met Thr Thr Phe Pro
 370 375 380
 Asn Lys Glu Leu Ala Asp Glu Ser Gln Thr Leu Lys Glu Ala Asn Leu
 385 390 395 400
 Leu Asn Ala Val Ile Val Gln Arg Leu Thr
 405 410

<210> 97
 <211> 379
 <212> PRT
 <213> Homo sapiens

<400> 97
 Met Cys Ser Thr Met Ser Ala Pro Thr Cys Leu Ala His Leu Pro Pro
 1 5 10 15
 Cys Phe Leu Leu Leu Ala Leu Val Leu Val Pro Ser Asp Ala Ser Gly
 20 25 30
 Gln Ser Ser Arg Asn Asp Trp Gln Val Leu Gln Pro Glu Gly Pro Met
 35 40 45
 Leu Val Ala Glu Gly Glu Thr Leu Leu Arg Cys Met Val Val Gly
 50 55 60
 Ser Cys Thr Asp Gly Met Ile Lys Trp Val Lys Ile Ala Leu Ala Ser

```

65          70          75          80
Phe Tyr Glu Asp Gly Asp Glu Asp Ile Val Thr Ile Ser Gln Ala
85
Thr Pro Ser Ser Val Ser Arg Gly Thr Ala Pro Ser Asp Asn Arg Val
100
Thr Ser Phe Arg Asp Leu Ile His Asp Gln Asp Glu Asp Glu Glu Glu
115
Glu Glu Gly Gln Arg Phe Tyr Ala Gly Gly Ser Glu Arg Ser Gly Gln
130
Gln Ile Val Gly Pro Pro Arg Lys Lys Ser Pro Asn Glu Leu Val Asp
145
Asp Leu Phe Lys Gly Ala Lys Glu His Gly Ala Val Ala Val Glu Arg
165
Val Thr Lys Ser Pro Gly Glu Thr Ser Lys Pro Arg Val His Val Val
180
Leu Lys Leu Trp Lys Ser Gly Phe Ser Leu Asp Asn Gly Glu Leu Arg
195
Ser Tyr Gln Asp Pro Ser Asn Ala Gln Phe Leu Glu Ser Ile Arg Arg
210
Gly Glu Val Pro Ala Glu Leu Arg Arg Leu Ala His Gly Gly Gln Val
225
Asn Leu Asp Met Glu Asp His Arg Asp Glu Asp Phe Val Lys Pro Lys
245
Gly Ala Phe Lys Ala Phe Thr Gly Glu Gly Gln Lys Leu Gly Ser Thr
260
Ala Pro Gln Val Leu Ser Thr Ser Pro Ala Gln Gln Ala Glu Asn
275
Glu Ala Lys Ala Ser Ser Ser Ile Leu Ile Asp Glu Ser Glu Pro Thr
290
Thr Asn Ile Gln Ile Arg Leu Ala Asp Gly Gly Arg Leu Val Gln Lys
305
Phe Asn His Ser His Arg Ile Ser Asp Ile Arg Leu Phe Ile Val Asp
325
Ala Arg Pro Ala Met Ala Ala Thr Ser Phe Ile Leu Met Thr Thr Phe
340
Pro Asn Lys Glu Leu Ala Asp Glu Ser Gln Thr Leu Lys Glu Ala Asn
355
Leu Leu Asn Ala Val Ile Val Gln Arg Leu Thr
370          375

```

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<210> 98
<211> 196
<212> PRT
<213> Homo sapiens

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```

<400> 98
Met Ala Ala Glu Arg Gln Glu Ala Leu Arg Glu Phe Val Ala Val Thr
1          5          10          15
Gly Ala Glu Glu Asp Arg Ala Arg Phe Phe Leu Glu Ser Ala Gly Trp
20
Asp Leu Gln Ile Ala Leu Ala Ser Phe Tyr Glu Asp Gly Gly Asp Glu
35          40          45
Asp Ile Val Thr Ile Ser Gln Ala Thr Pro Ser Ser Val Ser Arg Gly
50          55          60
Thr Ala Pro Ser Asp Asn Arg Val Thr Ser Phe Arg Asp Leu Ile His
65          70          75          80
Asp Gln Asp Glu Asp Glu Glu Glu Glu Gly Gln Arg Ser Arg Phe
85          90          95

```

```

Tyr Ala Gly Gly Ser Glu Arg Ser Gly Gln Gln Ile Val Gly Pro Pro
      100      105      110
Arg Lys Lys Ser Pro Asn Glu Leu Val Asp Asp Leu Phe Lys Gly Ala
      115      120      125
Lys Glu His Gly Ala Val Ala Val Glu Arg Val Thr Lys Ser Pro Gly
      130      135      140
Glu Thr Ser Lys Pro Arg Pro Phe Ala Gly Gly Gly Tyr Arg Leu Gly
      145      150      155      160
Ala Ser Thr Arg Gly Arg Val Cys Leu Cys Gly Arg Arg Lys Glu Ala
      165      170      175
Ala Phe Gln Pro Arg Cys Ser Cys Ser Ile Glu Thr Leu Glu Trp
      180      185      190
Ile Gln Pro Gly
      195

```

```

<210> 99
<211> 100
<212> PRT
<213> Homo sapiens

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<400> 99
Met Phe Ala Pro Arg Leu Leu Asp Leu Gln Lys Thr Lys Tyr Ala Arg
  1      5      10      15
Phe Met Asn His Arg Val Pro Ala His Lys Arg Tyr Gln Pro Thr Glu
      20      25      30
Tyr Glu His Ala Ala Asn Cys Ala Thr His Ala Phe Trp Ile Ile Pro
      35      40      45
Ser Ile Leu Gly Ser Ser Asn Leu Tyr Phe Leu Ser Asp Asp Asp Trp
      50      55      60
Glu Thr Ile Ser Ala Trp Ile Tyr Gly Leu Gly Leu Cys Gly Leu Phe
      65      70      75      80
Val Val Ser Thr Val Phe His Thr Ile Ser Trp Lys Lys Ser His Leu
      85      90      95
Arg Trp Gly Phe
      100

```

```

<210> 100
<211> 580
<212> PRT
<213> Homo sapiens

```

```

<400> 100
Met Arg Pro Trp Leu Arg His Leu Val Leu Gln Ala Leu Arg Asn Ser
  1      5      10      15
Arg Ala Phe Cys Gly Ser His Gly Lys Pro Ala Pro Leu Pro Val Pro
      20      25      30
Gln Lys Ile Val Ala Thr Trp Glu Ala Ile Ser Leu Gly Arg Gln Leu
      35      40      45
Val Pro Glu Tyr Phe Asn Phe Ala His Asp Val Leu Asp Val Trp Ser
      50      55      60
Arg Leu Glu Glu Ala Gly His Arg Pro Pro Asn Pro Ala Phe Trp Trp
      65      70      75      80
Val Asn Gly Thr Gly Ala Glu Ile Lys Trp Ser Phe Glu Glu Leu Gly
      85      90      95
Lys Gln Ser Arg Lys Ala Ala Asn Val Leu Gly Gly Ala Cys Gly Leu

```

[illegible]

<210> 101
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 101
 Met Asp Leu Pro Arg Gly Leu Val Val Ala Trp Ala Leu Ser Leu Trp
 1 5 10 15
 Pro Gly Phe Thr Asp Thr Phe Asn Met Asp Thr Arg Lys Pro Arg Val
 20 25 30
 Ile Pro Gly Ser Arg Thr Ala Phe Phe Gly Tyr Thr Val Gln Gln His
 35 40 45
 Asp Ile Ser Gly Asn Lys Trp Leu Val Val Gly Ala Pro Leu Glu Thr
 50 55 60
 Asn Gly Tyr Gln Lys Thr Gly Asp Val Tyr Lys Cys Pro Val Ile His
 65 70 75 80
 Gly Asn Cys Thr Lys Leu Asn Leu Gly Asn Val Gly Trp Trp Ser Leu
 85 90 95
 His Asn Glu Ala Ser Gly Cys Leu Thr Gln Gly Arg Leu
 100 105

<210> 102
 <211> 156
 <212> PRT
 <213> Homo sapiens

<400> 102
 Met Gln Lys Leu Glu Leu Gly Arg Tyr Asn Glu Thr His Ala Ile Ala
 1 5 10 15
 Lys Trp Leu Leu Glu Lys Gln Glu Leu Gly Gly Gly Phe Arg Ser Thr
 20 25 30
 Gln Thr Thr Val Val Ala Leu Glu Ala Leu Thr Arg Phe Arg Glu Ala
 35 40 45
 Val Pro Phe Lys Gly Ile Gln Asp Leu His Val Gln Ile Arg Ala Pro
 50 55 60
 Lys Thr Ala Leu Asn Val Asn Trp Tyr Ile Asp His Ser Asn Ala Tyr
 65 70 75 80
 Gln Gln Arg Ser Ala Lys Phe Leu Ala Gln Asp Asp Leu Glu Ile Lys
 85 90 95
 Ala Ser Gly Asn Gly Arg Gly Thr Ile Ser Ile Leu Thr Met Tyr His
 100 105 110
 Lys Ser Pro Glu Ser Arg Glu Asp Asn Cys Asn Leu Tyr His Leu Asn
 115 120 125
 Ala Thr Leu His Ser Ala Leu Glu Glu Asn Lys Lys Gly Gly Glu Thr
 130 135 140
 Phe Arg Leu Arg Met Glu Thr Arg Phe Gln Asn Asn
 145 150 155

<210> 103
 <211> 198
 <212> PRT
 <213> Homo sapiens

<400> 103

```

Met Ala Leu Arg His Leu Ala Leu Leu Ala Gly Leu Leu Val Gly Val
 1          5          10          15
Ala Ser Lys Ser Met Glu Asn Thr Ala Gln Leu Pro Glu Cys Cys Val
 20          25          30
Asp Val Val Gly Val Asn Ala Ser Cys Pro Gly Ala Ser Leu Cys Gly
 35          40          45
Pro Gly Cys Tyr Arg Arg Trp Asn Ala Asp Gly Ser Ala Ser Cys Val
 50          55          60
Arg Cys Gly Asn Gly Thr Leu Pro Ala Tyr Asn Gly Ser Glu Cys Arg
 65          70          75          80
Ser Phe Ala Gly Pro Gly Ala Pro Phe Pro Met Asn Arg Ser Ser Gly
 85          90          95
Thr Pro Gly Arg Pro His Pro Gly Ala Pro Arg Val Ala Ala Ser Leu
100          105          110
Phe Leu Gly Thr Phe Phe Ile Ser Ser Gly Leu Ile Leu Ser Val Ala
115          120          125
Gly Phe Phe Tyr Leu Lys Arg Ser Ser Lys Leu Pro Arg Ala Cys Tyr
130          135          140
Arg Arg Asn Lys Ala Pro Ala Leu Gln Pro Gly Glu Ala Ala Ala Met
145          150          155          160
Ile Pro Pro Pro Gln Ser Ser Val Arg Lys Pro Arg Tyr Val Arg Arg
165          170          175
Glu Arg Pro Leu Asp Arg Ala Thr Asp Pro Ala Ala Phe Pro Gly Glu
180          185          190
Ala Arg Ile Ser Asn Val
195

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<210> 104

<211> 254

<212> PRT

<213> Homo sapiens

<400> 104

```

Met Gly Leu Ser Ile Phe Leu Leu Leu Cys Val Leu Gly Leu Ser Gln
 1          5          10          15
Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg Asn Ser
 20          25          30
Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu Arg Cys Gly
 35          40          45
Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala Ala His Cys Ser
 50          55          60
Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His Ser Leu Ser Gln Leu
 65          70          75          80
Asp Trp Thr Glu Gln Ile Arg His Ser Gly Phe Ser Val Thr His Pro
 85          90          95
Gly Tyr Leu Gly Ala Ser Thr Ser His Glu His Asp Leu Arg Leu Leu
100          105          110
Arg Leu Arg Leu Pro Val Arg Val Thr Ser Ser Val Gln Pro Leu Pro
115          120          125
Leu Pro Asn Asp Cys Ala Thr Ala Gly Thr Glu Cys His Val Ser Gly
130          135          140
Trp Gly Ile Thr Asn His Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln
145          150          155          160
Cys Leu Asn Leu Ser Ile Val Ser His Ala Thr Cys His Gly Val Tyr
165          170          175

```

Pro Gly Arg Ile Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly
 180 185 190
 Gln Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly
 195 200 205
 Val Leu Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln
 210 215 220
 Asp Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Ser Ser Thr Leu Val
 225 230 235 240
 Gly Leu Gly Thr Ser Trp Asn Phe Asn Ser Cys Gln Pro Phe
 245 250

<210> 105
 <211> 404
 <212> PRT
 <213> Homo sapiens

<400> 105
 Met Ile Trp Lys Arg Ser Ala Val Leu Arg Phe Tyr Ser Val Cys Gly
 1 5 10 15
 Leu Leu Leu Gln Ala Ala Ala Ser Lys Asn Lys Val Lys Gly Ser Gln
 20 25 30
 Gly Gln Phe Pro Leu Thr Gln Asn Val Thr Val Val Glu Gly Gly Thr
 35 40 45
 Ala Ile Leu Thr Cys Arg Val Asp Gln Asn Asp Asn Thr Ser Leu Gln
 50 55 60
 Trp Ser Asn Pro Ala Gln Gln Thr Leu Tyr Phe Asp Asp Lys Lys Ala
 65 70 75 80
 Leu Arg Asp Asn Arg Ile Glu Leu Val Arg Ala Ser Trp His Glu Leu
 85 90 95
 Ser Ile Ser Val Ser Asp Val Ser Leu Ser Asp Glu Gly Gln Tyr Thr
 100 105 110
 Cys Ser Leu Phe Thr Met Pro Val Lys Thr Ser Lys Ala Tyr Leu Thr
 115 120 125
 Val Leu Gly Val Pro Glu Lys Pro Gln Ile Ser Gly Phe Ser Ser Pro
 130 135 140
 Val Met Glu Gly Asp Leu Met Gln Leu Thr Cys Lys Thr Ser Gly Ser
 145 150 155 160
 Lys Pro Ala Ala Asp Ile Arg Trp Phe Lys Asn Asp Lys Glu Ile Lys
 165 170 175
 Asp Val Lys Tyr Leu Lys Glu Glu Asp Ala Asn Arg Lys Thr Phe Thr
 180 185 190
 Val Ser Ser Thr Leu Asp Phe Arg Val Asp Arg Ser Asp Asp Gly Val
 195 200 205
 Ala Val Ile Cys Arg Val Asp His Glu Ser Leu Asn Ala Thr Pro Gln
 210 215 220
 Val Ala Met Gln Val Leu Glu Ile His Tyr Thr Pro Ser Val Lys Ile
 225 230 235 240
 Ile Pro Ser Thr Pro Phe Pro Gln Glu Gly Gln Pro Leu Ile Leu Thr
 245 250 255
 Cys Glu Ser Lys Gly Lys Pro Leu Pro Glu Pro Val Leu Trp Thr Lys
 260 265 270
 Asp Gly Gly Glu Leu Pro Asp Pro Asp Arg Met Val Val Ser Gly Arg
 275 280 285
 Glu Leu Asn Ile Leu Phe Leu Asn Lys Thr Asp Asn Gly Thr Tyr Arg
 290 295 300
 Cys Glu Ala Thr Asn Thr Ile Gly Gln Ser Ser Ala Glu Tyr Val Leu
 305 310 315 320
 Ile Val His Asp Pro Asn Ala Leu Ala Gly Asn Gly Pro Asp His

Ala	Leu	Ile	Gly	325	Gly	Ile	Val	Ala	Val	Val	Val	Phe	Val	Thr	Leu	Cys
			340						345					350		
Ser	Ile	Phe	Leu	Leu	Gly	Arg	Tyr	Leu	Ala	Arg	His	Lys	Gly	Thr	Tyr	
		355					360					365				
Leu	Thr	Asn	Glu	Ala	Lys	Gly	Ala	Glu	Asp	Ala	Pro	Asp	Ala	Asp	Thr	
		370				375					380					
Ala	Ile	Ile	Asn	Ala	Glu	Gly	Ser	Gln	Val	Asn	Ala	Glu	Glu	Lys	Lys	
		385			390					395					400	
Glu	Tyr	Phe	Ile													

<210> 106
 <211> 1600
 <212> PRT
 <213> Homo sapiens

<400> 106

Met	Thr	Leu	Glu	Gly	Leu	Tyr	Leu	Ala	Arg	Gly	Pro	Leu	Ala	Arg	Leu	
1				5					10					15		
Leu	Leu	Ala	Trp	Ser	Ala	Leu	Leu	Cys	Met	Ala	Gly	Gly	Gln	Gly	Arg	
		20						25					30			
Trp	Asp	Gly	Ala	Leu	Glu	Ala	Ala	Gly	Pro	Gly	Arg	Val	Arg	Arg	Arg	
		35					40					45				
Gly	Ser	Pro	Gly	Ile	Leu	Gln	Gly	Cys	Val	Val	Pro	Gly	Met	Leu	Gly	
		50				55					60					
Asp	Pro	Phe	Gly	Val	Asp	Trp	Ala	Val	Leu	Gly	Pro	Ala	Glu	Tyr	Pro	
		65			70					75				80		
Gly	Gly	Cys	Pro	His	Gly	Gln	Gly	Leu	Thr	Arg	Pro	Ile	Ser	Leu	Ser	
				85					90					95		
Pro	Lys	Ala	Glu	Cys	Val	Arg	Leu	Pro	Val	Pro	Cys	Leu	Leu	Leu	Ser	
		100						105					110			
Arg	Leu	Glu	Asp	Ile	Pro	Trp	Gln	Glu	Pro	Val	Cys	Arg	Thr	Arg	Ala	
		115					120					125				
Cys	Gly	Glu	Gly	Phe	Cys	Ser	Gln	Pro	Asn	Leu	Cys	Thr	Cys	Ala	Asp	
		130				135					140					
Gly	Thr	Leu	Ala	Pro	Ser	Cys	Gly	Val	Ser	Arg	Gly	Ser	Gly	Cys	Ser	
		145				150				155				160		
Val	Ser	Cys	Met	Asn	Gly	Gly	Thr	Cys	Arg	Gly	Ala	Ser	Cys	Leu	Cys	
			165						170					175		
Gln	Lys	Gly	Tyr	Thr	Gly	Thr	Val	Cys	Gly	Gln	Pro	Ile	Cys	Asp	Arg	
		180						185					190			
Gly	Cys	His	Asn	Gly	Gly	Arg	Cys	Ile	Gly	Pro	Asn	Arg	Cys	Ala	Cys	
		195				200					205					
Val	Tyr	Gly	Phe	Met	Gly	Pro	Gln	Cys	Glu	Arg	Asp	Tyr	Arg	Thr	Gly	
		210				215					220					
Pro	Cys	Phe	Gly	Gln	Val	Gly	Pro	Glu	Gly	Cys	Gln	His	Gln	Leu	Thr	
		225			230					235				240		
Gly	Leu	Val	Cys	Thr	Lys	Ala	Leu	Cys	Cys	Ala	Thr	Val	Gly	Arg	Ala	
			245						250					255		
Trp	Gly	Leu	Pro	Cys	Glu	Leu	Cys	Pro	Ala	Gln	Pro	His	Pro	Cys	Arg	
		260						265					270			
Arg	Gly	Phe	Ile	Pro	Asn	Ile	His	Thr	Gly	Ala	Cys	Gln	Asp	Val	Asp	
		275				280						285				
Glu	Cys	Gln	Ala	Val	Pro	Gly	Leu	Cys	Gln	Gly	Gly	Ser	Cys	Val	Asn	
		290				295					300					
Met	Val	Gly	Ser	Phe	His	Cys	Arg	Cys	Pro	Val	Gly	His	Arg	Leu	Ser	
		305			310					315				320		

Asp Ser Ser Ala Ala Cys Glu Asp Tyr Arg Ala Gly Ala Cys Phe Ser
 325 330 335
 Val Leu Phe Gly Gly Arg Cys Ala Gly Asp Leu Ala Gly His Tyr Thr
 340 345 350
 Arg Arg Gln Cys Cys Cys Asp Arg Gly Gln Val Leu Gly Ser Val Ala
 355 360 365
 Arg Ser Leu Ser Cys Val Leu Leu Gly Ala Pro Val Asn Glu Phe Gln
 370 375 380
 Gln Leu Cys Ala Gln Arg Leu Pro Leu Leu Pro Gly His Pro Gly Leu
 385 390 395 400
 Phe Pro Gly Leu Leu Gly Phe Gly Ser Asn Gly Met Gly Pro Pro Leu
 405 410 415
 Gly Pro Ala Arg Leu Asn Pro His Gly Ser Asp Ala Arg Gly Ile Pro
 420 425 430
 Ser Leu Gly Pro Gly Asn Ser Asn Ile Gly Thr Ala Thr Leu Asn Gln
 435 440 445
 Thr Ile Asp Ile Cys Arg His Phe Thr Asn Leu Cys Leu Asn Gly Arg
 450 455 460
 Cys Leu Pro Thr Pro Ser Ser Tyr Arg Cys Glu Cys Asn Val Gly Tyr
 465 470 475 480
 Thr Gln Asp Val Arg Gly Glu Cys Ile Asp Val Asp Glu Cys Thr Ser
 485 490 495
 Ser Pro Cys His His Gly Asp Cys Val Asn Ile Pro Gly Thr Tyr His
 500 505 510
 Cys Arg Cys Tyr Pro Gly Phe Gln Ala Thr Pro Thr Arg Gln Ala Cys
 515 520 525
 Val Asp Val Asp Glu Cys Ile Val Ser Gly Gly Leu Cys His Leu Gly
 530 535 540
 Arg Cys Val Asn Thr Glu Gly Ser Phe Gln Cys Val Cys Asn Ala Gly
 545 550 555 560
 Phe Glu Leu Ser Pro Asp Gly Lys Asn Cys Val Ala Ala Ala Pro Gly
 565 570 575
 Arg Gln Thr His Leu Arg Leu Gly Glu Ala Glu Gly Phe Lys Asp Asn
 580 585 590
 Ser Thr Val Gln Glu Pro Tyr Pro His Ile Thr Asp Pro Gly Arg Pro
 595 600 605
 Ser Gly Val Thr Leu Ala Ser Ala Leu Arg Cys Leu Arg Pro Cys Leu
 610 615 620
 Ser Ser Asp Trp Ser Arg Trp Glu His Ser Pro Ile Trp Ser Pro Leu
 625 630 635 640
 Leu Pro Glu Met Leu Trp Leu Cys Ser Ser Val His Thr Pro Thr Leu
 645 650 655
 Pro Gly Arg Pro Glu Pro Leu Gly Arg Ala Val Gly Trp Cys Thr Gly
 660 665 670
 Glu Ala Gln Ile Ser Pro Gly Leu Ser Gly His Pro Gly Tyr Pro Glu
 675 680 685
 Ser Gly Ala Leu Leu Glu Gly Gln Ser Arg Gly Ser Pro Glu Ala Arg
 690 695 700
 Ala Gly Ala Asn Arg Gly Asp His Asn Glu Cys Ala Thr Ser Thr Met
 705 710 715 720
 Cys Val Asn Gly Val Cys Leu Asn Glu Asp Trp Gln Leu Leu Leu Pro
 725 730 735
 Leu Gln Thr Arg Ala Ser Cys Trp Arg Leu Ala Ala Ile Thr Ala Leu
 740 745 750
 Asp Ala Arg His Leu Arg Glu Arg His Cys Thr Asn Thr Glu Gly Ser
 755 760 765
 Phe Arg Cys Gln Cys Leu Gly Gly Leu Ala Val Gly Thr Asp Gly Arg
 770 775 780
 Val Cys Val Asp Thr His Val Arg Ser Thr Cys Tyr Gly Ala Ile Glu
 785 790 795 800
 Lys Gly Ser Cys Ala Arg Pro Phe Pro Gly Thr Val Thr Lys Ser Glu

Cys	Cys	Cys	Ala	805	Asn	Pro	Asp	His	Gly	810	Phe	Gly	Glu	Pro	815	Cys	Gln	Leu
Cys	Pro	Ala	820	Lys	Asp	Ser	Ala	Glu	825	Phe	Gln	Ala	Leu	Cys	830	Ser	Ser	Gly
Leu	Gly	Ile	835	Thr	Thr	Asp	Gly	Arg	840	Asp	Ile	Asn	Glu	Cys	845	Ala	Leu	Asp
Pro	Glu	Val	850	Cys	Ala	Asn	Gly	Val	855	Cys	Glu	Asn	Leu	Arg	860	Gly	Ser	Thr
Arg	Cys	Val	865	Cys	Asn	Leu	Gly	Tyr	870	Glu	Ala	Gly	Ala	Ser	875	Gly	Lys	Asp
Cys	Thr	Asp	900	Val	Asp	Glu	Cys	Ala	905	Leu	Asn	Ser	Leu	Leu	910	Cys	Asp	Asn
Gly	Trp	Cys	915	Gln	Asn	Ser	Pro	Gly	920	Ser	Tyr	Ser	Cys	Ser	925	Cys	Pro	Pro
Gly	Phe	His	930	Phe	Trp	Gln	Asp	Thr	935	Glu	Ile	Cys	Lys	Asp	940	Val	Asp	Glu
Cys	Leu	Ser	945	Ser	Pro	Cys	Val	Ser	950	Gly	Val	Cys	Arg	Asn	955	Leu	Ala	Gly
Ser	Tyr	Thr	960	Cys	Lys	Cys	Gly	Pro	965	Gly	Ser	Arg	Leu	Asp	970	Pro	Ser	Gly
Thr	Phe	Cys	980	Leu	Asp	Ser	Thr	Lys	985	Gly	Thr	Cys	Trp	Leu	990	Lys	Ile	Gln
Glu	Ser	Arg	995	Cys	Glu	Val	Asn	Leu	1000	Gln	Gly	Ala	Ser	Leu	1005	Arg	Ser	Glu
Cys	Cys	Ala	1010	Thr	Leu	Gly	Ala	Ala	1015	Trp	Gly	Ser	Pro	Cys	1020	Glu	Arg	Cys
Glu	Ile	Gly	1025	Ser	Ile	Leu	Leu	Glu	1030	Ala	Ser	Gln	Ala	Pro	1035	Met	Gly	Lys
Ala	Leu	His	1040	Gly	Ala	Gly	Pro	Pro	1045	Leu	Gly	Trp	His	Glu	1050	Lys	Met	Thr
Pro	Leu	Phe	1055	Thr	Leu	Val	Leu	Pro	1060	Val	Ala	Asp	Ser	Thr	1065	Pro	Glu	Val
Thr	Val	Arg	1070	Asn	Ser	Arg	Val	Asp	1075	Glu	Cys	Leu	Ser	Ser	1080	Pro	Cys	Val
Ser	Gly	Val	1085	Cys	Arg	Asn	Leu	Ala	1090	Gly	Ser	Tyr	Thr	Cys	1095	Lys	Cys	Gly
Pro	Gly	Ser	1100	Arg	Leu	Asp	Pro	Ser	1105	Gly	Thr	Phe	Cys	Leu	1110	Asp	Ser	Thr
Lys	Gly	Thr	1120	Cys	Trp	Leu	Lys	Ile	1125	Gln	Glu	Ser	Arg	Cys	1130	Glu	Val	Asn
Leu	Gln	Gly	1135	Ala	Ser	Leu	Arg	Ser	1140	Glu	Cys	Cys	Ala	Thr	1145	Leu	Gly	Ala
Ala	Trp	Gly	1150	Ser	Pro	Cys	Glu	Arg	1155	Cys	Glu	Ile	Asp	Pro	1160	Ala	Cys	Ala
Arg	Gly	Phe	1165	Ala	Arg	Met	Thr	Gly	1170	Val	Thr	Cys	Asn	Asp	1175	Val	Asn	Glu
Cys	Glu	Ser	1185	Phe	Pro	Gly	Val	Cys	1190	Pro	Asn	Gly	Arg	Cys	1195	Val	Asn	Thr
Ala	Gly	Ser	1200	Phe	Arg	Cys	Glu	Cys	1205	Pro	Glu	Gly	Leu	Met	1210	Leu	Asp	Ala
Ser	Gly	Arg	1215	Leu	Cys	Val	Asp	Val	1220	Arg	Leu	Glu	Pro	Cys	1225	Phe	Leu	Arg
Trp	Asp	Glu	1230	Asp	Glu	Cys	Gly	Val	1235	Thr	Leu	Pro	Gly	Lys	1240	Tyr	Arg	Met
Asp	Val	Cys	1245	Cys	Cys	Ser	Ser	Ile	1250	Gly	Ala	Val	Trp	Gly	1255	Val	Cys	Glu
Ala	Cys	Pro	1260	Asp	Pro	Glu	Ser	Leu	1265	Glu	Phe	Ala	Ser	Leu	1270	Cys	Pro	Arg
Gly	Leu	Gly	1275	Phe	Ala	Ser	Arg	Asp	1280	Phe	Leu	Ser	Gly	Arg	1285	Pro	Phe	Tyr

Lys Asp Val Asn Glu Cys Lys Val Phe Pro Gly Leu Cys Thr His Gly
 1300 1305 1310
 Thr Cys Arg Asn Thr Val Gly Ser Phe His Cys Ala Cys Ala Gly Gly
 1315 1320 1325
 Phe Ala Leu Asp Ala Gln Glu Arg Asn Cys Thr Asp Ile Asp Glu Cys
 1330 1335 1340
 Arg Ile Ser Pro Asp Leu Cys Gly Gln Gly Thr Cys Val Asn Thr Pro
 1345 1350 1355 1360
 Gly Ser Phe Glu Cys Glu Cys Phe Pro Gly Tyr Glu Ser Gly Phe Met
 1365 1370 1375
 Leu Met Lys Asn Cys Met Asp Val Asp Glu Cys Ala Arg Asp Pro Leu
 1380 1385 1390
 Leu Cys Arg Gly Gly Thr Cys Thr Asn Thr Asp Gly Ser Tyr Lys Cys
 1395 1400 1405
 Gln Cys Pro Pro Gly His Glu Leu Thr Ala Lys Gly Thr Ala Cys Glu
 1410 1415 1420
 Asp Ile Asp Glu Cys Ser Leu Ser Asp Gly Leu Cys Pro His Gly Gln
 1425 1430 1435 1440
 Cys Val Asn Val Ile Gly Ala Phe Gln Cys Ser Cys His Ala Gly Phe
 1445 1450 1455
 Gln Ser Thr Pro Asp Arg Gln Gly Cys Val Asp Ile Asn Glu Cys Arg
 1460 1465 1470
 Val Gln Asn Gly Gly Cys Asp Val His Cys Ile Asn Thr Glu Gly Ser
 1475 1480 1485
 Tyr Arg Cys Ser Cys Gly Gln Gly Tyr Ser Leu Met Pro Asp Gly Arg
 1490 1495 1500
 Ala Cys Ala Asp Val Asp Glu Cys Glu Glu Asn Pro Arg Val Cys Asp
 1505 1510 1515 1520
 Gln Gly His Cys Thr Asn Met Pro Gly Gly His Arg Cys Leu Cys Tyr
 1525 1530 1535
 Asp Gly Phe Met Ala Thr Pro Asp Met Arg Thr Cys Val Asp Val Ala
 1540 1545 1550
 Leu Leu Pro Pro Ala Leu Tyr Pro Gly Pro Gly His Leu Pro His Cys
 1555 1560 1565
 Leu Pro Gly Thr Gly Gln Ala Leu Gln Val Ser Pro Gly Leu Asp Ala
 1570 1575 1580
 Val Leu Trp Gly Thr Glu Pro Ala Pro Gln Leu Gly Ile Pro Gly Arg
 1585 1590 1595 1600

<210> 107
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 107
 Met Asp Ser Tyr Gly Thr Ser Asn Asn Cys Trp Leu Ser Leu Ala Ser
 1 5 10 15
 Gly Ala Ile Trp Ala Phe Val Ala Pro Ala Leu Phe Val Ile Val Val
 20 25 30
 Asn Ile Gly Ile Leu Ile Ala Val Thr Arg Val Ile Ser Gln Ile Ser
 35 40 45
 Ala Asp Asn Tyr Lys Ile His Gly Asp Pro Ser Ala Phe Lys Leu Thr
 50 55 60
 Ala Lys Ala Val Ala Val Leu Leu Pro Ile Leu Gly Thr Ser Trp Val
 65 70 75 80
 Phe Gly Val Leu Ala Val Asn Gly Cys Ala Val Val Phe Gln Tyr Met

[illegible]

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<210> 108
<211> 374
<212> PRT
<213> Homo sapiens
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<400> 108																	
Met	Met	Pro	Gly	Thr	Ala	Leu	Glu	Gly	Val	Leu	Leu	Ala	Val	Leu	Leu		
1				5					10					15			
Val	Gly	Leu	Glu	Thr	Ala	Thr	Gly	Arg	Leu	Leu	Ser	Gly	Gln	Pro	Val		
			20					25					30				
Cys	Arg	Gly	Gly	Thr	Gln	Arg	Pro	Cys	Tyr	Lys	Val	Ile	Tyr	Phe	His		
		35					40					45					
Asp	Thr	Ser	Arg	Arg	Leu	Asn	Phe	Glu	Glu	Ala	Lys	Glu	Ala	Cys	Arg		
50						55					60						
Arg	Asp	Gly	Gly	Gln	Leu	Val	Ser	Ile	Glu	Ser	Glu	Asp	Glu	Gln	Lys		
65					70					75							
Leu	Ile	Glu	Lys	Phe	Ile	Glu	Asn	Leu	Leu	Pro	Ser	Asp	Gly	Asp	Phe		
			85					90					95				
Trp	Ile	Gly	Leu	Arg	Arg	Arg	Glu	Gly	Lys	Gln	Ser	Asn	Ser	Thr	Ala		
			100				105						110				
Cys	Gln	Asp	Leu	Tyr	Ala	Trp	Thr	Asp	Gly	Ser	Ile	Ser	Gln	Phe	Arg		
		115					120					125					
Asn	Trp	Tyr	Val	Asp	Glu	Pro	Ser	Cys	Gly	Ser	Glu	Val	Cys	Val	Val		
		130				135					140						
Met	Tyr	His	Gln	Pro	Ser	Ala	Pro	Ala	Gly	Ile	Gly	Gly	Pro	Tyr	Met		
145					150					155					160		
Phe	Gln	Trp	Asn	Asp	Asp	Arg	Cys	Asn	Met	Lys	Asn	Asn	Phe	Ile	Cys		
			165						170				175				
Lys	Tyr	Ser	Asp	Glu	Lys	Pro	Ala	Val	Pro	Ser	Arg	Glu	Ala	Glu	Gly		
		180						185					190				
Glu	Glu	Thr	Glu	Leu	Thr	Thr	Pro	Val	Leu	Pro	Glu	Glu	Thr	Gln	Glu		
		195					200					205					
Glu	Asp	Ala	Lys	Lys	Thr	Phe	Lys	Glu	Ser	Arg	Glu	Ala	Ala	Leu	Asn		
		210				215					220						
Leu	Ala	Tyr	Ile	Leu	Ile	Pro	Ser	Ile	Pro	Leu	Leu	Leu	Leu	Leu	Val		
225					230					235					240		
Val	Thr	Thr	Val	Val	Cys	Trp	Val	Trp	Ile	Cys	Arg	Lys	Arg	Lys	Arg		
			245						250					255			
Glu	Gln	Pro	Asp	Pro	Ser	Thr	Lys	Lys	Gln	His	Thr	Ile	Trp	Pro	Ser		
		260					265						270				
Pro	His	Gln	Gly	Asn	Ser	Pro	Asp	Leu	Glu	Val	Tyr	Asn	Val	Ile	Arg		
		275					280					285					
Lys	Gln	Ser	Glu	Ala	Asp	Leu	Ala	Glu	Thr	Arg	Pro	Asp	Leu	Lys	Asn		
		290				295					300						

Ile Ser Phe Arg Val Cys Ser Gly Glu Ala Thr Pro Asp Asp Met Ser
 305 310 315 320
 Cys Asp Tyr Asp Asn Met Ala Val Asn Pro Ser Glu Ser Gly Phe Val
 325 330 335
 Thr Leu Val Ser Val Glu Ser Gly Phe Val Thr Asn Asp Ile Tyr Glu
 340 345 350
 Phe Ser Pro Asp Gln Met Gly Arg Ser Lys Glu Ser Gly Trp Val Glu
 355 360 365
 Asn Glu Ile Tyr Gly Tyr
 370

<210> 109
 <211> 503
 <212> PRT
 <213> Homo sapiens

<400> 109
 Met Tyr Leu Val Ala Gly Asp Arg Gly Leu Ala Gly Cys Gly His Leu
 1 5 10 15
 Leu Val Ser Leu Leu Gly Leu Leu Leu Leu Ala Arg Ser Gly Thr
 20 25 30
 Arg Ala Leu Val Cys Leu Pro Cys Asp Glu Ser Lys Cys Glu Glu Pro
 35 40 45
 Arg Asn Cys Pro Gly Ser Ile Val Gln Gly Val Cys Gly Cys Tyr
 50 55 60
 Thr Cys Ala Ser Gln Arg Asn Glu Ser Cys Gly Gly Thr Phe Gly Ile
 65 70 75 80
 Tyr Gly Thr Cys Asp Arg Gly Leu Arg Cys Val Ile Arg Pro Pro Leu
 85 90 95
 Asn Gly Asp Ser Leu Thr Glu Tyr Glu Ala Gly Val Cys Glu Asp Glu
 100 105 110
 Asn Trp Thr Asp Asp Gln Leu Leu Gly Phe Lys Pro Cys Asn Glu Asn
 115 120 125
 Leu Ile Ala Gly Cys Asn Ile Ile Asn Gly Lys Cys Glu Cys Asn Thr
 130 135 140
 Ile Arg Thr Cys Ser Asn Pro Phe Glu Phe Pro Ser Gln Asp Met Cys
 145 150 155 160
 Leu Ser Ala Leu Lys Arg Ile Glu Glu Glu Lys Pro Asp Cys Ser Lys
 165 170 175
 Ala Arg Cys Glu Val Gln Phe Ser Pro Arg Cys Pro Glu Asp Ser Val
 180 185 190
 Leu Ile Glu Gly Tyr Ala Pro Pro Gly Glu Cys Cys Pro Leu Pro Ser
 195 200 205
 Arg Cys Val Cys Asn Pro Ala Gly Cys Leu Arg Lys Val Cys Gln Pro
 210 215 220
 Gly Asn Leu Asn Ile Leu Val Ser Lys Ala Ser Gly Lys Pro Gly Glu
 225 230 235 240
 Cys Cys Asp Leu Tyr Glu Cys Lys Pro Val Phe Gly Val Asp Cys Arg
 245 250 255
 Thr Val Glu Cys Pro Pro Val Gln Gln Thr Ala Arg Cys Pro Pro Asp
 260 265 270
 Ser Tyr Glu Thr Gln Val Arg Leu Thr Ala Asp Gly Cys Cys Pro Leu
 275 280 285
 Pro Pro Arg Cys Glu Cys Leu Ser Gly Leu Cys Gly Phe Pro Val Cys
 290 295 300
 Glu Val Gly Ser Thr Pro Arg Ile Val Ser Arg Gly Asp Gly Thr Pro
 305 310 315 320
 Gly Lys Cys Cys Asp Val Phe Glu Cys Val Asn Asp Thr Lys Pro Ala


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          325          330          335
Cys Val Phe Asn Asn Val Glu Tyr Tyr Asp Gly Asp Met Phe Arg Met
          340          345          350
Asp Asn Cys Arg Phe Cys Arg Cys Gln Gly Gly Val Ala Ile Cys Phe
          355          360          365
Thr Ala Gln Cys Gly Glu Ile Asn Cys Glu Arg Tyr Tyr Val Pro Glu
          370          375          380
Gly Glu Cys Cys Pro Val Cys Glu Asp Pro Val Tyr Pro Phe Asn Asn
          385          390          395          400
Pro Ala Gly Cys Tyr Ala Asn Gly Leu Ile Leu Ala His Gly Asp Arg
          405          410          415
Trp Arg Glu Asp Asp Cys Thr Phe Cys Gln Cys Val Asn Gly Glu Arg
          420          425          430
His Cys Val Ala Thr Val Cys Gly Gln Thr Cys Thr Asn Pro Val Lys
          435          440          445
Val Pro Gly Glu Cys Cys Pro Val Cys Glu Glu Pro Thr Ile Ile Thr
          450          455          460
Val Asp Pro Pro Ala Cys Gly Glu Leu Ser Asn Cys Thr Leu Thr Gly
          465          470          475          480
Lys Asp Cys Ile Asn Gly Phe Lys Arg Asp His Asn Gly Cys Arg Thr
          485          490          495
Cys Gln Cys Ile Asn Ser Glu
          500

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<210> 110
<211> 123
<212> PRT
<213> Homo sapiens

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          <400> 110
Met Trp Leu Pro Pro Ala Leu Leu Leu Leu Ser Leu Ser Gly Cys Phe
          1          5          10          15
Ser Ile Gln Gly Pro Glu Ser Val Arg Ala Pro Glu Gln Gly Ser Leu
          20          25          30
Thr Val Gln Cys His Tyr Lys Gln Gly Trp Glu Thr Tyr Ile Lys Trp
          35          40          45
Trp Cys Arg Gly Val Arg Trp Asp Thr Cys Lys Ile Leu Ile Glu Thr
          50          55          60
Arg Gly Ser Glu Gln Gly Glu Lys Ser Asp Arg Val Ser Ile Lys Asp
          65          70          75          80
Asn Gln Lys Asp Arg Thr Phe Thr Val Thr Met Glu Gly Leu Arg Arg
          85          90          95
Asp Asp Ala Asp Val Tyr Trp Cys Gly Ile Glu Arg Arg Gly Pro Asp
          100          105          110
Leu Gly Thr Gln Val Lys Val Ile Val Asp Pro
          115          120

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<210> 111
<211> 120
<212> PRT
<213> Homo sapiens

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```

          <400> 111
Met Ser Cys Ile Leu Gly Phe Cys Phe Pro Gly Cys Phe Ser Ile Gln
          1          5          10          15

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Gly Pro Glu Ser Val Arg Ala Pro Glu Gln Gly Ser Leu Thr Val Gln
 20 25 30
 Cys His Tyr Lys Gln Gly Trp Glu Thr Tyr Ile Lys Trp Trp Cys Arg
 35 40 45
 Gly Val Arg Trp Asp Thr Cys Lys Ile Leu Ile Glu Thr Arg Gly Ser
 50 55 60
 Glu Gln Gly Glu Lys Ser Asp Arg Val Ser Ile Lys Asp Asn Gln Lys
 65 70 75 80
 Asp Arg Thr Phe Thr Val Thr Met Glu Gly Leu Arg Arg Asp Asp Ala
 85 90 95
 Asp Val Tyr Trp Cys Gly Ile Glu Arg Arg Gly Pro Asp Leu Gly Thr
 100 105 110
 Gln Val Lys Val Ile Val Asp Pro
 115 120

<210> 112
 <211> 346
 <212> PRT
 <213> Homo sapiens

<400> 112
 Met Glu Arg Lys Phe Met Ser Leu Gln Pro Ser Ile Ser Val Ser Glu
 1 5 10 15
 Met Glu Pro Asn Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr
 20 25 30
 Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile
 35 40 45
 Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu
 50 55 60
 Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu
 65 70 75 80
 Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp
 85 90 95
 Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg
 100 105 110
 Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe
 115 120 125
 Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe
 130 135 140
 Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly
 145 150 155 160
 Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser
 165 170 175
 Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu
 180 185 190
 Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val
 195 200 205
 Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile
 210 215 220
 Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val
 225 230 235 240
 Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe
 245 250 255
 Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr
 260 265 270
 Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val
 275 280 285
 Ile Thr Leu Ala Leu Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu

290		295		300	
Tyr Tyr Phe Ala Gly	Glu Asn Phe Lys Asp Arg	Leu Lys Ser	Ala Leu		
305	310	315	320		
Arg Lys Gly His Pro	Gln Lys Ala Lys Thr Lys	Cys Val Phe	Pro Val		
	325	330	335		
Ser Val Trp Leu Arg	Lys Glu Thr Arg Val				
	340	345			

<210> 113
 <211> 403
 <212> PRT
 <213> Homo sapiens

<400> 113

Met Glu Thr Tyr	Ala Glu Val Gly Lys	Glu Gly Lys Pro Ser Cys Ala
1	5	10 15
Ser Val Asp Leu	Gln Gly Asp Ser Ser Leu	Gln Val Glu Ile Ser Asp
	20	25 30
Ala Val Ser Glu	Arg Asp Lys Val Lys Phe Thr	Val Gln Thr Lys Ser
	35	40 45
Cys Leu Pro His	Phe Ala Gln Thr Glu Phe Ser	Val Val Arg Gln His
	50	55 60
Glu Glu Phe Ile	Trp Leu His Asp Ala Tyr Val	Glu Asn Glu Glu Tyr
	65	70 75
Ala Gly Leu Ile	Ile Pro Pro Ala Pro Pro Arg	Pro Asp Phe Glu Ala
	85	90 95
Ser Arg Glu Lys	Leu Gln Lys Leu Gly Glu Gly Asp Ser	Ser Val Thr
	100	105 110
Arg Glu Glu Phe	Ala Lys Met Lys Gln Glu Leu Glu Ala	Glu Tyr Leu
	115	120 125
Ala Ile Phe Lys	Lys Thr Val Ala Met His Glu Val Phe	Leu Gln Arg
	130	135 140
Leu Ala Ala His	Pro Thr Leu Arg Arg Asp His Asn Phe	Phe Val Phe
	145	150 155
Leu Glu Tyr Gly	Gln Asp Leu Ser Val Arg Gly Lys	Asn Arg Lys Glu
	165	170 175
Leu Leu Gly Gly	Phe Leu Arg Asn Ile Val Lys Ser Ala	Asp Glu Ala
	180	185 190
Leu Ile Thr Gly	Met Ser Gly Leu Lys Glu Val Asp Asp Phe	Phe Glu
	195	200 205
His Glu Arg Thr	Phe Leu Leu Glu Tyr His Thr Arg Ile	Arg Asp Ala
	210	215 220
Cys Leu Arg Ala	Asp Arg Val Met Arg Ala His Lys Cys	Leu Ala Asp
	225	230 235
Asp Tyr Ile Pro	Ile Ser Ala Ala Leu Ser Ser Leu Gly	Thr Gln Glu
	245	250 255
Val Asn Gln Leu	Arg Thr Ser Phe Leu Lys Leu Ala Glu	Leu Phe Glu
	260	265 270
Arg Leu Arg Lys	Leu Glu Gly Arg Val Ala Ser Asp Glu	Asp Leu Lys
	275	280 285
Leu Ser Asp Met	Leu Arg Tyr Tyr Met Arg Asp Ser	Gln Ala Ala Lys
	290	295 300
Asp Leu Leu Tyr	Arg Arg Leu Arg Ala Leu Ala Asp Tyr	Glu Asn Ala
	305	310 315
Asn Lys Ala Leu	Asp Lys Ala Arg Thr Arg Asn Arg Glu	Val Arg Pro
	325	330 335
Ala Glu Ser His	Gln Gln Leu Cys Cys Gln Arg Phe Glu	Arg Leu Ser
	340	345 350

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Asp Ser Ala Lys Gln Glu Leu Met Asp Phe Lys Ser Arg Arg Val Ser
    355                      360                      365
Ser Phe Arg Lys Asn Leu Ile Glu Leu Ala Glu Leu Glu Lys His
    370                      375                      380
Ala Lys Ala Ser Thr Leu Ile Leu Arg Asn Thr Leu Val Ala Leu Lys
    385                      390                      395                      400
Gly Glu Pro

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<210> 114
<211> 806
<212> PRT
<213> Homo sapiens

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<400> 114
Met Ala Val Arg Ala Leu Lys Leu Leu Thr Thr Leu Leu Ala Val Val
    1                      5                      10                      15
Ala Ala Ala Ser Gln Ala Glu Val Glu Ser Glu Ala Gly Trp Gly Met
    20                      25                      30
Val Thr Pro Asp Leu Leu Phe Ala Glu Gly Thr Ala Ala Tyr Ala Arg
    35                      40                      45
Gly Asp Trp Pro Gly Val Val Leu Ser Met Glu Arg Ala Leu Arg Ser
    50                      55                      60
Arg Ala Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala
    65                      70                      75                      80
Ala Asp Phe Pro Trp Glu Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala
    85                      90                      95
Gln Ala Ser Gly Ala Ala Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly
    100                      105                      110
Leu Leu Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala
    115                      120                      125
Ala His Ser Leu Ser Glu Glu Met Glu Leu Glu Phe Arg Lys Arg Ser
    130                      135                      140
Pro Tyr Asn Tyr Leu Gln Val Ala Tyr Phe Lys Val Gln Thr Cys Leu
    145                      150                      155                      160
Glu Pro Gly Gly Arg Gly Pro Ser Gly Glu Arg Ser Val Ala Gly Asp
    165                      170                      175
Leu Arg Ser Leu Gly Asp Arg Gly Ser Val Arg Arg Glu Gly Lys Val
    180                      185                      190
Ala Ser Trp Leu Gly Ser Ser Pro Arg Ser Arg Gly Glu Leu Leu Pro
    195                      200                      205
Gly Arg Arg Pro Ser Ser Pro Ser Ser His Gly Gln Met Leu Thr Pro
    210                      215                      220
Lys Ile Asn Lys Leu Glu Lys Ala Val Ala Ala Ala His Thr Phe Phe
    225                      230                      235                      240
Val Gly Asn Pro Glu His Met Glu Met Gln Gln Asn Leu Asp Tyr Tyr
    245                      250                      255
Gln Thr Met Ser Gly Val Lys Glu Ala Asp Phe Lys Asp Leu Glu Thr
    260                      265                      270
Gln Pro His Met Gln Glu Phe Arg Leu Gly Val Arg Leu Tyr Ser Glu
    275                      280                      285
Glu Gln Pro Gln Glu Ala Val Pro His Leu Glu Ala Ala Leu Gln Glu
    290                      295                      300
Tyr Phe Val Ala Tyr Glu Glu Cys Arg Ala Leu Cys Glu Gly Pro Tyr
    305                      310                      315                      320
Asp Tyr Asp Gly Tyr Asn Tyr Leu Glu Tyr Asn Ala Asp Leu Phe Gln
    325                      330                      335
Ala Ile Thr Asp His Tyr Ile Gln Val Leu Asn Cys Lys Gln Asn Cys

```

340
 Val Thr Glu Leu Ala Ser His Pro Ser Arg Glu Lys Pro Phe Glu Asp
 355
 Phe Leu Pro Ser His Tyr Asn Tyr Leu Gln Phe Ala Tyr Tyr Asn Ile
 370
 Gly Asn Tyr Thr Gln Ala Val Glu Cys Ala Lys Thr Tyr Leu Leu Phe
 385
 Phe Pro Asn Asp Glu Val Met Asn Gln Asn Leu Ala Tyr Tyr Ala Ala
 405
 Met Leu Gly Glu Glu His Thr Arg Ser Ile Gly Pro Arg Glu Ser Ala
 420
 Lys Glu Tyr Arg Gln Arg Ser Leu Leu Glu Lys Glu Leu Leu Phe Phe
 435
 Ala Tyr Asp Val Phe Gly Ile Pro Phe Val Asp Pro Asp Ser Trp Thr
 450
 Pro Glu Glu Val Ile Pro Lys Arg Leu Gln Glu Lys Gln Lys Ser Glu
 465
 Arg Glu Thr Ala Val Arg Ile Ser Gln Glu Ile Gly Asn Leu Met Lys
 485
 Glu Ile Glu Thr Leu Val Glu Glu Lys Thr Lys Glu Ser Leu Asp Val
 500
 Ser Arg Leu Thr Arg Glu Gly Gly Pro Leu Leu Tyr Glu Gly Ile Ser
 515
 Leu Thr Met Asn Ser Lys Leu Leu Asn Gly Ser Gln Arg Val Val Met
 530
 Asp Gly Val Ile Ser Asp His Glu Cys Gln Glu Leu Gln Arg Leu Thr
 545
 Asn Val Ala Ala Thr Ser Gly Asp Gly Tyr Arg Gly Gln Thr Ser Pro
 565
 His Thr Pro Asn Glu Lys Phe Tyr Gly Val Thr Val Phe Lys Ala Leu
 580
 Lys Leu Gly Gln Glu Gly Lys Val Pro Leu Gln Ser Ala His Leu Tyr
 595
 Tyr Asn Val Thr Glu Lys Val Arg Arg Ile Met Glu Ser Tyr Phe Arg
 610
 Leu Asp Thr Pro Leu Tyr Phe Ser Tyr Ser His Leu Val Cys Arg Thr
 625
 Ala Ile Glu Glu Val Gln Ala Glu Arg Lys Asp Asp Ser His Pro Val
 645
 His Val Asp Asn Cys Ile Leu Asn Ala Glu Thr Leu Val Cys Val Lys
 660
 Glu Pro Pro Ala Tyr Thr Phe Arg Asp Tyr Ser Ala Ile Leu Tyr Leu
 675
 Asn Gly Asp Phe Asp Gly Gly Asn Phe Tyr Phe Thr Glu Leu Asp Ala
 690
 Lys Thr Val Thr Ala Glu Val Gln Pro Gln Cys Gly Arg Ala Val Gly
 705
 Phe Ser Ser Gly Thr Glu Asn Pro His Gly Val Lys Ala Val Thr Arg
 725
 Gly Gln Arg Cys Ala Ile Ala Leu Trp Phe Thr Leu Asp Pro Arg His
 740
 Ser Glu Arg Asp Arg Val Gln Ala Asp Asp Leu Val Lys Met Leu Phe
 755
 Ser Pro Glu Glu Met Asp Leu Ser Gln Glu Gln Pro Leu Asp Ala Gln
 770
 Gln Gly Pro Pro Glu Pro Ala Gln Glu Ser Leu Ser Gly Ser Glu Ser
 785
 Lys Pro Lys Asp Glu Leu
 805

<210> 115
 <211> 906
 <212> PRT
 <213> Homo sapiens

<400> 115
 Met Ala Leu Glu Gln Ala Leu Gln Ala Ala Arg Gln Gly Glu Leu Asp
 1 5 10 15
 Val Leu Arg Ser Leu His Ala Ala Gly Leu Leu Gly Pro Ser Leu Arg
 20 25 30
 Asp Pro Leu Asp Ala Leu Pro Val His His Ala Ala Arg Ala Gly Lys
 35 40 45
 Leu His Cys Leu Arg Phe Leu Val Glu Glu Ala Ala Leu Pro Ala Ala
 50 55 60
 Ala Arg Ala Arg Asn Gly Ala Thr Pro Ala His Asp Ala Ser Ala Thr
 65 70 75 80
 Gly His Leu Ala Cys Leu Gln Trp Leu Leu Ser Gln Gly Gly Cys Arg
 85 90 95
 Val Gln Ala Phe Pro Glu Ser Leu Gly Val Arg Ala Val Ala Leu Gly
 100 105 110
 Leu Val Pro Val Ser Cys Arg Asp Asn Gln Asp Lys Asp Asn Ser Gly
 115 120 125
 Ala Thr Val Leu His Leu Ala Ala Arg Phe Gly His Pro Glu Val Val
 130 135 140
 Asn Trp Leu Leu His His Gly Gly Gly Asp Pro Thr Ala Ala Thr Asp
 145 150 155 160
 Met Gly Ala Leu Pro Ile His Tyr Ala Ala Ala Lys Gly Asp Phe Pro
 165 170 175
 Ser Leu Arg Leu Leu Val Glu His Tyr Pro Glu Gly Val Asn Ala Gln
 180 185 190
 Thr Lys Asn Gly Ala Thr Pro Leu Tyr Leu Ala Cys Gln Glu Gly His
 195 200 205
 Leu Glu Val Thr Gln Tyr Leu Val Gln Glu Cys Gly Ala Asp Pro His
 210 215 220
 Ala Arg Ala His Asp Gly Met Thr Pro Leu His Ala Ala Ala Gln Met
 225 230 235 240
 Gly His Ser Pro Val Ile Val Trp Leu Val Ser Cys Thr Asp Val Ser
 245 250 255
 Leu Ser Glu Gln Asp Lys Asp Gly Ala Thr Ala Met His Phe Ala Ala
 260 265 270
 Ser Arg Gly His Thr Lys Val Leu Ser Trp Leu Leu Leu His Gly Gly
 275 280 285
 Glu Ile Ser Ala Asp Leu Trp Gly Gly Thr Pro Leu His Asp Ala Ala
 290 295 300
 Glu Asn Gly Glu Leu Glu Cys Cys Gln Ile Leu Val Val Asn Gly Ala
 305 310 315 320
 Glu Leu Asp Val Arg Asp Arg Asp Gly Tyr Thr Ala Ala Asp Leu Ser
 325 330 335
 Asp Phe Asn Gly His Ser His Cys Thr Arg Tyr Leu Arg Thr Val Glu
 340 345 350
 Asn Leu His Arg Gly Met Val Leu Ala Leu Gly Ala Ala Glu His Ser
 355 360 365
 Lys Ala Gln Arg Pro Glu Ala Ala Gly Gly Pro Glu Asp Glu Leu Pro
 370 375 380
 Pro Ala Lys Glu Ser Leu Glu Glu Asn Glu Trp Pro Ser Arg Gly Gln
 385 390 395 400
 Gly Leu Val Pro Ser Ala Pro Thr Ala Val Gly Gln Ser Val Glu His
 405 410 415
 Arg Val Leu Ser Arg Asp Pro Ser Ala Glu Leu Glu Ala Lys Gln Pro

Asp Ser Gly 420
 435 Met Ser Ser Pro Asn 425 Thr Thr Val Ser Val 430 Gln Pro Leu
 Asn Phe 440 Thr Ser Thr Leu Ser Asn 445 Tyr Asp Ser
 450 Ser Ser Ser His Ser Ser Ile Lys Gly Gln His 460 Pro Pro Cys Gly
 465 Ser Ser Ala Arg Ala Ala Asp Ile Gln Ser Tyr Met Asp Met Leu
 485 Leu Ser Pro Glu Leu Gly Leu Pro Arg Gly Thr Ile Gly Lys Pro Thr Pro
 500 505 510 515 520 525 530 535 540 545 550 555 560
 Pro Pro Pro Pro Ser Phe Pro Pro Pro Pro Pro Gly Thr
 Gln Leu Pro Pro Pro Pro Pro Gly Tyr Pro Ala Pro Lys Pro Pro Val
 575 580 585 590 595 600 605 610 615 620 625 630 635 640
 Gly Pro Gln Ala Ala Asp Ile Tyr Met Gln Thr Lys Asn Lys Leu Arg
 His Val Glu Thr Glu Ala Leu Lys Lys Glu Leu Ser Ser Cys Asp Gly
 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640
 His Asp Gly Leu Arg Arg Gln Asp Ser Ser Arg Lys Pro Arg Ala Phe
 Ser. Lys Gln Pro Ser Thr Gly Asp Tyr Tyr Arg Gln Leu Gly Arg Cys
 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905
 Pro Gly Glu Thr Leu Ala Ala Arg Pro Gly Met Ala His Ser Glu Glu
 Ala Ala Leu Leu Pro Gly Asn His Val Pro Asn Gly Cys Ala Ala Asp
 Pro Lys Ala Ser Arg Glu Leu Pro Pro Pro Pro Pro Pro Pro Pro
 Pro Leu Pro Glu Ala Ala Ser Ser Pro Pro Pro Ala Pro Pro Leu Pro
 Leu Glu Ser Ala Gly Pro Gly Cys Gly Gln Arg Arg Ser Ser Ser Ser
 Thr Gly Ser Thr Lys Ser Phe Asn Met Met Ser Pro Thr Gly Asp Asn
 Ser Glu Leu Leu Ala Glu Ile Lys Ala Gly Lys Ser Leu Lys Pro Thr
 Pro Gln Ser Lys Gly Leu Thr Thr Val Phe Ser Gly Ile Gly Gln Pro
 Ala Phe Gln Pro Asp Ser Pro Leu Pro Ser Val Ser Pro Ala Leu Ser
 Pro Val Arg Ser Pro Thr Pro Pro Ala Ala Gly Phe Gln Pro Leu Leu
 Asn Gly Ser Leu Val Pro Val Pro Pro Thr Thr Pro Ala Pro Gly Val
 Gln Leu Asp Val Glu Ala Leu Ile Pro Thr His Asp Glu Gln Gly Arg
 Pro Ile Pro Glu Trp Lys Arg Gln Val Met Val Arg Lys Met Gln Leu
 Lys Met Gln Glu Glu Glu Gln Arg Arg Lys Glu Glu Glu Glu
 Ala Arg Leu Ala Ser Met Pro Ala Trp Arg Arg Asp Leu Leu Arg Lys
 Lys Leu Glu Glu Glu Arg Glu Gln Lys Arg Lys Glu Glu Glu Arg Gln
 Lys Gln Glu Glu Leu Arg Arg Glu Lys Glu Gln Ser Glu Lys Leu Arg
 Thr Leu Gly Tyr Asp Glu Ser Lys Leu Ala Pro Trp Gln Arg Gln Val
 Ile Leu Lys Lys Gly Asp Ile Ala Lys Tyr

<210> 116
 <211> 848
 <212> PRT
 <213> Homo sapiens

<400> 116
 Met Ala Leu Glu Gln Ala Leu Gln Ala Ala Arg Gln Gly Glu Leu Asp
 1 5 10 15
 Val Leu Arg Ser Leu His Ala Ala Gly Leu Leu Gly Pro Ser Leu Arg
 20 25 30
 Asp Pro Leu Asp Ala Leu Pro Val His Ala Ala Arg Ala Gly Lys
 35 40 45
 Leu His Cys Leu Arg Phe Leu Val Glu Glu Ala Ala Leu Pro Ala Ala
 50 55 60
 Ala Arg Ala Arg Asn Gly Ala Thr Pro Ala His Asp Ala Ser Ala Thr
 65 70 75 80
 Gly His Leu Ala Cys Leu Gln Trp Leu Leu Ser Gln Gly Gly Cys Arg
 85 90 95
 Val Gln Ala Phe Pro Glu Ser Leu Gly Val Arg Ala Val Ala Leu Gly
 100 105 110
 Leu Val Pro Val Ser Cys Arg Asp Asn Gln Asp Lys Asp Asn Ser Gly
 115 120 125
 Ala Thr Val Leu His Leu Ala Ala Arg Phe Gly His Pro Glu Val Val
 130 135 140
 Asn Trp Leu Leu His His Gly Gly Gly Asp Pro Thr Ala Ala Thr Asp
 145 150 155 160
 Met Gly Ala Leu Pro Ile His Tyr Ala Ala Ala Lys Gly Asp Phe Pro
 165 170 175
 Ser Leu Arg Leu Leu Val Glu His Tyr Pro Glu Gly Val Asn Ala Gln
 180 185 190
 Thr Lys Asn Gly Ala Thr Pro Leu Tyr Leu Ala Cys Gln Glu Gly His
 195 200 205
 Leu Glu Val Thr Gln Tyr Leu Val Gln Glu Cys Gly Ala Asp Pro His
 210 215 220
 Ala Arg Ala His Asp Gly Met Thr Pro Leu His Ala Ala Ala Gln Met
 225 230 235 240
 Gly His Ser Pro Val Ile Val Trp Leu Val Ser Cys Thr Asp Val Ser
 245 250 255
 Leu Ser Glu Gln Asp Lys Asp Gly Ala Thr Ala Met His Phe Ala Ala
 260 265 270
 Ser Arg Gly His Thr Lys Val Leu Ser Trp Leu Leu Leu His Gly Gly
 275 280 285
 Glu Ile Ser Ala Asp Leu Trp Gly Gly Thr Pro Leu His Asp Ala Ala
 290 295 300
 Glu Asn Gly Glu Leu Glu Cys Cys Gln Ile Leu Val Val Asn Gly Ala
 305 310 315 320
 Glu Leu Asp Val Arg Asp Arg Asp Gly Tyr Thr Ala Ala Asp Leu Ser
 325 330 335
 Asp Phe Asn Gly His Ser His Cys Thr Arg Tyr Leu Arg Thr Val Glu
 340 345 350
 Asn Leu Ser Val Glu His Arg Val Leu Ser Arg Asp Pro Ser Ala Glu
 355 360 365
 Leu Glu Ala Lys Gln Pro Asp Ser Gly Met Ser Ser Pro Asn Thr Thr
 370 375 380
 Val Ser Val Gln Pro Leu Asn Phe Asp Leu Ser Ser Pro Thr Ser Thr
 385 390 395 400
 Leu Ser Asn Tyr Asp Ser Cys Ser Ser Ser Ser Ile Lys Gly

Gln	His	Pro	Pro	405	Cys	Gly	Leu	Ser	Ser	410	Ala	Arg	Ala	Ala	Asp	415	Ile	Gln
Ser	Tyr	Met	Met	420	Asp	Met	Leu	Asn	Pro	425	Glu	Leu	Gly	Leu	Pro	430	Arg	Gly
Ile	Gly	Gly	Lys	435	Pro	Thr	Pro	Pro	Pro	440	Pro	Pro	Pro	Ser	Phe	Pro	Pro	Pro
Pro	Pro	Pro	Pro	450	Pro	Gly	Thr	Gln	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Gly	Tyr	Pro
Ala	Pro	Lys	Pro	465	Pro	Val	Gly	Pro	Gln	Ala	Ala	Ala	Asp	Ile	Tyr	Met	480	Gln
Thr	Lys	Asn	Lys	485	Lys	Leu	Arg	His	Val	Glu	Thr	Glu	Ala	Leu	Lys	Lys	495	Glu
Leu	Ser	Ser	Cys	500	Asp	Gly	His	Asp	Gly	Leu	Arg	Arg	Arg	Gln	Asp	Ser	Ser	Ser
Arg	Lys	Pro	Arg	515	Ala	Phe	Ser	Lys	Gln	Pro	Ser	Thr	Thr	Gly	Asp	Tyr	Tyr	Tyr
Arg	Gln	Leu	Gly	530	Arg	Cys	Pro	Gly	Glu	Thr	Leu	Ala	Ala	Arg	Pro	Gly	560	Gly
Met	Ala	His	Ser	545	Glu	Glu	Ala	Ala	Leu	Leu	Pro	Gly	Asn	His	Val	Pro	575	Pro
Asn	Gly	Cys	Ala	580	Ala	Asp	Pro	Lys	Ala	Ser	Arg	Glu	Leu	Pro	Pro	Pro	590	Pro
Pro	Pro	Pro	Pro	595	Pro	Pro	Pro	Leu	Pro	600	Glu	Ala	Ala	Ser	Ser	Pro	Pro	Pro
Pro	Ala	Pro	Pro	610	Leu	Pro	Leu	Glu	Glu	Ser	Ala	Gly	Pro	Gly	Cys	Gly	Gln	Gln
Arg	Arg	Ser	Ser	625	Ser	Ser	Thr	Gly	Ser	Thr	Lys	Ser	Phe	Asn	Met	Met	640	Gly
Ser	Ser	Pro	Thr	645	Asp	Asn	Ser	Glu	Leu	Leu	Ala	Glu	Ile	Lys	Ala	Gly	655	Gly
Lys	Ser	Leu	Lys	660	Pro	Thr	Pro	Gln	Ser	Lys	Gly	Leu	Thr	Thr	Val	Phe	670	Phe
Ser	Gly	Ile	Gly	675	Gln	Pro	Ala	Phe	Gln	Pro	Asp	Ser	Pro	Leu	Pro	Ser	685	Ser
Val	Ser	Pro	Ala	690	Leu	Ser	Pro	Val	Arg	Ser	Pro	Thr	Thr	Pro	Ala	Ala	700	Ala
Gly	Phe	Gln	Pro	705	Leu	Leu	Asn	Gly	Ser	Leu	Val	Val	Pro	Val	Pro	Pro	715	Thr
Thr	Pro	Ala	Pro	720	Gly	Val	Gln	Leu	Asp	Val	Glu	Ala	Leu	Ile	Pro	Thr	730	Thr
His	Asp	Glu	Gln	740	Gly	Arg	Pro	Ile	Pro	Glu	Trp	Lys	Arg	Gln	Val	Met	745	Met
Val	Arg	Lys	Met	755	Gln	Leu	Lys	Met	Gln	Glu	Glu	Glu	Glu	Gln	Arg	Arg	760	Arg
Lys	Glu	Glu	Glu	770	Glu	Glu	Ala	Arg	Leu	Ala	Ser	Met	Pro	Ala	Trp	Arg	775	Arg
Arg	Asp	Leu	Leu	785	Arg	Lys	Lys	Lys	Leu	Glu	Glu	Glu	Arg	Glu	Gln	Lys	800	Arg
Lys	Glu	Glu	Glu	805	Arg	Gln	Lys	Gln	Glu	Glu	Leu	Arg	Arg	Glu	Lys	Glu	810	Glu
Gln	Ser	Glu	Lys	820	Leu	Arg	Thr	Leu	Gly	Tyr	Asp	Glu	Ser	Lys	Leu	Ala	825	Ala
Pro	Trp	Gln	Arg	835	Gln	Val	Ile	Leu	Lys	Lys	Gly	Asp	Ile	Ala	Lys	Tyr	840	Tyr

<211> 588
 <212> PRT
 <213> Homo sapiens

<400> 117
 Met Leu Arg Leu Gln Ala Pro Gly Pro Ala Gly Arg Pro Arg Cys Phe
 1 5 10 15
 Pro Leu Arg Ala Ala Arg Leu Phe Thr Arg Phe Ala Glu Ala Gly Arg
 20 25 30
 Ser Thr Leu Arg Leu Pro Ala His Asp Thr Pro Gly Ala Gly Ala Val
 35 40 45
 Gln Leu Leu Leu Ser Asp Cys Pro Pro Asp Arg Leu Arg Arg Phe Leu
 50 55 60
 Arg Thr Leu Arg Leu Lys Leu Ala Ala Ala Pro Gly Pro Gly Pro Ala
 65 70 75 80
 Ser Ala Arg Ala Gln Leu Leu Gly Pro Arg Pro Arg Asp Phe Val Thr
 85 90 95
 Ile Ser Pro Val Gln Pro Glu Glu Arg Arg Leu Arg Ala Ala Thr Arg
 100 105 110
 Val Pro Asp Thr Thr Leu Val Lys Arg Pro Val Glu Pro Gln Ala Gly
 115 120 125
 Ala Glu Pro Ser Thr Glu Ala Pro Arg Trp Pro Leu Pro Val Lys Arg
 130 135 140
 Leu Ser Leu Pro Ser Thr Lys Pro Gln Leu Ser Glu Glu Gln Ala Ala
 145 150 155 160
 Val Leu Arg Ala Ala Leu Lys Gly Gln Ser Ile Phe Phe Thr Gly Ser
 165 170 175
 Ala Gly Thr Gly Lys Ser Tyr Leu Leu Lys Arg Ile Leu Gly Ser Leu
 180 185 190
 Pro Pro Thr Gly Thr Glu Ala Thr Ala Ser Thr Gly Val Ala Ala Cys
 195 200 205
 His Ile Gly Gly Thr Thr Leu His Ala Phe Ala Gly Ile Gly Ser Gly
 210 215 220
 Gln Ala Pro Leu Ala Gln Cys Val Ala Leu Ala Gln Arg Pro Gly Val
 225 230 235 240
 Arg Gln Gly Trp Leu Asn Cys Gln Arg Leu Val Ile Asp Glu Ile Ser
 245 250 255
 Met Val Glu Ala Asp Leu Phe Asp Lys Leu Glu Ala Val Ala Arg Ala
 260 265 270
 Val Arg Gln Gln Asn Lys Pro Phe Gly Gly Ile Gln Leu Ile Ile Cys
 275 280 285
 Gly Asp Phe Leu Gln Leu Pro Pro Val Thr Lys Gly Ser Gln Pro Pro
 290 295 300
 Arg Phe Cys Phe Gln Ser Lys Ser Trp Lys Arg Gly Val Pro Val Thr
 305 310 315 320
 Leu Glu Leu Thr Lys Gly Gly Arg Gln Ala Asn Gln Thr Phe Phe Phe
 325 330 335
 Leu Leu Gln Ala Val Arg Leu Gly Arg Cys Ser Asp Glu Val Thr Arg
 340 345 350
 Gln Leu Gln Ala Thr Ala Ser His Lys Val Gly Arg Asp Gly Ile Val
 355 360 365
 Ala Thr Arg Leu Cys Thr His Gln Asp Asp Val Ala Leu Thr Asn Glu
 370 375 380
 Arg Arg Leu Gln Glu Leu Pro Gly Lys Val His Arg Phe Glu Ala Met
 385 390 395 400
 Asp Ser Asn Pro Glu Leu Ala Ser Thr Leu Asp Ala Gln Cys Pro Val
 405 410 415
 Ser Gln Leu Leu Gln Leu Lys Leu Gly Ala Gln Val Met Leu Val Lys
 420 425 430
 Asn Leu Ser Val Ser Arg Gly Leu Val Asn Gly Ala Arg Gly Val Val

```

      435      440      445
Val Gly Phe Glu Ala Glu Gly Arg Gly Leu Pro Gln Val Arg Phe Leu
  450      455      460
Cys Gly Val Thr Glu Val Ile His Ala Asp Arg Trp Thr Val Gln Ala
  465      470      475      480
Thr Gly Gly Gln Leu Leu Ser Arg Gln Gln Leu Pro Leu Gln Leu Ala
      485      490      495
Trp Ala Met Ser Ile His Lys Ser Gln Gly Met Thr Leu Asp Cys Val
      500      505      510
Glu Ile Ser Leu Gly Arg Val Phe Ala Ser Gly Gln Ala Tyr Val Ala
      515      520      525
Leu Ser Arg Ala Arg Ser Leu Gln Gly Leu Arg Val Leu Asp Phe Asp
      530      535      540
Pro Met Ala Val Arg Cys Asp Pro Arg Val Leu His Phe Tyr Ala Thr
  545      550      555      560
Leu Arg Arg Gly Arg Ser Leu Ser Leu Glu Ser Pro Asp Asp Asp Glu
      565      570      575
Ala Ala Ser Asp Gln Glu Asn Met Asp Pro Ile Leu
      580      585

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<210> 118
 <211> 526
 <212> PRT
 <213> Homo sapiens

```

      <400> 118
Met Leu Arg Leu Gln Ala Pro Gly Pro Ala Gly Arg Pro Arg Cys Phe
  1      5      10      15
Pro Leu Arg Ala Ala Arg Leu Phe Thr Arg Phe Ala Glu Ala Gly Arg
      20      25      30
Ser Thr Leu Arg Leu Pro Ala His Asp Thr Pro Gly Ala Gly Ala Val
      35      40      45
Gln Leu Leu Leu Ser Asp Cys Pro Pro Asp Arg Leu Arg Arg Phe Leu
      50      55      60
Arg Thr Leu Arg Leu Lys Leu Ala Ala Ala Pro Gly Pro Gly Pro Ala
      65      70      75      80
Ser Ala Arg Ala Gln Leu Leu Gly Pro Arg Pro Arg Asp Phe Val Thr
      85      90      95
Ile Ser Pro Val Gln Pro Glu Glu Arg Arg Leu Arg Ala Ala Thr Arg
      100      105      110
Val Pro Asp Thr Thr Leu Val Lys Arg Pro Val Glu Pro Gln Ala Gly
      115      120      125
Ala Glu Pro Ser Thr Glu Ala Pro Arg Trp Pro Leu Pro Val Lys Arg
      130      135      140
Leu Ser Leu Pro Ser Thr Lys Pro Gln Leu Ser Glu Glu Gln Ala Ala
      145      150      155      160
Val Leu Arg Ala Ala Leu Lys Gly Gln Ser Ile Phe Phe Thr Gly Ser
      165      170      175
Ala Gly Thr Gly Lys Ser Tyr Leu Leu Lys Arg Ile Leu Gly Ser Leu
      180      185      190
Pro Pro Thr Gly Thr Glu Ala Thr Ala Ser Thr Gly Val Ala Ala Cys
      195      200      205
His Ile Gly Gly Thr Thr Leu His Ala Phe Ala Gly Ile Gly Ser Gly
      210      215      220
Gln Ala Pro Leu Ala Gln Cys Val Ala Leu Ala Gln Arg Pro Gly Val
      225      230      235      240
Arg Gln Gly Trp Leu Asn Cys Gln Arg Leu Val Ile Asp Glu Ile Ser
      245      250      255

```

Met Val Glu Ala Asp Leu Phe Asp Lys Leu Glu Ala Val Ala Arg Ala
 260 265 270
 Val Arg Gln Gln Asn Lys Pro Phe Gly Gly Ile Gln Leu Ile Ile Cys
 275 280 285
 Gly Asp Phe Leu Gln Leu Pro Pro Val Thr Lys Gly Ser Gln Pro Pro
 290 295 300
 Arg Phe Cys Phe Gln Ser Ser Pro Asn Arg Cys Ser Asp Glu Val Thr
 305 310 315 320
 Arg Gln Leu Gln Ala Thr Ala Ser His Lys Val Gly Arg Asp Gly Ile
 325 330 335
 Val Ala Thr Arg Leu Cys Thr His Gln Asp Asp Val Ala Leu Thr Asn
 340 345 350
 Glu Arg Arg Leu Gln Glu Leu Pro Gly Lys Val His Arg Phe Glu Ala
 355 360 365
 Met Asp Ser Asn Pro Glu Leu Ala Ser Thr Leu Asp Ala Gln Cys Pro
 370 375 380
 Val Ser Gln Leu Leu Gln Leu Lys Leu Gly Ala Gln Val Met Leu Val
 385 390 395 400
 Lys Asn Leu Ser Val Ser Arg Gly Leu Val Asn Gly Ala Arg Gly Val
 405 410 415
 Val Val Gly Phe Glu Ala Glu Gly Arg Gly Leu Pro Gln Val Arg Phe
 420 425 430
 Leu Cys Gly Val Thr Glu Val Ile His Ala Asp Arg Trp Thr Val Gln
 435 440 445
 Ala Thr Gly Gly Gln Leu Leu Ser Arg Gln Gln Leu Pro Leu Gln Leu
 450 455 460
 Ala Trp Ala Met Ser Ile His Lys Ser Gln Gly Leu Arg Val Leu Asp
 465 470 475 480
 Phe Asp Pro Met Ala Val Arg Cys Asp Pro Arg Val Leu His Phe Tyr
 485 490 495
 Ala Thr Leu Arg Arg Gly Arg Ser Leu Ser Leu Glu Ser Pro Asp Asp
 500 505 510
 Asp Glu Ala Ala Ser Asp Gln Glu Asn Met Asp Pro Ile Leu
 515 520 525

<210> 119
 <211> 674
 <212> PRT
 <213> Homo sapiens

<400> 119
 Met Gln Thr Ser Ser Ser Arg Ser Val His Leu Ser Glu Trp Gln Lys
 1 5 10 15
 Asn Tyr Phe Ala Ile Thr Ser Gly Ile Cys Thr Gly Pro Lys Ala Asp
 20 25 30
 Ala Tyr Arg Ala Gln Ile Leu Arg Ile Gln Tyr Ala Trp Ala Asn Ser
 35 40 45
 Glu Ile Ser Gln Val Cys Ala Thr Lys Leu Phe Lys Lys Tyr Ala Glu
 50 55 60
 Lys Tyr Ser Ala Ile Ile Asp Ser Asp Asn Val Glu Ser Gly Leu Asn
 65 70 75 80
 Asn Tyr Ala Glu Asn Ile Leu Thr Leu Ala Gly Ser Gln Gln Thr Asp
 85 90 95
 Ser Asp Lys Trp Gln Ser Gly Leu Ser Ile Asn Asn Val Phe Lys Met
 100 105 110
 Ser Ser Val Gln Lys Met Met Gln Ala Gly Lys Lys Phe Lys Asp Ser
 115 120 125
 Leu Leu Glu Pro Ala Leu Ala Ser Val Val Ile His Lys Glu Ala Thr

130	Val	Phe	Asp	Leu	Pro	Lys	135	Phe	Ser	Val	Cys	Gly	140	Ser	Ser	Gln	Glu	Ser
145	Asp	Ser	Leu	Pro	Asn	150	Ala	His	Asp	Arg	Arg	155	Thr	Gln	Asp	160	Phe	
	Pro	Glu	Ser	Asn	Arg	165	Leu	Lys	Leu	Leu	Gln	170	Asn	Ala	Gln	Pro	Pro	Met
	Val	Thr	Asn	Thr	Ala	180	Arg	Thr	Cys	Pro	Thr	185	Phe	Ser	Ala	190	Val	Gly
	Glu	Ser	Ala	Thr	Ala	195	Lys	Phe	His	Val	Thr	200	Leu	Phe	Gly	Asn	Val	
	Lys	Lys	Glu	Asn	His	210	Ser	Ser	Ala	Lys	Glu	215	Asn	Ile	Gly	Leu	Asn	Val
	225	Phe	Leu	Ser	Asn	230	Gln	Ser	Cys	Phe	Pro	235	Ala	Ala	Cys	Glu	Asn	Pro
	Arg	Lys	Ser	Phe	Tyr	245	Gly	Ser	Gly	Thr	Ile	250	Asp	Ala	Leu	Ser	Asn	Pro
	1	Ile	Leu	Asn	Lys	260	Ala	Cys	Ser	Lys	Thr	265	Glu	Asp	Asn	Gly	Pro	Lys
	Asp	Ser	Ser	Leu	Pro	275	Thr	Phe	Lys	Thr	Ala	280	Lys	Glu	Gln	Leu	Trp	Val
	290	Asp	Gln	Gln	Lys	305	Lys	Tyr	His	Gln	Pro	310	Gln	Arg	Ala	Ser	Gly	Ser
	320	Tyr	Gly	Gly	Val	330	Lys	Ser	Leu	Gly	Ala	335	Ser	Arg	Ser	Arg	Gly	Ile
	340	Leu	Gly	Lys	Phe	355	Val	Pro	Pro	Ile	Pro	360	Lys	Gln	Asp	Gly	Gly	Glu
	370	Asn	Gly	Gly	Met	385	Gln	Cys	Lys	Pro	Tyr	390	Gly	Ala	Gly	Pro	Thr	Glu
	395	Ala	His	Pro	Val	405	Asp	Glu	Arg	Leu	Lys	410	Asn	Leu	Glu	Pro	Lys	Met
	420	Glu	Leu	Ile	Met	435	Asn	Glu	Ile	Met	Asp	440	His	Gly	Pro	Pro	Val	Asn
	450	385	Glu	Asp	Ile	465	Ala	Gly	Val	Glu	Phe	470	Ala	Lys	Ala	Thr	Ile	Lys
	480	Val	Val	Trp	Pro	495	Met	Leu	Arg	Pro	Asp	500	Ile	Phe	Thr	Gly	Leu	Arg
	510	Pro	Pro	Lys	Gly	525	Ile	Leu	Leu	Phe	Gly	530	Pro	Pro	Gly	Thr	Gly	Lys
	545	Leu	Ile	Gly	Lys	560	Cys	Ile	Ala	Ser	Gln	565	Ser	Gly	Ala	Thr	Phe	Phe
	575	Ile	Ser	Ala	Ser	590	Leu	Thr	Ser	Lys	Trp	600	Val	Val	Gly	Glu	Gly	Glu
	610	Met	Val	Arg	Ala	620	Leu	Phe	Ala	Val	Ala	630	Arg	Cys	Gln	Gln	Pro	Ala
	645	Ile	Phe	Ile	Asp	655	Glu	Asp	Leu	Leu	Ser	660	Gln	Arg	Gly	Arg	Gly	Asp
	675	Glu	His	Glu	Ser	690	Ser	Arg	Arg	Arg	Thr	700	Glu	Phe	Leu	Val	Gln	Leu
	715	Asp	Gly	Ala	Thr	730	Ser	Ser	Glu	Asp	Arg	740	Ile	Leu	Val	Val	Gly	Ala
	755	Thr	Asn	Arg	Pro	770	Gln	Glu	Ile	Asp	Glu	780	Ala	Ala	Arg	Arg	Arg	Leu
	795	Lys	Arg	Leu	Tyr	810	Ile	Pro	Leu	Pro	Glu	820	Ala	Ser	Ala	Arg	Lys	Gln
	835	Val	Ile	Asn	Leu	850	Met	Ser	Lys	Glu	Gln	860	Cys	Cys	Leu	Ser	Glu	Glu
	875	Ile	Glu	Gln	Ile	890	Val	Gln	Gln	Ser	Asp	900	Ala	Phe	Ser	Gly	Ala	Asp
	915	Thr	Gln	Leu	Cys	930	Arg	Glu	Ala	Ser	Leu	940	Gly	Pro	Ile	Arg	Ser	Leu

Thr Ala Asp Ile Ala Thr Ile Thr Pro Asp Gln Val Arg Pro Ile Ala
 625 630 635 640
 Tyr Ile Asp Phe Glu Asn Ala Phe Arg Thr Val Arg Pro Ser Val Ser
 645 650 655
 Pro Lys Asp Leu Glu Leu Tyr Glu Asn Trp Asn Lys Thr Phe Gly Cys
 660 665 670
 Gly Lys.

<210> 120
 <211> 333
 <212> PRT
 <213> Homo sapiens

<400> 120
 Met Asn Leu Ser Leu Val Leu Ala Ala Phe Cys Leu Gly Ile Ala Ser
 1 5 10 15
 Ala Val Pro Lys Phe Asp Gln Asn Leu Asp Thr Lys Trp Tyr Gln Trp
 20 25 30
 Lys Ala Thr His Arg Arg Leu Tyr Gly Ala Asn Glu Gly Trp Arg
 35 40 45
 Arg Ala Val Trp Glu Lys Asn Met Lys Met Ile Glu Leu His Asn Gly
 50 55 60
 Glu Tyr Ser Gln Gly Lys His Ser Phe Thr Met Ala Met Asn Ala Phe
 65 70 75 80
 Gly Asp Met Thr Asn Glu Glu Phe Arg Gln Val Met Asn Gly Phe Gln
 85 90 95
 Tyr Gln Lys His Arg Lys Gly Lys Gln Phe Gln Glu Arg Leu Leu Leu
 100 105 110
 Glu Ile Pro Thr Ser Val Asp Trp Arg Glu Lys Gly Tyr Met Thr Pro
 115 120 125
 Val Lys Asp Gln Gly Gln Cys Gly Ser Cys Trp Ala Phe Ser Ala Thr
 130 135 140
 Gly Ala Leu Glu Gly Gln Met Phe Trp Lys Thr Gly Lys Leu Ile Ser
 145 150 155 160
 Leu Asn Glu Gln Asn Leu Val Asp Cys Ser Gly Pro Gln Gly Asn Glu
 165 170 175
 Gly Cys Asn Gly Asp Phe Met Asp Asn Pro Phe Arg Tyr Val Gln Glu
 180 185 190
 Asn Gly Gly Leu Asp Ser Glu Glu Ser Tyr Pro Tyr Glu Ala Thr Glu
 195 200 205
 Glu Ser Cys Lys Tyr Asn Pro Lys Tyr Ser Val Ala Asn Asp Thr Gly
 210 215 220
 Phe Val Asp Ile Pro Lys Gln Glu Lys Ala Leu Met Lys Ala Val Ala
 225 230 235 240
 Thr Val Gly Pro Ile Ser Val Ala Ile Asp Ala Gly His Glu Ser Phe
 245 250 255
 Leu Phe Tyr Lys Glu Gly Ile Tyr Phe Glu Pro Asp Cys Ser Ser Glu
 260 265 270
 Asp Met Asp His Gly Val Leu Val Val Gly Tyr Gly Phe Glu Ser Thr
 275 280 285
 Glu Ser Asp Asn Asn Lys Tyr Trp Leu Val Lys Asn Ser Trp Gly Glu
 290 295 300
 Glu Trp Gly Met Gly Gly Tyr Val Lys Met Ala Lys Asp Arg Arg Asn
 305 310 315 320
 His Cys Gly Ile Ala Ser Ala Ala Ser Tyr Pro Thr Val
 325 330

<210> 121
 <211> 794
 <212> PRT
 <213> Homo sapiens

<400> 121
 Met Leu Cys Gly Arg Trp Arg Arg Cys Arg Arg Pro Pro Glu Glu Pro
 1 5 10 15
 Pro Val Ala Ala Gln Val Ala Ala Gln Val Ala Ala Pro Val Ala Leu
 20 25 30
 Pro Ser Pro Pro Thr Pro Ser Asp Gly Gly Thr Lys Arg Pro Gly Leu
 35 40 45
 Arg Ala Leu Lys Lys Met Gly Leu Thr Glu Asp Glu Asp Val Arg Ala
 50 55 60
 Met Leu Arg Gly Ser Arg Leu Arg Lys Ile Arg Ser Arg Thr Trp His
 65 70 75 80
 Lys Glu Arg Leu Tyr Arg Leu Gln Glu Asp Gly Leu Ser Val Trp Phe
 85 90 95
 Gln Arg Arg Ile Pro Arg Ala Pro Ser Gln His Ile Phe Phe Val Gln
 100 105 110
 His Ile Glu Ala Val Arg Glu Gly His Gln Ser Glu Gly Leu Arg Arg
 115 120 125
 Phe Gly Gly Ala Phe Ala Pro Ala Arg Cys Leu Thr Ile Ala Phe Lys
 130 135 140
 Gly Arg Arg Lys Asn Leu Asp Leu Ala Ala Pro Thr Ala Glu Glu Ala
 145 150 155 160
 Gln Arg Trp Val Arg Gly Leu Thr Lys Leu Arg Ala Arg Leu Asp Ala
 165 170 175
 Met Ser Gln Arg Glu Arg Leu Asp His Trp Ile His Ser Tyr Leu His
 180 185 190
 Arg Ala Asp Ser Asn Gln Asp Ser Lys Met Ser Phe Lys Glu Ile Lys
 195 200 205
 Ser Leu Leu Arg Met Val Asn Val Asp Met Asn Asp Met Tyr Ala Tyr
 210 215 220
 Leu Leu Phe Lys Glu Cys Asp His Ser Asn Asn Asp Arg Leu Glu Gly
 225 230 235 240
 Ala Glu Ile Glu Glu Phe Leu Arg Arg Leu Leu Lys Arg Pro Glu Leu
 245 250 255
 Glu Glu Ile Phe His Gln Tyr Ser Gly Glu Asp Arg Val Leu Ser Ala
 260 265 270
 Pro Glu Leu Leu Glu Phe Leu Glu Asp Gln Gly Glu Glu Gly Ala Thr
 275 280 285
 Leu Ala Arg Ala Gln Gln Leu Ile Gln Thr Tyr Glu Leu Asn Glu Thr
 290 295 300
 Ala Lys Gln His Glu Leu Met Thr Leu Asp Gly Phe Met Met Tyr Leu
 305 310 315 320
 Leu Ser Pro Glu Gly Ala Ala Leu Asp Asn Thr His Thr Cys Val Phe
 325 330 335
 Gln Asp Met Asn Gln Pro Leu Ala His Tyr Phe Ile Ser Ser Ser His
 340 345 350
 Asn Thr Tyr Leu Thr Asp Ser Gln Ile Gly Gly Pro Ser Ser Thr Glu
 355 360 365
 Ala Tyr Val Arg Tyr Cys Ser Arg Gly Ala Phe Ala Gln Gly Cys Arg
 370 375 380
 Cys Val Glu Leu Asp Cys Trp Glu Gly Pro Gly Gly Glu Pro Val Ile
 385 390 395 400
 Tyr His Gly His Thr Leu Thr Ser Lys Ile Leu Phe Arg Asp Val Val
 405 410 415

Gln Ala Val Arg Asp His Ala Phe Thr Leu Ser Pro Tyr Pro Val Ile
 420 425 430
 Leu Ser Leu Glu Asn His Cys Gly Leu Glu Gln Gln Ala Ala Met Ala
 435 440 445
 Arg His Leu Cys Thr Ile Leu Gly Asp Met Leu Val Thr Gln Ala Leu
 450 455 460
 Asp Ser Pro Asn Pro Glu Glu Leu Pro Ser Pro Glu Gln Leu Lys Gly
 465 470 475 480
 Arg Val Leu Val Lys Gly Lys Lys Leu Pro Ala Ala Arg Ser Glu Asp
 485 490 495
 Gly Arg Ala Leu Ser Asp Arg Glu Glu Glu Glu Asp Asp Glu Glu
 500 505 510
 Glu Glu Glu Glu Val Glu Ala Ala Ala Gln Arg Arg Leu Ala Lys Gln
 515 520 525
 Ile Ser Pro Glu Leu Ser Ala Leu Ala Val Tyr Cys His Ala Thr Arg
 530 535 540
 Leu Arg Thr Leu His Pro Ala Pro Asn Ala Pro Gln Pro Cys Gln Val
 545 550 555 560
 Ser Ser Leu Ser Glu Arg Lys Ala Lys Lys Leu Ile Arg Glu Ala Gly
 565 570 575
 Asn Ser Phe Val Arg His Asn Ala Arg Gln Leu Thr Arg Val Tyr Pro
 580 585 590
 Leu Gly Leu Arg Met Asn Ser Ala Asn Tyr Ser Pro Gln Glu Met Trp
 595 600 605
 Asn Ser Gly Cys Gln Leu Val Ala Leu Asn Phe Gln Thr Pro Gly Tyr
 610 615 620
 Glu Met Asp Leu Asn Ala Gly Arg Phe Leu Val Asn Gly Gln Cys Gly
 625 630 635 640
 Tyr Val Leu Lys Pro Ala Cys Leu Arg Gln Pro Asp Ser Thr Phe Asp
 645 650 655
 Pro Glu Tyr Pro Gly Pro Pro Arg Thr Thr Leu Ser Ile Gln Val Leu
 660 665 670
 Thr Ala Gln Gln Leu Pro Lys Leu Asn Ala Glu Lys Pro His Ser Ile
 675 680 685
 Val Asp Pro Leu Val Arg Ile Glu Ile His Gly Val Pro Ala Asp Cys
 690 695 700
 Ala Arg Gln Glu Thr Asp Tyr Val Leu Asn Asn Gly Phe Asn Pro Arg
 705 710 715 720
 Trp Gly Gln Thr Leu Gln Phe Gln Leu Arg Ala Pro Glu Leu Ala Leu
 725 730 735
 Val Arg Phe Val Val Glu Asp Tyr Asp Ala Thr Ser Pro Asn Asp Phe
 740 745 750
 Val Gly Gln Phe Thr Leu Pro Leu Ser Ser Leu Lys Gln Gly Tyr Arg
 755 760 765
 His Ile His Leu Leu Ser Lys Asp Gly Ala Ser Leu Ser Pro Ala Thr
 770 775 780
 Leu Phe Ile Gln Ile Arg Ile Gln Arg Ser
 785 790

<210> 122

<211> 286

<212> PRT

<213> Homo sapiens

<400> 122

Met Val Asp Leu Ser Val Ser Pro Asp Ser Leu Lys Pro Val Ser Leu
 1 5 10 15
 Thr Ser Ser Leu Val Phe Leu Met His Leu Leu Leu Leu Gln Pro Gly

[illegible]

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<210> 123
<211> 551
<212> PRT
<213> Homo sapiens
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<400> 123																	
Met	Thr	Ser	Pro	Gln	Ala	Asp	Phe	Cys	Leu	Gly	Thr	Ala	Leu	His	Ser		
1				5					10					15			
Trp	Gly	Leu	Trp	Phe	Thr	Glu	Glu	Gly	Ser	Pro	Ser	Thr	Met	Leu	Thr		
			20					25					30				
Gly	Ile	Ala	Val	Gly	Ala	Leu	Leu	Ala	Leu	Ala	Leu	Val	Gly	Val	Leu		
		35					40					45					
Ile	Leu	Phe	Met	Phe	Arg	Arg	Leu	Arg	Gln	Phe	Arg	Gln	Ala	Gln	Pro		
	50					55					60						
Thr	Pro	Gln	Tyr	Arg	Phe	Arg	Lys	Arg	Asp	Lys	Val	Met	Phe	Tyr	Gly		
65					70					75					80		
Arg	Lys	Ile	Met	Arg	Lys	Val	Thr	Thr	Leu	Pro	Asn	Thr	Leu	Val	Glu		
				85					90					95			
Asn	Thr	Ala	Leu	Pro	Arg	Gln	Arg	Ala	Arg	Lys	Arg	Thr	Lys	Val	Leu		
			100					105					110				
Ser	Leu	Ala	Lys	Arg	Ile	Leu	Arg	Phe	Lys	Lys	Glu	Tyr	Pro	Ala	Leu		
	115						120					125					
Gln	Pro	Lys	Glu	Pro	Pro	Pro	Ser	Leu	Leu	Glu	Ala	Asp	Leu	Thr	Glu		
	130					135					140						

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Phe Asp Val Lys Asn Ser His Leu Pro Ser Glu Val Leu Tyr Met Leu
145          150          155          160
Lys Asn Val Arg Val Leu Gly His Phe Glu Lys Pro Leu Phe Leu Glu
          165          170          175
Leu Cys Lys His Ile Val Phe Val Gln Leu Gln Glu Gly Glu His Val
          180          185          190
Phe Gln Pro Arg Glu Pro Asp Pro Ser Ile Cys Val Val Gln Asp Gly
          195          200          205
Arg Leu Glu Val Cys Ile Gln Asp Thr Asp Gly Thr Glu Val Val Val
          210          215          220
Lys Glu Val Leu Ala Gly Asp Ser Val His Ser Leu Leu Ser Ile Leu
          225          230          235          240
Asp Ile Ile Thr Gly His Ala Ala Pro Tyr Lys Thr Val Ser Val Arg
          245          250          255
Ala Ala Ile Pro Ser Thr Ile Leu Arg Leu Pro Ala Ala Phe His
          260          265          270
Gly Val Phe Glu Lys Tyr Pro Glu Thr Leu Val Arg Val Val Gln Ile
          275          280          285
Ile Met Val Arg Leu Gln Arg Val Thr Phe Leu Ala Leu His Asn Tyr
          290          295          300
Leu Gly Leu Thr Thr Glu Leu Phe Asn Ala Glu Ser Gln Ala Ile Pro
          305          310          315          320
Leu Val Ser Val Ala Ser Val Ala Ala Glu Lys Ala Lys Lys Gln Val
          325          330          335
Phe Tyr Gly Glu Glu Glu Arg Leu Lys Lys Pro Pro Arg Leu Gln Glu
          340          345          350
Ser Cys Asp Ser Gly Thr Val Leu His Gln Gly Gly Gln Cys Pro Ala
          355          360          365
Pro Glu Ser Gly Gly Ser Cys Ser His Cys Leu Arg Ser Pro Gln Val
          370          375          380
Ile Leu His Met Pro Glu Ala Thr Thr His Ile Pro Gly Ser Pro His
          385          390          395          400
Thr Ala Gln Val Thr Leu Gln Val Pro Gln Val Thr Ser His Ala Pro
          405          410          415
Gln Val Tyr Ser His Ala Pro Gln Val Pro Ser Arg Ala Ser Gly Pro
          420          425          430
Leu Thr Arg Ala Pro Gly His Leu Thr Cys Pro Pro Gly Leu Ile Arg
          435          440          445
Trp Pro Pro Arg Ser Pro His Val Ser Pro Ser Pro His Met Arg Ala
          450          455          460
Gly Cys Pro Gln Thr Ser Pro Gly Leu Ile Arg Cys Ala His Leu Leu
          465          470          475          480
Thr Cys Gly Leu Asp Val Leu Lys Pro Pro Thr Val Ser Leu Arg Val
          485          490          495
Pro Val Ser Ser His Glu Ala Arg Met Ser Ser Asp Arg Pro Arg Thr
          500          505          510
Leu His Pro Pro Phe Phe Ser Cys Ser Gln Asn Ser Pro Leu Gly Gln
          515          520          525
Val Pro Gly Gly Glu Trp Ala Ser Arg Asp Gly Leu Ser Pro Ala Val
          530          535          540
Leu Ser Ala Asn Arg Gly Ala
          545          550

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<210> 124

<211> 328

<212> PRT

<213> Homo sapiens

<400> 124
 Met Ala Leu Pro Ala Leu Gly Leu Asp Pro Trp Ser Leu Leu Gly Leu
 1 5 10 15
 Phe Leu Phe Gln Leu Leu Gln Leu Leu Leu Pro Thr Thr Thr Ala Gly
 20 25 30
 Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr Ala Gly Asp
 35 40 45
 Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly Leu Gln Asp Phe
 50 55 60
 Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr Leu Tyr Val Gly Ala
 65 70 75 80
 Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln Asp Pro Gly Val Pro Arg
 85 90 95
 Leu Lys Asn Met Ile Pro Trp Pro Ala Ser Asp Arg Lys Lys Ser Glu
 100 105 110
 Cys Ala Phe Lys Lys Lys Ser Asn Glu Thr Gln Cys Phe Asn Phe Ile
 115 120 125
 Arg Val Leu Val Ser Tyr Asn Val Thr His Leu Tyr Thr Cys Gly Thr
 130 135 140
 Phe Ala Phe Ser Pro Ala Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr
 145 150 155 160
 Leu Leu Pro Ile Ser Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser
 165 170 175
 Pro Phe Asp Pro Ala His Lys His Thr Ala Val Leu Val Asp Gly Met
 180 185 190
 Leu Tyr Ser Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu
 195 200 205
 Met Arg Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu
 210 215 220
 Arg Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr
 225 230 235 240
 Gln Val Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp Phe
 245 250 255
 Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys Asn Asp
 260 265 270
 Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr Phe Leu Lys
 275 280 285
 Ala Gln Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro Phe Asn Val Ile
 290 295 300
 Arg His Ala Val Leu Leu Pro Ala Asp Ser Pro Thr Ala Pro His Ile
 305 310 315 320
 Tyr Ala Val Phe Thr Ser Gln Trp
 325

<210> 125
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 125
 Met Met Glu Thr Met Gln Leu Lys Val Asn Arg His Pro Phe Cys Phe
 1 5 10 15
 Ser Val Lys Gly Gln Val Lys Met Leu Gln Leu Met Arg Leu Gly Leu
 20 25 30
 Arg Val Arg Gly Val Val Glu Ser Ala Cys Gly Arg Glu Met Trp Leu
 35 40 45
 Cys Gly Tyr Lys Gly
 50

<210> 126
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 126
 Met Ala Cys Val Ser Val Asp His Tyr Pro Ala Val Val Cys Ala His
 1 5 10 15
 Trp Gly Pro Cys Leu Arg Thr Ala Gly Arg Ala Arg Leu Val Cys Val
 20 25 30
 Ala Ile Trp Thr Leu Val Leu Leu Gln Thr Met Pro Leu Leu Met
 35 40 45
 Pro Met Thr Lys Pro Leu Val Gly Lys Leu Ala Cys Met Glu Tyr Ser
 50 55 60
 Ser Met Glu Ser Val Leu Gly Leu Pro Leu Met Val Leu Val Ala Phe
 65 70 75 80
 Ala Ile Gly Phe Cys Gly Pro Val Gly Ile Ile Leu Ser Cys Tyr Met
 85 90 95
 Lys Ile Thr Trp Lys Leu Cys Ser Thr Ala Gly Arg Thr Gln
 100 105 110

<210> 127
 <211> 212
 <212> PRT
 <213> Homo sapiens

<400> 127
 Met Leu Ser Ser Val Val Phe Trp Gly Leu Ile Ala Leu Ile Gly Thr
 1 5 10 15
 Ser Arg Gly Ser Tyr Pro Phe Ser His Ser Met Lys Pro His Leu His
 20 25 30
 Pro Arg Leu Tyr His Gly Cys Tyr Gly Asp Ile Met Thr Met Lys Thr
 35 40 45
 Ser Gly Ala Thr Cys Asp Ala Asn Ser Val Met Asn Cys Gly Ile Arg
 50 55 60
 Gly Ser Glu Met Phe Ala Glu Met Asp Leu Arg Ala Ile Lys Pro Tyr
 65 70 75 80
 Gln Thr Leu Ile Lys Glu Val Gly Gln Arg His Cys Val Asp Pro Ala
 85 90 95
 Val Ile Ala Ala Ile Ile Ser Arg Glu Ser His Gly Gly Ser Val Leu
 100 105 110
 Gln Asp Gly Trp Asp His Arg Gly Leu Lys Phe Gly Leu Met Gln Leu
 115 120 125
 Asp Lys Gln Thr Tyr His Pro Val Gly Ala Trp Asp Ser Lys Glu His
 130 135 140
 Leu Ser Gln Ala Thr Gly Ile Leu Thr Glu Arg Ile Lys Ala Ile Gln
 145 150 155 160
 Lys Lys Phe Pro Thr Trp Ser Val Ala Gln His Leu Lys Gly Gly Leu
 165 170 175
 Ser Ala Phe Lys Ser Gly Ile Glu Ala Ile Ala Thr Pro Ser Asp Ile
 180 185 190
 Asp Asn Asp Phe Val Asn Asp Ile Ile Ala Arg Ala Lys Phe Tyr Lys
 195 200 205
 Arg Gln Ser Phe

210

<210> 128
 <211> 267
 <212> PRT
 <213> Homo sapiens

<400> 128
 Met Ile Gly Asn Asn Met Ile Thr Cys Ile Asn Gly Ile Trp Thr Glu
 1 5 10 15
 Leu Pro Met Cys Val Ala Thr His Gln Leu Lys Arg Cys Lys Ile Ala
 20 25 30
 Gly Val Asn Ile Lys Thr Leu Leu Lys Leu Ser Gly Lys Glu Phe Asn
 35 40 45
 His Asn Ser Arg Ile Arg Tyr Arg Cys Ser Asp Ile Phe Arg Tyr Arg
 50 55 60
 His Ser Val Cys Ile Asn Gly Lys Trp Asn Pro Glu Val Asp Cys Thr
 65 70 75 80
 Glu Lys Arg Glu Gln Phe Cys Pro Pro Pro Glu Ile Pro Asn Ala
 85 90 95
 Gln Asn Met Thr Thr Thr Val Asn Tyr Gln Asp Gly Glu Lys Val Ala
 100 105 110
 Val Leu Cys Lys Glu Asn Tyr Leu Leu Pro Glu Ala Lys Glu Ile Val
 115 120 125
 Cys Lys Asp Gly Arg Trp Gln Ser Leu Pro Arg Cys Val Glu Ser Thr
 130 135 140
 Ala Tyr Cys Gly Pro Pro Pro Ser Ile Asn Asn Gly Asp Thr Thr Ser
 145 150 155 160
 Phe Pro Leu Ser Val Tyr Pro Pro Gly Ser Thr Val Thr Tyr Arg Cys
 165 170 175
 Gln Ser Phe Tyr Lys Leu Gln Gly Ser Val Thr Val Thr Cys Arg Asn
 180 185 190
 Lys Gln Trp Ser Glu Pro Pro Arg Cys Leu Asp Pro Cys Val Val Ser
 195 200 205
 Glu Glu Asn Met Asn Lys Asn Asn Ile Gln Leu Lys Trp Arg Asn Asp
 210 215 220
 Gly Lys Leu Tyr Ala Lys Thr Gly Asp Ala Val Glu Phe Gln Cys Lys
 225 230 235 240
 Phe Pro His Lys Ala Met Ile Ser Ser Pro Pro Phe Arg Ala Ile Cys
 245 250 255
 Gln Glu Gly Lys Phe Glu Tyr Pro Ile Cys Glu
 260 265

<210> 129
 <211> 1364
 <212> PRT
 <213> Homo sapiens

<400> 129
 Met Gly Pro Asp Glu Ala Thr Pro Pro Asp Leu Val Leu Pro Ala Trp
 1 5 10 15
 Arg Leu Arg His Gly Ala Phe Arg Thr Leu Val Thr Arg Glu Pro Gly
 20 25 30
 Ala Pro Arg Met Gly Ala Pro Ser Ala Cys Arg Thr Leu Val Leu Ala
 35 40 45

272

Leu Ala Ala Met Leu Val Val Pro Gln Ala Glu Thr Gln Gly Pro Val
 50 55 60
 Glu Pro Ser Trp Glu Asn Ala Gly His Thr Met Asp Gly Gly Ala Pro
 65 70 75 80
 Thr Ser Ser Pro Thr Arg Arg Val Ser Phe Val Pro Pro Val Thr Val
 85 90 95
 Phe Pro Ser Leu Ser Pro Leu Asn Pro Ala His Asn Gly Arg Val Cys
 100 105 110
 Ser Thr Trp Gly Asp Phe His Tyr Thr Phe Asp Gly Asp Val Phe
 115 120 125
 Arg Phe Pro Gly Leu Cys Asn Tyr Val Phe Ser Glu His Cys Arg Ala
 130 135 140
 Ala Tyr Glu Asp Phe Asn Val Gln Leu Arg Arg Gly Leu Val Gly Ser
 145 150 155 160
 Arg Pro Val Val Thr Arg Val Val Ile Lys Ala Gln Gly Leu Val Leu
 165 170 175
 Glu Ala Ser Asn Gly Ser Val Leu Ile Asn Gly Gln Arg Glu Glu Leu
 180 185 190
 Pro Tyr Ser Arg Thr Gly Leu Leu Val Glu Gln Ser Gly Asp Tyr Ile
 195 200 205
 Lys Val Ser Ile Arg Leu Val Leu Thr Phe Leu Trp Asn Gly Glu Asp
 210 215 220
 Ser Ala Leu Leu Glu Leu Asp Pro Lys Tyr Ala Asn Gln Thr Cys Gly
 225 230 235 240
 Leu Cys Gly Asp Phe Asn Gly Leu Pro Ala Phe Asn Glu Phe Tyr Ala
 245 250 255
 His Ser Glu Cys His Leu Asp Ala Arg Leu Thr Pro Leu Gln Phe Gly
 260 265 270
 Asn Leu Gln Lys Leu Asp Gly Pro Thr Glu Gln Cys Pro Asp Pro Leu
 275 280 285
 Pro Leu Pro Ala Gly Asn Cys Thr Asp Glu Glu Gly Ile Cys His Arg
 290 295 300
 Thr Leu Leu Gly Pro Ala Phe Ala Glu Cys His Ala Leu Val Asp Ser
 305 310 315 320
 Thr Ala Tyr Leu Ala Ala Cys Ala Gln Asp Leu Cys Arg Cys Pro Thr
 325 330 335
 Cys Pro Cys Ala Thr Phe Val Glu Tyr Ser Arg Gln Cys Ala His Ala
 340 345 350
 Gly Gly Gln Pro Arg Asn Trp Arg Cys Pro Glu Leu Cys Pro Arg Thr
 355 360 365
 Cys Pro Leu Asn Met Gln His Gln Glu Cys Gly Ser Pro Cys Thr Asp
 370 375 380
 Thr Cys Ser Asn Pro Gln Arg Ala Gln Leu Cys Glu Asp His Cys Val
 385 390 395 400
 Asp Gly Cys Phe Cys Pro Pro Gly Thr Val Leu Asp Asp Ile Thr His
 405 410 415
 Ser Gly Cys Leu Pro Leu Gly Gln Cys Pro Cys Thr His Gly Gly Arg
 420 425 430
 Thr Tyr Ser Pro Gly Thr Ser Phe Asn Thr Thr Cys Ser Ser Cys Thr
 435 440 445
 Cys Ser Gly Gly Leu Trp Gln Cys Gln Asp Leu Pro Cys Pro Gly Thr
 450 455 460
 Cys Ser Val Gln Gly Gly Ala His Ile Ser Thr Tyr Asp Glu Lys Leu
 465 470 475 480
 Tyr Asp Leu His Gly Asp Cys Ser Tyr Val Leu Ser Lys Lys Cys Ala
 485 490 495
 Asp Ser Ser Phe Thr Val Leu Ala Glu Leu Arg Lys Cys Gly Leu Thr
 500 505 510
 Asp Asn Glu Asn Cys Leu Lys Ala Val Thr Leu Ser Leu Asp Gly Gly
 515 520 525
 Asp Thr Ala Ile Arg Val Gln Ala Asp Gly Gly Val Phe Leu Asn Ser

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530          535          540
Ile Tyr Thr Gln Leu Pro Leu Ser Ala Ala Asn Ile Thr Leu Phe Thr
545          550          555          560
Pro Ser Ser Phe Phe Ile Val Val Gln Thr Gly Leu Gly Leu Gln Leu
          565          570          575
Leu Val Gln Leu Val Pro Leu Met Gln Val Phe Val Arg Leu Asp Pro
          580          585          590
Ala His Gln Gly Gln Met Cys Gly Leu Cys Gly Asn Phe Asn Gln Asn
          595          600          605
Gln Ala Asp Asp Phe Thr Ala Leu Ser Gly Val Val Glu Ala Thr Gly
          610          615          620
Ala Ala Phe Ala Asn Thr Trp Lys Ala Gln Ala Ala Cys Ala Asn Ala
          625          630          635
Arg Asn Ser Phe Glu Asp Pro Cys Ser Leu Ser Val Glu Asn Glu Asn
          645          650          655
Tyr Ala Arg His Trp Cys Ser Arg Leu Thr Asp Pro Asn Ser Ala Phe
          660          665          670
Ser Arg Cys His Ser Ile Ile Asn Pro Lys Pro Phe His Ser Asn Cys
          675          680          685
Met Phe Asp Thr Cys Asn Cys Glu Arg Ser Glu Asp Cys Leu Cys Ala
          690          695          700
Ala Leu Ser Ser Tyr Val His Ala Cys Ala Ala Lys Gly Val Gln Leu
          705          710          715          720
Ser Asp Trp Arg Asp Gly Val Cys Thr Lys Tyr Met Gln Asn Cys Pro
          725          730          735
Lys Ser Gln Arg Tyr Ala Tyr Val Val Asp Ala Cys Gln Pro Thr Cys
          740          745          750
Arg Gly Leu Ser Glu Ala Asp Val Thr Cys Ser Val Ser Phe Val Pro
          755          760          765
Val Asp Gly Cys Thr Cys Pro Ala Gly Thr Phe Leu Asn Asp Ala Gly
          770          775          780
Ala Cys Val Pro Ala Gln Lys Cys Pro Cys Tyr Ala His Gly Thr Val
          785          790          795          800
Leu Ala Pro Gly Glu Val Val His Asp Glu Gly Ala Val Cys Ser Cys
          805          810          815
Thr Gly Gly Lys Leu Ser Cys Leu Gly Ala Ser Leu Gln Lys Ser Thr
          820          825          830
Gly Cys Ala Ala Pro Met Val Tyr Leu Asp Cys Ser Asn Ser Ser Ala
          835          840          845
Gly Thr Pro Gly Ala Glu Cys Leu Arg Ser Cys His Thr Leu Asp Val
          850          855          860
Gly Cys Phe Ser Thr His Cys Val Ser Gly Cys Val Cys Pro Pro Gly
          865          870          875          880
Leu Val Ser Asp Gly Ser Gly Gly Cys Ile Ala Glu Glu Asp Cys Pro
          885          890          895
Cys Val His Asn Glu Ala Thr Tyr Lys Pro Gly Glu Thr Ile Arg Val
          900          905          910
Asp Cys Asn Thr Cys Thr Cys Arg Asn Arg Arg Trp Glu Cys Ser His
          915          920          925
Arg Leu Cys Leu Gly Thr Cys Val Ala Tyr Gly Asp Gly His Phe Ile
          930          935          940
Thr Phe Asp Gly Asp Arg Tyr Ser Phe Glu Gly Ser Cys Glu Tyr Ile
          945          950          955          960
Leu Ala Gln Asp Tyr Cys Gly Asp Asn Thr Thr His Gly Thr Phe Arg
          965          970          975
Ile Val Thr Glu Asn Ile Pro Cys Gly Thr Thr Gly Thr Thr Cys Ser
          980          985          990
Lys Ala Ile Lys Leu Phe Val Glu Ser Tyr Glu Leu Ile Leu Gln Glu
          995          1000          1005
Gly Thr Phe Lys Ala Val Ala Arg Gly Pro Gly Gly Asp Pro Pro Tyr
1010          1015          1020

```

Lys Ile Arg Tyr Met Gly Ile Phe Leu Val Ile Glu Thr His Gly Met
 1025 1030 1035 1040
 Ala Val Ser Trp Asp Arg Lys Thr Ser Val Phe Ile Arg Leu His Gln
 1045 1050 1055
 Asp Tyr Lys Gly Arg Val Cys Gly Leu Cys Gly Asn Phe Asp Asp Asn
 1060 1065 1070
 Ala Ile Asn Asp Phe Ala Thr Arg Ser Arg Ser Val Val Gly Asp Ala
 1075 1080 1085
 Leu Glu Phe Gly Asn Ser Trp Lys Leu Ser Pro Ser Cys Pro Asp Ala
 1090 1095 1100
 Leu Ala Pro Lys Asp Pro Cys Thr Ala Asn Pro Phe Arg Lys Ser Trp
 1105 1110 1115
 Ala Gln Lys Gln Cys Ser Ile Leu His Gly Pro Thr Phe Ala Ala Cys
 1125 1130 1135
 Arg Ser Gln Val Asp Ser Thr Lys Tyr Trp Glu Ala Cys Val Asn Asp
 1140 1145 1150
 Ala Cys Ala Cys Asp Ser Gly Gly Asp Cys Glu Cys Phe Cys Thr Ala
 1155 1160 1165
 Val Ala Ala Tyr Ala Gln Ala Cys His Asp Ala Gly Leu Cys Val Ser
 1170 1175 1180
 Trp Arg Thr Pro Asp Thr Cys Pro Leu Phe Cys Asp Phe Tyr Asn Pro
 1185 1190 1195 1200
 His Gly Gly Cys Glu Trp His Tyr Gln Pro Cys Gly Ala Pro Cys Leu
 1205 1210 1215
 Lys Thr Cys Arg Asn Pro Ser Gly His Cys Leu Val Asp Leu Pro Gly
 1220 1225 1230
 Leu Glu Gly Cys Tyr Pro Lys Cys Pro Pro Ser Gln Pro Phe Phe Asn
 1235 1240 1245
 Glu Asp Gln Met Lys Cys Val Ala Gln Cys Gly Cys Tyr Asp Lys Asp
 1250 1255 1260
 Gly Asn Tyr Tyr Asp Val Gly Ala Arg Val Pro Thr Ala Glu Asn Cys
 1265 1270 1275 1280
 Gln Ser Cys Asn Cys Thr Pro Ser Gly Ile Gln Cys Ala His Ser Leu
 1285 1290 1295
 Glu Ala Cys Thr Cys Thr Tyr Glu Asp Arg Thr Tyr Ser Tyr Gln Asp
 1300 1305 1310
 Val Ile Tyr Asn Thr Thr Asp Gly Leu Gly Ala Cys Leu Ile Ala Ile
 1315 1320 1325
 Cys Gly Ser Asn Gly Thr Ile Ile Arg Lys Ala Val Ala Cys Pro Gly
 1330 1335 1340
 Thr Pro Ala Thr Thr Pro Phe Thr Phe Thr Thr Ala Trp Val Pro His
 1345 1350 1355 1360
 Ser Thr Thr Ser

<210> 130
 <211> 1296
 <212> PRT
 <213> Homo sapiens

<400> 130
 Met Ser Thr Ser Ser Asp Ile Pro Ser Ser Pro Ser Ile Gln Asn Thr Glu
 1 5 10 15
 Thr Ser Ser Leu Val Ser Met Thr Ser Ala Thr Ile Pro Ser Val Arg
 20 25 30
 Pro Thr Phe Thr Ser Thr His Asn Thr Leu Thr Ser Ser Leu Leu Thr
 35 40 45
 Thr Phe Pro Gly Thr Tyr Ser Phe Ser Ser Met Ser Ala Ser Ser

	50					55					60				
Asp 65	Gly	Thr	Thr	His	Thr	Glu	Thr	Ile	Thr	Ser	Leu	Pro	Ala	Ser	
Ser	Thr	Leu	His	Thr	Thr	Ala	Glu	Ser	Thr	Thr	Ala	His	Thr	Thr	
Thr	Ser	Phe	Thr	Thr	Ser	Thr	Thr	Met	Glu	Ser	Pro	Ser	Ser	Val	
Ala	Thr	Thr	Ser	Thr	Gly	Gln	Thr	Thr	Phe	Ser	Ser	Ser	Thr	Ala	
Phe	Thr	Glu	Thr	Thr	Met	Leu	Thr	Pro	Thr	Thr	Asp	Phe	Ser	Glu	
Thr	Leu	Thr	Thr	Ala	Met	Thr	Ser	Thr	Pro	Pro	Ile	Thr	Ser	Ser	
Thr	Pro	Thr	Asn	Thr	Val	Thr	Ser	Met	Thr	Thr	Met	Thr	Ser	Trp	
Thr	Ala	Thr	Asn	Thr	Leu	Ser	Ser	Leu	Thr	Thr	Asn	Ile	Leu	Ser	
Thr	Pro	Val	Pro	Ser	Thr	Glu	Arg	Thr	Thr	Ser	His	Thr	Thr	Asn	
Asn	Pro	Val	Ser	Thr	Leu	Val	Thr	Thr	Leu	Pro	Thr	Thr	Ile	Thr	
Ser	Thr	Pro	Thr	Ser	Glu	Thr	Thr	Tyr	Pro	Ile	Ser	Ser	Thr	Ser	
Val	Thr	Glu	Ser	Thr	Thr	Glu	Ile	Thr	Tyr	Ser	Thr	Thr	Met	Thr	
Thr	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Leu	Thr	Ser	Pro	Leu	Ser	
Thr	Thr	Glu	Thr	Ala	Lys	Thr	Pro	Thr	Thr	Ile	Leu	Val	Thr	Thr	
Thr	Lys	Thr	Thr	Ser	His	Ser	Thr	Thr	Ser	Phe	Thr	Ser	Ser	Thr	
Tyr	Ser	Ser	Ala	Ser	Thr	His	Thr	Thr	Ala	Ile	Thr	Ser	Val	Pro	
Thr	Leu	Gly	Thr	Met	Val	Thr	Ser	Thr	Ser	Arg	Ile	Pro	Ser	Thr	
Ser	Thr	Ser	Ile	Pro	Thr	Ser	Gln	Pro	Lys	Thr	Val	Asn	Ser	Ser	
Gly	Gly	Ile	Thr	Gly	Ser	Leu	Pro	Met	Met	Thr	Asp	Leu	Thr	Ser	
Tyr	Thr	Val	Ser	Ser	Met	Ser	Ala	Ile	Pro	Thr	Thr	Val	Ile	Pro	
Ser	Leu	Thr	Val	Gln	Asn	Thr	Glu	Thr	Ser	Ile	Phe	Val	Ser	Met	
Ser	Ala	Thr	Thr	Pro	Ser	Gly	Arg	Pro	Thr	Phe	Thr	Ser	Thr	Val	
Thr	Pro	Thr	Arg	Ser	Leu	Leu	Thr	Ser	Thr	Phe	Pro	Thr	Thr	His	
Ser	Ser	Ser	Met	Ser	Glu	Ser	Ser	Ala	Gly	Thr	Thr	His	Thr	Glu	
Ile	Ser	Ser	Pro	Pro	Ala	Thr	Thr	Ser	Thr	Leu	His	Thr	Thr	Ala	
Ser	Thr	Pro	Ser	Cys	Thr	Thr	Thr	Thr	Ser	Phe	Ile	Thr	Ser	Thr	
Met	Glu	Pro	Leu	Ser	Thr	Ile	Val	Ala	Thr	Thr	Gly	Thr	Val	Lys	
Thr	Val	Thr	Ser	Ser	Ser	Thr	Ala	Thr	Phe	Arg	Glu	Thr	Thr	Leu	
Ser	Thr	Thr	Asp	Ile	Ser	Thr	Glu	Ser	Leu	Met	Thr	Ala	Met	Ser	
Thr	Thr	Arg	Leu	Thr	Ser	Ala	Ile	Thr	Ser	Lys	Thr	Thr	Leu	Ser	

Leu Lys Thr Thr Ala Ser Arg Pro Thr Ala Asn Ser Thr Leu Ser Ser
 545 550 555 560
 Leu Thr Ser Ser Ile Leu Ser Ser Thr Leu Val Pro Ser Thr Asp Met
 565 570 575
 Ile Thr Ser His Thr Thr Asn Leu Thr Arg Ser Ser Pro Leu Leu Ala
 580 585 590
 Thr Leu Pro Thr Thr Thr Ile Thr Arg Ser Thr Pro Thr Ser Glu Thr Thr
 595 600 605
 Tyr Pro Thr Ser Pro Thr Ser Thr Thr Val Lys Gly Ser Thr Thr Ser Ile
 610 615 620
 Arg Tyr Ser Thr Ser Met Thr Thr Gly Thr Leu Ser Met Glu Thr Ser Leu
 625 630 635 640
 Pro Pro Thr Ser Ser Ser Leu Pro Thr Thr Glu Thr Ala Thr Met Thr
 645 650 655
 Pro Thr Thr Thr Leu Ile Thr Thr Thr Pro Asn Thr Thr Ser His Ser
 660 665 670
 Thr Pro Ser Phe Thr Ser Ser Thr Ile Tyr Ser Thr Val Ser Thr Ser
 675 680 685
 Thr Thr Ala Ile Thr Ser His Phe Thr Thr Ser Glu Thr Ala Val Thr
 690 695 700
 Pro Thr Pro Val Thr Pro Ser Ser Leu Ser Thr Asp Ile Pro Thr Thr
 705 710 715 720
 Ser Leu Arg Thr Leu Thr Pro Ser Ser Val Gly Thr Ser Thr Ser Leu
 725 730 735
 Thr Thr Thr Thr Asp Phe Pro Ser Ile Pro Thr Asp Ile Ser Thr Leu
 740 745 750
 Pro Thr Arg Thr His Ile Ile Ser Ser Ser Pro Ser Ile Gln Ser Thr
 755 760 765
 Glu Thr Ser Ser Leu Val Gly Thr Thr Ser Pro Thr Met Ser Thr Val
 770 775 780
 Arg Met Thr Leu Arg Ile Thr Glu Asn Thr Pro Ile Ser Ser Phe Ser
 785 790 795 800
 Thr Ser Ile Val Val Ile Pro Glu Thr Pro Thr Gln Thr Pro Pro Val
 805 810 815
 Leu Thr Ser Ala Thr Gly Thr Gln Thr Ser Pro Ala Pro Thr Thr Val
 820 825 830
 Thr Phe Gly Ser Thr Asp Ser Ser Thr Ser Thr Leu His Thr Leu Thr
 835 840 845
 Pro Ser Thr Ala Leu Ser Thr Ile Val Ser Thr Ser Gln Val Pro Ile
 850 855 860
 Pro Ser Thr His Ser Ser Thr Leu Gln Thr Thr Pro Ser Thr Pro Ser
 865 870 875 880
 Leu Gln Thr Ser Leu Thr Ser Thr Ser Glu Phe Thr Thr Glu Ser Phe
 885 890 895
 Thr Arg Gly Ser Thr Ser Thr Asn Ala Ile Leu Thr Ser Phe Ser Thr
 900 905 910
 Ile Ile Trp Ser Ser Thr Pro Thr Ile Ile Met Ser Ser Ser Pro Ser
 915 920 925
 Ser Ala Ser Ile Thr Pro Val Phe Ser Thr Thr Ile His Ser Val Pro
 930 935 940
 Ser Ser Pro Tyr Ile Phe Ser Thr Glu Asn Val Gly Ser Ala Ser Ile
 945 950 955 960
 Thr Gly Phe Pro Ser Leu Ser Ser Ser Ala Thr Thr Ser Thr Ser Ser
 965 970 975
 Thr Ser Ser Ser Leu Thr Thr Ala Leu Thr Glu Ile Thr Pro Phe Ser
 980 985 990
 Tyr Ile Ser Leu Pro Ser Thr Thr Pro Cys Pro Gly Thr Ile Thr Ile
 995 1000 1005
 Thr Ile Val Pro Ala Ser Pro Thr Asp Pro Cys Val Glu Met Asp Pro
 1010 1015 1020
 Ser Thr Glu Ala Thr Ser Pro Pro Thr Pro Leu Thr Val Phe Pro

1025 1030 1035 1040
 Phe Thr Thr Glu Met Val Thr Cys Pro Thr Ser Ile Ser Ile Gln Thr
 1045 1050 1055
 Thr Leu Thr Thr Tyr Met Asp Thr Ser Ser Met Met Pro Glu Ser Glu
 1060 1065 1070
 Ser Ser Ile Ser Pro Asn Ala Ser Ser Ser Thr Gly Thr Gly Thr Val
 1075 1080 1085
 Pro Thr Asn Thr Val Phe Thr Ser Thr Arg Leu Pro Thr Ser Glu Thr
 1090 1095 1100
 Trp Leu Ser Asn Ser Ser Val Ile Pro Leu Pro Leu Pro Gly Val Ser
 1105 1110 1115 1120
 Thr Ile Pro Leu Thr Met Lys Pro Ser Ser Ser Leu Pro Thr Ile Leu
 1125 1130 1135
 Arg Thr Ser Ser Lys Ser Thr His Pro Ser Pro Pro Thr Thr Arg Thr
 1140 1145 1150
 Ser Glu Thr Pro Val Ala Thr Thr Gln Thr Pro Thr Thr Leu Thr Ser
 1155 1160 1165
 Arg Arg Thr Thr Arg Ile Thr Ser Gln Met Thr Thr Gln Ser Thr Leu
 1170 1175 1180
 Thr Thr Thr Ala Gly Thr Cys Asp Asn Gly Gly Thr Trp Glu Gln Gly
 1185 1190 1195 1200
 Gln Cys Ala Cys Leu Pro Gly Phe Ser Gly Asp Arg Cys Gln Leu Gln
 1205 1210 1215
 Thr Arg Cys Gln Asn Gly Gly Gln Trp Asp Gly Leu Lys Cys Gln Cys
 1220 1225 1230
 Pro Ser Thr Phe Tyr Gly Ser Ser Cys Glu Phe Ala Val Glu Gln Val
 1235 1240 1245
 Asp Leu Asp Ala Glu Asp Phe Cys Arg His Ala Gly Leu His Leu Gln
 1250 1255 1260
 Gly Cys Gly Asp Pro Val Pro Glu Glu Trp Gln His Arg Gly Gly Leu
 1265 1270 1275 1280
 Pro Gly Pro Ala Gly Asp Ala Leu Gln Pro Pro Ala Gly Glu Arg Val
 1285 1290 1295

<210> 131
 <211> 319
 <212> PRT
 <213> Homo sapiens

<400> 131
 Met Thr Arg Thr Tyr Glu Asn Phe Gln Tyr Leu Glu Asn Lys Val Lys
 1 5 10 15
 Val Gln Gly Phe Lys Asn Gly Pro Leu Pro Leu Gln Ser Leu Leu Gln
 20 25 30
 Arg Leu Cys Ser Gly Pro Cys His Leu Leu Leu Ser Leu Gly Leu Gly
 35 40 45
 Leu Leu Leu Leu Val Ile Ile Cys Val Val Gly Phe Gln Asn Ser Lys
 50 55 60
 Phe Gln Arg Asp Leu Val Thr Leu Arg Thr Asp Phe Ser Asn Phe Thr
 65 70 75 80
 Ser Asn Thr Val Ala Glu Ile Gln Ala Leu Thr Ser Gln Gly Ser Ser
 85 90 95
 Leu Glu Glu Thr Ile Ala Ser Leu Lys Ala Glu Val Glu Gly Phe Lys
 100 105 110
 Gln Glu Arg Gln Ala Gly Val Ser Glu Leu Gln Glu His Thr Thr Gln
 115 120 125

Lys Ala His Leu Gly His Cys Pro His Cys Pro Ser Val Cys Val Pro
 130 135 140
 Val His Ser Glu Met Leu Leu Arg Val Gln Gln Leu Val Gln Asp Leu
 145 150 155 160
 Lys Lys Leu Thr Cys Gln Val Ala Thr Leu Asn Asn Asn Gly Glu Glu
 165 170 175
 Ala Ser Thr Glu Gly Thr Cys Cys Pro Val Asn Trp Val Glu His Gln
 180 185 190
 Asp Ser Cys Tyr Trp Phe Ser His Ser Gly Met Ser Trp Ala Glu Ala
 195 200 205
 Glu Lys Tyr Cys Gln Leu Lys Asn Ala His Leu Val Val Ile Asn Ser
 210 215 220
 Arg Glu Glu Gln Asn Phe Val Gln Lys Tyr Leu Gly Ser Ala Tyr Thr
 225 230 235 240
 Trp Met Gly Leu Ser Asp Pro Glu Gly Ala Trp Lys Trp Val Asp Gly
 245 250 255
 Thr Asp Tyr Ala Thr Gly Phe Gln Asn Trp Lys Pro Gly Gln Pro Asp
 260 265 270
 Asp Trp Gln Gly His Gly Leu Gly Gly Glu Asp Cys Ala His Phe
 275 280 285
 His Pro Asp Gly Arg Trp Asn Asp Asp Val Cys Gln Arg Pro Tyr His
 290 295 300
 Trp Val Cys Glu Ala Gly Leu Gly Gln Thr Ser Gln Glu Ser His
 305 310 315

<210> 132
 <211> 590
 <212> PRT
 <213> Homo sapiens

<400> 132
 Met Lys Glu Val Thr Phe His Cys His Glu Gly Tyr Ile Leu His Gly
 1 5 10 15
 Ala Pro Lys Leu Thr Cys Gln Ser Asp Gly Asn Trp Asp Ala Glu Ile
 20 25 30
 Pro Leu Cys Lys Pro Val Asn Cys Gly Pro Pro Glu Asp Leu Ala His
 35 40 45
 Gly Phe Pro Asn Gly Phe Ser Phe Ile His Gly Gly His Ile Gln Tyr
 50 55 60
 Gln Cys Phe Pro Gly Tyr Lys Leu His Gly Asn Ser Ser Arg Arg Cys
 65 70 75 80
 Leu Ser Asn Gly Ser Trp Ser Gly Ser Ser Pro Ser Cys Leu Pro Cys
 85 90 95
 Arg Cys Ser Thr Pro Val Ile Glu Tyr Gly Thr Val Asn Gly Thr Asp
 100 105 110
 Phe Asp Cys Gly Lys Ala Ala Arg Ile Gln Cys Phe Lys Gly Phe Lys
 115 120 125
 Leu Leu Gly Leu Ser Glu Ile Thr Cys Glu Ala Asp Gly Gln Trp Ser
 130 135 140
 Ser Gly Phe His His Phe Glu His Thr Ser Cys Gly Ser Leu Pro Met
 145 150 155 160
 Ile Pro Asn Ala Phe Ile Ser Glu Thr Ser Ser Trp Lys Glu Asn Val
 165 170 175
 Ile Thr Tyr Ser Cys Arg Ser Gly Tyr Val Ile Gln Gly Ser Ser Asp
 180 185 190
 Leu Ile Cys Thr Glu Lys Gly Val Trp Ser Gln Pro Tyr Pro Val Cys
 195 200 205
 Glu Pro Leu Ser Cys Gly Ser Pro Ser Val Ala Asn Ala Val Ala

210 215 220
 Thr Gly Glu Ala His Thr Tyr Glu Ser Glu Val Lys Leu Arg Cys Leu
 225 230 235 240
 Glu Gly Tyr Thr Met Asp Thr Asp Thr Arg Ser Ile Thr Cys Gln Lys
 245 250 255
 Asp Gly Arg Trp Phe Pro Glu Arg Ile Ser Cys Ser Pro Lys Lys Cys
 260 265 270
 Pro Leu Pro Glu Asn Ile Thr His Ile Leu Val His Gly Asp Asp Phe
 275 280 285
 Ser Val Asn Arg Gln Val Ser Val Ser Cys Ala Glu Gly Tyr Thr Phe
 290 295 300
 Glu Gly Val Asn Ile Ser Val Cys Gln Leu Asp Gly Thr Trp Glu Pro
 305 310 315 320
 Pro Phe Ser Asp Glu Ser Cys Ser Pro Val Ser Cys Gly Lys Pro Glu
 325 330 335
 Ser Pro Glu His Gly Phe Val Val Gly Ser Lys Tyr Thr Phe Glu Ser
 340 345 350
 Thr Ile Ile Tyr Gln Cys Glu Pro Gly Tyr Glu Leu Glu Gly Asn Arg
 355 360 365
 Glu Arg Val Cys Gln Glu Asn Arg Gln Trp Ser Gly Gly Val Ala Ile
 370 375 380
 Cys Lys Glu Thr Arg Cys Glu Thr Pro Leu Glu Phe Leu Asn Gly Lys
 385 390 395 400
 Ala Asp Ile Glu Asn Arg Thr Thr Gly Pro Asn Val Val Tyr Ser Cys
 405 410 415
 Asn Arg Gly Tyr Ser Leu Glu Gly Pro Ser Glu Ala His Cys Thr Glu
 420 425 430
 Asn Gly Thr Trp Ser His Pro Val Pro Leu Cys Lys Pro Asn Pro Cys
 435 440 445
 Pro Val Pro Phe Val Ile Pro Glu Asn Ala Leu Leu Ser Glu Lys Glu
 450 455 460
 Phe Tyr Val Asp Gln Asn Val Ser Ile Lys Cys Arg Glu Gly Phe Leu
 465 470 475 480
 Leu Gln Gly His Gly Ile Ile Thr Cys Asn Pro Asp Glu Thr Trp Thr
 485 490 495
 Gln Thr Ser Ala Lys Cys Glu Lys Ile Ser Cys Gly Pro Pro Ala His
 500 505 510
 Val Glu Asn Ala Ile Ala Arg Gly Val His Tyr Gln Tyr Gly Asp Met
 515 520 525
 Ile Thr Tyr Ser Cys Tyr Ser Gly Tyr Met Leu Glu Gly Phe Leu Arg
 530 535 540
 Ser Val Cys Leu Glu Asn Gly Thr Trp Thr Ser Pro Pro Ile Cys Arg
 545 550 555 560
 Ala Val Cys Arg Phe Pro Cys Gln Asn Gly Gly Ile Cys Gln Arg Pro
 565 570 575
 Asn Ala Cys Ser Cys Pro Glu Gly Trp Asp Gly Ala Pro Leu
 580 585 590

<210> 133
 <211> 1544
 <212> PRT
 <213> Homo sapiens

<400> 133
 Met Ser Gly Thr Gln Ser Thr Ile Thr Asp Arg Phe Pro Leu Lys Lys
 1 5 10 15
 Pro Ile Arg His Gly Ser Ile Leu Asn Arg Glu Ser Pro Thr Asp Lys
 20 25 30

Lys Gln Lys Val Glu Arg Ile Ala Ser His Asp Phe Asp Pro Thr Asp
 35 40 45
 Ser Ser Ser Lys Lys Thr Lys Ser Ser Ser Glu Glu Ser Arg Ser Glu
 50 55 60
 Ile Tyr Gly Leu Val Gln Arg Cys Val Ile Ile Gln Lys Asp Asp Asn
 65 70 75 80
 Gly Phe Gly Leu Thr Val Ser Gly Asp Asn Pro Val Phe Val Gln Ser
 85 90 95
 Val Lys Glu Asp Gly Ala Ala Met Arg Ala Gly Val Gln Thr Gly Asp
 100 105 110
 Arg Ile Ile Lys Val Asn Gly Thr Leu Val Thr His Ser Asn His Leu
 115 120 125
 Glu Val Val Lys Leu Ile Lys Ser Gly Ser Tyr Val Ala Leu Thr Val
 130 135 140
 Gln Gly Arg Pro Pro Gly Ser Pro Gln Ile Pro Leu Ala Asp Ser Glu
 145 150 155 160
 Val Glu Pro Ser Val Ile Gly His Met Ser Pro Ile Met Thr Ser Pro
 165 170 175
 His Ser Pro Gly Ala Ser Gly Asn Met Glu Arg Ile Thr Ser Pro Val
 180 185 190
 Leu Met Gly Glu Glu Asn Asn Val Val His Asn Gln Lys Val Glu Ile
 195 200 205
 Leu Arg Lys Met Leu Gln Lys Glu Gln Glu Arg Leu Leu Lys Glu Ile Gln
 210 215 220
 Glu Asp Tyr Asn Arg Thr Pro Ala Gln Arg Leu Leu Lys Glu Ile Gln
 225 230 235 240
 Glu Ala Lys Lys His Ile Pro Gln Leu Gln Glu Gln Leu Ser Lys Ala
 245 250 255
 Thr Gly Ser Ala Gln Asp Gly Ala Val Val Thr Pro Ser Arg Pro Leu
 260 265 270
 Gly Asp Thr Leu Thr Val Ser Glu Ala Glu Thr Asp Pro Gly Asp Val
 275 280 285
 Leu Gly Arg Thr Asp Cys Ser Ser Gly Asp Ala Ser Arg Pro Ser Ser
 290 295 300
 Asp Asn Ala Asp Ser Pro Lys Ser Gly Pro Lys Glu Arg Ile Tyr Leu
 305 310 315 320
 Glu Glu Asn Pro Glu Lys Ser Glu Thr Ile Gln Asp Thr Asp Thr Gln
 325 330 335
 Ser Leu Val Gly Ser Pro Ser Thr Arg Ile Ala Pro His Ile Ile Gly
 340 345 350
 Ala Glu Asp Asp Asp Phe Gly Thr Glu His Glu Gln Ile Asn Gly Gln
 355 360 365
 Cys Ser Cys Phe Gln Ser Ile Glu Leu Leu Lys Ser Arg Pro Ala His
 370 375 380
 Leu Ala Val Phe Leu His His Val Val Ser Gln Phe Asp Pro Ala Thr
 385 390 395 400
 Leu Leu Cys Tyr Leu Tyr Ser Asp Leu Tyr Lys His Thr Asn Ser Lys
 405 410 415
 Glu Thr Arg Arg Ile Phe Leu Glu Phe His Gln Phe Phe Leu Asp Arg
 420 425 430
 Ser Ala His Leu Lys Val Ser Val Pro Asp Glu Met Ser Ala Asp Leu
 435 440 445
 Glu Lys Arg Arg Pro Glu Leu Ile Pro Glu Asp Leu His Arg His Tyr
 450 455 460
 Ile Gln Thr Met Gln Glu Arg Val His Pro Glu Val Gln Arg His Leu
 465 470 475 480
 Lys Asp Phe Arg Gln Lys Arg Ser Met Gly Leu Thr Leu Ala Glu Ser
 485 490 495
 Glu Leu Thr Lys Leu Asp Ala Glu Arg Asp Lys Asp Arg Leu Thr Leu
 500 505 510
 Glu Lys Glu Arg Thr Cys Ala Glu Gln Ile Val Ala Lys Ile Glu Glu

515				520				525							
Val	Leu	Met	Thr	Ala	Gln	Ala	Val	Glu	Glu	Asp	Lys	Ser	Ser	Thr	Met
530				535							540				
Gln	Tyr	Val	Ile	Leu	Met	Tyr	Met	Lys	His	Leu	Gly	Val	Lys	Val	Lys
545				550				555							560
Glu	Pro	Arg	Asn	Leu	Glu	His	Lys	Arg	Gly	Arg	Ile	Gly	Phe	Leu	Pro
			565					570							575
Lys	Ile	Lys	Gln	Ser	Met	Lys	Lys	Asp	Lys	Glu	Gly	Glu	Glu	Lys	Gly
			580					585							590
Lys	Arg	Arg	Gly	Phe	Pro	Ser	Ile	Leu	Gly	Pro	Pro	Arg	Arg	Pro	Ser
			595					600							
Arg	His	Asp	Asn	Ser	Ala	Ile	Gly	Arg	Ala	Met	Glu	Leu	Gln	Lys	Ala
			610				615				620				
Arg	His	Pro	Lys	His	Leu	Ser	Thr	Pro	Ser	Ser	Val	Ser	Pro	Glu	Pro
			625				630				635				640
Gln	Asp	Ser	Ala	Lys	Leu	Arg	Gln	Ser	Gly	Leu	Ala	Asn	Glu	Gly	Thr
			645							650					655
Asp	Ala	Gly	Tyr	Leu	Pro	Ala	Asn	Ser	Met	Ser	Ser	Val	Ala	Ser	Gly
			660					665							670
Ala	Ser	Phe	Ser	Gln	Glu	Gly	Gly	Lys	Glu	Asn	Asp	Thr	Gly	Ser	Lys
			675					680							
Gln	Val	Gly	Glu	Thr	Ser	Ala	Pro	Gly	Asp	Thr	Leu	Asp	Gly	Thr	Pro
			690				695				700				
Arg	Thr	Leu	Asn	Thr	Val	Phe	Val	Phe	Pro	Pro	Pro	Pro	Leu	Asp	Gln
			705				710				715				720
Val	Gln	Glu	Glu	Glu	Cys	Glu	Val	Glu	Arg	Val	Thr	Glu	His	Gly	Thr
			725					730							735
Pro	Lys	Pro	Phe	Arg	Lys	Phe	Asp	Ser	Val	Ala	Phe	Gly	Glu	Ser	Gln
			740					745							750
Ser	Glu	Asp	Glu	Gln	Phe	Glu	Asn	Asp	Leu	Glu	Thr	Asp	Pro	Pro	Asn
			755				760								
Trp	Gln	Gln	Leu	Val	Ser	Arg	Glu	Val	Leu	Leu	Gly	Leu	Lys	Pro	Cys
			770				775				780				
Glu	Ile	Lys	Arg	Gln	Glu	Val	Ile	Asn	Glu	Leu	Phe	Tyr	Thr	Glu	Arg
			785				790				795				800
Ala	His	Val	Arg	Thr	Leu	Lys	Val	Leu	Asp	Gln	Val	Phe	Tyr	Gln	Arg
			805							810					815
Val	Ser	Arg	Glu	Gly	Ile	Leu	Ser	Pro	Ser	Glu	Leu	Trp	Lys	Ile	Phe
			820					825							830
Ser	Asn	Leu	Glu	Asp	Ile	Leu	Gln	Leu	His	Ile	Gly	Leu	Asn	Glu	Gln
			835				840								845
Met	Lys	Ala	Val	Arg	Lys	Arg	Asn	Glu	Thr	Ser	Val	Ile	Asp	Gln	Ile
			850				855				860				
Gly	Glu	Asp	Leu	Leu	Thr	Trp	Phe	Ser	Gly	Pro	Gly	Glu	Glu	Lys	Leu
			865				870				875				880
Lys	His	Ala	Ala	Ala	Thr	Phe	Cys	Ser	Asn	Gln	Pro	Phe	Ala	Leu	Glu
			885					890							895
Met	Ile	Lys	Ser	Arg	Gln	Lys	Lys	Asp	Ser	Arg	Phe	Gln	Thr	Phe	Val
			900					905							910
Gln	Asp	Ala	Glu	Ser	Asn	Pro	Leu	Cys	Arg	Arg	Leu	Gln	Leu	Lys	Asp
			915				920								925
Ile	Ile	Pro	Thr	Gln	Met	Gln	Arg	Leu	Thr	Lys	Tyr	Pro	Leu	Leu	Leu
			930				935				940				
Asp	Asn	Ile	Ala	Lys	Tyr	Thr	Glu	Trp	Pro	Thr	Glu	Arg	Glu	Lys	Val
			945				950				955				960
Lys	Lys	Ala	Ala	Asp	His	Cys	Arg	Gln	Ile	Leu	Asn	Tyr	Val	Asn	Gln
			965							970					975
Ala	Val	Lys	Glu	Ala	Glu	Asn	Lys	Gln	Arg	Leu	Glu	Asp	Tyr	Gln	Arg
			980					985							990
Arg	Leu	Asp	Thr	Ser	Ser	Leu	Lys	Leu	Ser	Glu	Tyr	Pro	Asn	Val	Glu
			995				1000								1005

Glu Leu Arg Asn Leu Asp Leu Thr Lys Arg Lys Met Ile His Glu Gly
 1010 1015 1020
 Pro Leu Val Trp Lys Val Asn Arg Asp Lys Thr Ile Asp Leu Tyr Thr
 1025 1030 1035 1040
 Leu Leu Leu Glu Asp Ile Leu Val Leu Leu Gln Lys Gln Asp Asp Arg
 1045 1050 1055
 Leu Val Leu Arg Cys His Ser Lys Ile Leu Ala Ser Thr Ala Asp Ser
 1060 1065 1070
 Lys His Thr Phe Ser Pro Val Ile Lys Leu Ser Thr Val Leu Val Arg
 1075 1080 1085
 Gln Gly Ala Thr Asp Asn Lys Ala Leu Phe Val Ile Ser Met Ser Asp
 1090 1095 1100
 Asn Gly Ala Gln Ile Tyr Glu Leu Val Ala Gln Thr Val Ser Glu Lys
 1105 1110 1115 1120
 Thr Val Trp Gln Asp Leu Ile Cys Arg Met Ala Ala Ser Val Lys Glu
 1125 1130 1135
 Gln Ser Thr Lys Pro Ile Pro Leu Pro Gln Ser Thr Pro Gly Glu Gly
 1140 1145 1150
 Asp Asn Asp Glu Glu Asp Pro Ser Lys Leu Lys Glu Glu Gln His Gly
 1155 1160 1165
 Ile Ser Val Thr Gly Leu Gln Ser Pro Asp Arg Asp Leu Gly Leu Glu
 1170 1175 1180
 Ser Thr Leu Ile Ser Ser Lys Pro Gln Ser His Ser Leu Ser Thr Ser
 1185 1190 1195 1200
 Gly Lys Ser Glu Val Arg Asp Leu Phe Val Ala Glu Arg Gln Phe Ala
 1205 1210 1215
 Lys Glu Gln His Thr Asp Gly Thr Leu Lys Glu Val Gly Glu Asp Tyr
 1220 1225 1230
 Gln Ile Ala Ile Pro Asp Ser His Leu Pro Val Ser Glu Glu Arg Trp
 1235 1240 1245
 Ala Leu Asp Ala Leu Arg Asn Leu Gly Leu Leu Lys Gln Leu Leu Val
 1250 1255 1260
 Gln Gln Leu Gly Leu Thr Glu Lys Ser Val Gln Glu Asp Trp Gln His
 1265 1270 1275 1280
 Phe Pro Arg Tyr Arg Thr Ala Ser Gln Gly Pro Gln Thr Asp Ser Val
 1285 1290 1295
 Ile Gln Asn Ser Glu Asn Ile Lys Ala Tyr His Ser Gly Glu Gly His
 1300 1305 1310
 Met Pro Phe Arg Thr Gly Thr Gly Asp Ile Ala Thr Cys Tyr Ser Pro
 1315 1320 1325
 Arg Thr Ser Thr Glu Ser Phe Ala Pro Arg Asp Ser Val Gly Leu Ala
 1330 1335 1340
 Pro Gln Asp Ser Gln Ala Ser Asn Ile Leu Val Met Asp His Met Ile
 1345 1350 1355 1360
 Met Thr Pro Glu Met Pro Thr Met Glu Pro Glu Gly Gly Leu Asp Asp
 1365 1370 1375
 Ser Gly Glu His Phe Phe Asp Ala Arg Glu Ala His Ser Asp Glu Asn
 1380 1385 1390
 Pro Ser Glu Gly Asp Gly Ala Val Asn Lys Glu Glu Lys Asp Val Asn
 1395 1400 1405
 Leu Arg Ile Ser Gly Asn Tyr Leu Ile Leu Asp Gly Tyr Asp Pro Val
 1410 1415 1420
 Gln Glu Ser Ser Thr Asp Glu Glu Val Ala Ser Ser Leu Thr Leu Gln
 1425 1430 1435 1440
 Pro Met Thr Gly Ile Pro Ala Val Glu Ser Thr His Gln Gln Gln His
 1445 1450 1455
 Ser Pro Gln Asn Thr His Ser Asp Gly Ala Ile Ser Pro Phe Thr Pro
 1460 1465 1470
 Glu Phe Leu Val Gln Gln Arg Trp Gly Ala Met Glu Tyr Ser Cys Phe
 1475 1480 1485
 Glu Ile Gln Ser Pro Ser Ser Cys Ala Asp Ser Gln Ser Gln Ile Met

1490 1495 1500
 Glu Tyr Ile His Lys Ile Glu Ala Asp Leu Glu His Leu Lys Lys Val
 1505 1510 1515 1520
 Glu Glu Ser Tyr Thr Ile Leu Cys Gln Arg Leu Ala Gly Ser Ala Leu
 1525 1530 1535
 Thr Asp Lys His Ser Asp Lys Ser
 1540

<210> 134
 <211> 486
 <212> PRT
 <213> Homo sapiens

<400> 134
 Met Met Gly Gln Asp Lys Ile Gln Gly His Ser Val Ile Ser Glu Glu
 1 5 10 15
 Ser Asp Gly Lys Leu Ile Glu Asp Ser Leu Ile Gln Leu Arg Cys His
 20 25 30
 Phe Thr Trp Lys Leu Leu Ile Glu Ala Pro Glu Ile Pro Asp Leu Glu
 35 40 45
 Asn Arg Ile Trp Glu Glu Ile Gln Phe Leu Asp Thr Lys Tyr Asn Val
 50 55 60
 Gly Ile His Asn Leu Leu Ala Tyr Val Lys His Leu Lys Gly Gln Asn
 65 70 75
 Glu Glu Ala Leu Val Ser Leu Lys Lys Ala Glu Asp Leu Ile Gln Lys
 85 90 95
 Glu His Ala Asn Gln Ala Asp Ile Arg Ser Leu Val Thr Trp Gly Asn
 100 105 110
 Phe Ala Trp Val Tyr Tyr His Met Gly Arg Leu Ala Glu Ala Gln Thr
 115 120 125
 Tyr Leu Asp Lys Val Glu Asn Thr Cys Lys Lys Phe Ala Asn Pro Ser
 130 135 140
 Arg Tyr Arg Met Glu Cys Pro Glu Val Asp Cys Glu Gly Trp Ala
 145 150 155
 Leu Ala Lys Cys Gly Gly Lys Asn Tyr Glu Arg Ala Lys Thr Cys Phe
 165 170 175
 Glu Lys Ala Leu Glu Gly Asn Pro Glu Asn Pro Glu Phe Asn Thr Gly
 180 185 190
 Tyr Ala Ile Thr Val Tyr Arg Leu Asp Lys Phe Asn Thr Ala Ser Gly
 195 200 205
 Arg Asn Lys Ala Phe Ser Leu His Val Leu Lys Arg Ala Val Arg Leu
 210 215 220
 Asn Pro Asp Asp Val Tyr Ile Arg Val Leu Leu Ala Leu Lys Leu Gln
 225 230 235
 Asp Glu Gly Gln Glu Ala Glu Gly Glu Lys Tyr Ile Glu Glu Ala Leu
 245 250 255
 Thr Ser Ile Ser Ser Gln Ala Tyr Val Phe Gln Tyr Ala Ala Lys Phe
 260 265 270
 Tyr Arg Arg Lys Gly Ser Val Asp Lys Ala Leu Glu Leu Leu Lys Met
 275 280 285
 Ala Leu Glu Thr Thr Pro Thr Ser Ala Phe Leu His His Gln Met Gly
 290 295 300
 Leu Cys Tyr Arg Ala Gln Met Ile Gln Ile Lys Glu Ala Thr Asn Trp
 305 310 315
 Gln Pro Arg Gly Gln Asp Arg Glu Thr Val Asp Arg Leu Val Gln Leu
 325 330 335
 Ala Ile Cys Lys Phe Glu Lys Thr Ile Met Leu Lys Arg Thr Phe Glu
 340 345 350

```

Met Ala Tyr Val Asp Leu Ala Glu Thr Tyr Ala Glu Ile Gly His His
    355          360          365
Arg Lys Ala Glu Glu His Phe Gln Lys Gly Leu Arg Met Lys Ile Phe
    370          375          380
Glu Asp Gln Leu Lys Gln Glu Ile His Tyr His Tyr Gly Arg Phe Gln
    385          390          395
Glu His His Gly Lys Ser Gln Asp Lys Ala Ile Thr His Tyr Leu Lys
    405          410          415
Gly Leu Lys Ile Glu Lys Met Ser His Ser Arg Glu Lys Leu Leu Asn
    420          425          430
Ala Leu Glu Lys Leu Ala Lys Arg Cys Ile His Gln Asn Val Arg Val
    435          440          445
Val Glu Ser Val Ser Leu Leu Gly Leu Ile His Lys Leu Lys Gly Glu
    450          455          460
Val Ser Asp Ala Leu Leu Cys Tyr Glu Arg Ala Leu Arg Leu Ala Ala
    465          470          475
Asp Leu Asn Pro Ile Phe
    485

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<210> 135
<211> 403
<212> PRT
<213> Homo sapiens

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<400> 135
Met Glu Thr Tyr Ala Glu Val Gly Lys Glu Gly Lys Pro Ser Cys Ala
    1          5          10          15
Ser Val Asp Leu Gln Gly Asp Ser Ser Leu Gln Val Glu Ile Ser Asp
    20          25          30
Ala Val Ser Glu Arg Asp Lys Val Lys Phe Thr Val Gln Thr Lys Ser
    35          40          45
Cys Leu Pro His Phe Ala Gln Thr Glu Phe Ser Val Val Arg Gln His
    50          55          60
Glu Glu Phe Ile Trp Leu His Asp Ala Tyr Val Glu Asn Glu Glu Tyr
    65          70          75          80
Ala Gly Leu Ile Ile Pro Pro Ala Pro Pro Arg Pro Asp Phe Glu Ala
    85          90          95
Ser Arg Glu Lys Leu Gln Lys Leu Gly Glu Gly Asp Ser Ser Val Thr
    100          105          110
Arg Glu Glu Phe Ala Lys Met Lys Gln Glu Leu Glu Ala Glu Tyr Leu
    115          120          125
Ala Ile Phe Lys Lys Thr Val Ala Met His Glu Val Phe Leu Gln Arg
    130          135          140
Leu Ala Ala His Pro Thr Leu Arg Arg Asp His Asn Phe Phe Val Phe
    145          150          155          160
Leu Glu Tyr Gly Gln Asp Leu Ser Val Arg Gly Lys Asn Arg Lys Glu
    165          170          175          180
Leu Leu Gly Gly Phe Leu Arg Asn Ile Val Lys Ser Ala Asp Glu Ala
    180          185          190          195
Leu Ile Thr Gly Met Ser Gly Leu Lys Glu Val Asp Asp Phe Phe Glu
    195          200          205          210
His Glu Arg Thr Phe Leu Leu Glu Tyr His Thr Arg Ile Arg Asp Ala
    210          215          220          225
Cys Leu Arg Ala Asp Arg Val Met Arg Ala His Lys Cys Leu Ala Asp
    225          230          235          240
Asp Tyr Ile Pro Ile Ser Ala Ala Leu Ser Ser Leu Gly Thr Gln Glu
    245          250          255
Val Asn Gln Leu Arg Thr Ser Phe Leu Lys Leu Ala Glu Leu Phe Glu

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Arg	Leu	Arg	Lys	Leu	Glu	Gly	Arg	Val	Ala	Ser	Asp	Glu	Asp	Leu	Lys
		275					280					285			
Leu	Ser	Asp	Met	Leu	Arg	Tyr	Tyr	Met	Arg	Asp	Ser	Gln	Ala	Ala	Lys
		290				295					300				
Asp	Leu	Leu	Tyr	Arg	Arg	Leu	Arg	Ala	Leu	Ala	Asp	Tyr	Glu	Asn	Ala
305					310					315				320	
Asn	Lys	Ala	Leu	Asp	Lys	Ala	Arg	Thr	Arg	Asn	Arg	Glu	Val	Arg	Pro
			325					330						335	
Ala	Glu	Ser	His	Gln	Gln	Leu	Cys	Cys	Gln	Arg	Phe	Glu	Arg	Leu	Ser
			340					345					350		
Asp	Ser	Ala	Lys	Gln	Glu	Leu	Met	Asp	Phe	Lys	Ser	Arg	Arg	Val	Ser
			355				360					365			
Ser	Phe	Arg	Lys	Asn	Leu	Ile	Glu	Leu	Ala	Glu	Leu	Glu	Leu	Lys	His
		370				375					380				
Ala	Lys	Ala	Ser	Thr	Leu	Ile	Leu	Arg	Asn	Thr	Leu	Val	Ala	Leu	Lys
385					390					395				400	
Gly	Glu	Pro													

<210> 136
 <211> 273
 <212> PRT
 <213> Homo sapiens

Met	Thr	Leu	Ser	Pro	Leu	Leu	Leu	Phe	Leu	Pro	Pro	Leu	Leu	Leu	Leu
1				5					10					15	
Leu	Asp	Val	Pro	Thr	Ala	Ala	Val	Gln	Ala	Ser	Pro	Leu	Gln	Ala	Leu
			20					25					30		
Asp	Phe	Phe	Gly	Asn	Gly	Pro	Pro	Val	Asn	Tyr	Lys	Thr	Gly	Asn	Leu
		35					40					45			
Tyr	Leu	Arg	Gly	Pro	Leu	Lys	Lys	Ser	Asn	Ala	Pro	Leu	Val	Asn	Val
		50				55					60				
Thr	Leu	Tyr	Tyr	Glu	Ala	Leu	Cys	Gly	Gly	Cys	Arg	Ala	Phe	Leu	Ile
65				70					75					80	
Arg	Glu	Leu	Phe	Pro	Thr	Trp	Leu	Leu	Val	Met	Glu	Ile	Leu	Asn	Val
			85						90					95	
Thr	Leu	Val	Pro	Tyr	Gly	Asn	Ala	Gln	Glu	Gln	Asn	Val	Ser	Gly	Arg
			100					105					110		
Trp	Glu	Phe	Lys	Cys	Gln	His	Gly	Glu	Glu	Cys	Lys	Phe	Asn	Lys	
		115					120					125			
Val	Glu	Ala	Cys	Val	Leu	Asp	Glu	Leu	Asp	Met	Glu	Leu	Ala	Phe	Leu
		130				135					140				
Thr	Ile	Val	Cys	Met	Glu	Glu	Phe	Glu	Asp	Met	Glu	Arg	Ser	Leu	Pro
145				150					155					160	
Leu	Cys	Leu	Gln	Leu	Tyr	Ala	Pro	Gly	Leu	Ser	Pro	Asp	Thr	Ile	Met
			165					170					175		
Glu	Cys	Ala	Met	Gly	Asp	Arg	Gly	Met	Gln	Leu	Met	His	Ala	Asn	Ala
		180						185					190		
Gln	Arg	Thr	Asp	Ala	Leu	Gln	Pro	Pro	His	Glu	Tyr	Val	Pro	Trp	Val
		195					200					205			
Thr	Val	Asn	Gly	Lys	Pro	Leu	Gly	Arg	Ser	Asp	Pro	Ala	Pro	Tyr	Pro
		210				215					220				
Cys	Leu	Pro	Val	Val	Pro	Gly	Gln	Glu	Ala	Gly	Cys	Leu	Pro	Phe	Leu
225					230					235				240	
Asn	Gln	Leu	Pro	Gln	Glu	Cys	Leu	Leu	Gln	Val	Met	Ala	Gly	Glu	Leu
				245						250				255	

Arg Arg Ala His Gly Arg Arg Val Gly Thr Arg Leu Pro Ala Phe Phe
 260 265 270
 Phe

<210> 137
 <211> 806
 <212> PRT
 <213> Homo sapiens

<400> 137
 Met Ala Val Arg Ala Leu Lys Leu Leu Thr Thr Leu Leu Ala Val Val
 1 5 10 15
 Ala Ala Ala Ser Gln Ala Glu Val Glu Ser Glu Ala Gly Trp Gly Met
 20 25 30
 Val Thr Pro Asp Leu Leu Phe Ala Glu Gly Thr Ala Ala Tyr Ala Arg
 35 40 45
 Gly Asp Trp Pro Gly Val Val Leu Ser Met Glu Arg Ala Leu Arg Ser
 50 55 60
 Arg Ala Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala
 65 70 75 80
 Ala Asp Phe Pro Trp Glu Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala
 85 90 95
 Gln Ala Ser Gly Ala Ala Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly
 100 105 110
 Leu Leu Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala
 115 120 125
 Ala His Ser Leu Ser Glu Glu Met Glu Leu Glu Phe Arg Lys Arg Ser
 130 135 140
 Pro Tyr Asn Tyr Leu Gln Val Ala Tyr Phe Lys Val Gln Thr Cys Leu
 145 150 155 160
 Glu Pro Gly Gly Arg Gly Pro Ser Gly Glu Arg Ser Val Ala Gly Asp
 165 170 175
 Leu Arg Ser Leu Gly Asp Arg Gly Ser Val Arg Arg Glu Gly Lys Val
 180 185 190
 Ala Ser Trp Leu Gly Ser Ser Pro Arg Ser Arg Gly Glu Leu Leu Pro
 195 200 205
 Gly Arg Arg Pro Ser Ser Pro Ser Ser His Gly Gln Met Leu Thr Pro
 210 215 220
 Lys Ile Asn Lys Leu Glu Lys Ala Val Ala Ala His Thr Phe Phe
 225 230 235 240
 Val Gly Asn Pro Glu His Met Glu Met Gln Gln Asn Leu Asp Tyr Tyr
 245 250 255
 Gln Thr Met Ser Gly Val Lys Glu Ala Asp Phe Lys Asp Leu Glu Thr
 260 265 270
 Gln Pro His Met Gln Glu Phe Arg Leu Gly Val Arg Leu Tyr Ser Glu
 275 280 285
 Glu Gln Pro Gln Glu Ala Val Pro His Leu Glu Ala Ala Leu Gln Glu
 290 295 300
 Tyr Phe Val Ala Tyr Glu Glu Cys Arg Ala Leu Cys Glu Gly Pro Tyr
 305 310 315 320
 Asp Tyr Asp Gly Tyr Asn Tyr Leu Glu Tyr Asn Ala Asp Leu Phe Gln
 325 330 335
 Ala Ile Thr Asp His Tyr Ile Gln Val Leu Asn Cys Lys Gln Asn Cys
 340 345 350
 Val Thr Glu Leu Ala Ser His Pro Ser Arg Glu Lys Pro Phe Glu Asp
 355 360 365
 Phe Leu Pro Ser His Tyr Asn Tyr Leu Gln Phe Ala Tyr Tyr Asn Ile

370	375	380
Gly Asn Tyr Thr Gln Ala Val Glu Cys Ala Lys Thr Tyr Leu Leu Phe		
385	390	395
Phe Pro Asn Asp Glu Val Met Asn Gln Asn Leu Ala Tyr Tyr Ala Ala		400
	405	410
Met Leu Gly Glu Glu His Thr Arg Ser Ile Gly Pro Arg Glu Ser Ala		415
	420	425
Lys Glu Tyr Arg Gln Arg Ser Leu Leu Glu Lys Glu Leu Leu Phe Phe		430
	435	440
Ala Tyr Asp Val Phe Gly Ile Pro Phe Val Asp Pro Asp Ser Trp Thr		445
	450	455
Pro Glu Glu Val Ile Pro Lys Arg Leu Gln Glu Lys Gln Lys Ser Glu		460
	465	470
Arg Glu Thr Ala Val Arg Ile Ser Gln Glu Ile Gly Asn Leu Met Lys		475
	485	490
Glu Ile Glu Thr Leu Val Glu Glu Lys Thr Lys Glu Ser Leu Asp Val		495
	500	505
Ser Arg Leu Thr Arg, Glu Gly Gly Pro Leu Leu Tyr Glu Gly Ile Ser		510
	515	520
Leu Thr Met Asn Ser Lys Leu Leu Asn Gly Ser Gln Arg Val Val Met		525
	530	535
Asp Gly Val Ile Ser Asp His Glu Cys Gln Glu Leu Gln Arg Leu Thr		540
	545	550
Asn Val Ala Ala Thr Ser Gly Asp Gly Tyr Arg Gly Gln Thr Ser Pro		555
	565	570
His Thr Pro Asn Glu Lys Phe Tyr Gly Val Thr Val Phe Lys Ala Leu		575
	580	585
Lys Leu Gly Gln Glu Gly Lys Val Pro Leu Gln Ser Ala His Leu Tyr		590
	595	600
Tyr Asn Val Thr Glu Lys Val Arg Arg Ile Met Glu Ser Tyr Phe Arg		605
	610	615
Leu Asp Thr Pro Leu Tyr Phe Ser Tyr Ser His Leu Val Cys Arg Thr		620
	625	630
Ala Ile Glu Glu Val Gln Ala Glu Arg Lys Asp Ser His Pro Val		635
	645	650
His Val Asp Asn Cys Ile Leu Asn Ala Glu Thr Leu Val Cys Val Lys		655
	660	665
Glu Pro Pro Ala Tyr Thr Phe Arg Asp Tyr Ser Ala Ile Leu Tyr Leu		670
	675	680
Asn Gly Asp Phe Asp Gly Gly Asn Phe Tyr Phe Thr Glu Leu Asp Ala		685
	690	695
Lys Thr Val Thr Ala Glu Val Gln Pro Gln Cys Gly Arg Ala Val Gly		700
	705	710
Phe Ser Ser Gly Thr Glu Asn Pro His Gly Val Lys Ala Val Thr Arg		715
	725	730
Gly Gln Arg Cys Ala Ile Ala Leu Trp Phe Thr Leu Asp Pro Arg His		735
	740	745
Ser Glu Arg Asp Arg Val Gln Ala Asp Asp Leu Val Lys Met Leu Phe		750
	755	760
Ser Pro Glu Glu Met Asp Leu Ser Gln Glu Gln Pro Leu Asp Ala Gln		765
	770	775
Gln Gly Pro Pro Glu Pro Ala Gln Glu Ser Leu Ser Gly Ser Glu Ser		780
	785	790
Lys Pro Lys Asp Glu Leu		795
	805	800

<210> 138

<211> 244

<212> PRT

<213> Homo sapiens

<400> 138

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Met Arg Phe Val Leu Cys Val Lys Ala Lys Pro Ser Gly Leu Val Thr
 1      5      10      15
Ile Ser Arg Lys Ile Thr Gln Asp Tyr Gly Gln Asp Ala Ala Phe Thr
 20      25      30
Ala Ile Leu Asp Thr Leu Asp Ile Phe Leu Glu Ile Val Thr Asn Pro
 35      40      45
Asp Gly Phe Ala Phe Thr His Ser Thr Asn Arg Met Trp Arg Lys Thr
 50      55      60
Arg Ser His Thr Ala Gly Ser Leu Cys Ile Gly Val Asp Pro Asn Arg
 65      70      75      80
Asn Trp Asp Ala Gly Phe Gly Leu Ser Gly Ala Ser Ser Asn Pro Cys
 85      90      95
Ser Glu Thr Tyr His Gly Lys Phe Ala Asn Ser Glu Val Glu Val Lys
100      105      110
Ser Ile Val Asp Phe Val Lys Asp His Gly Asn Ile Lys Ala Phe Ile
115      120      125
Ser Ile His Ser Tyr Ser Gln Leu Leu Met Tyr Pro Tyr Gly Tyr Lys
130      135      140
Thr Glu Pro Val Pro Asp Gln Asp Glu Leu Asp Gln Leu Ser Lys Ala
145      150      155      160
Ala Val Thr Ala Leu Ala Ser Leu Tyr Gly Thr Lys Phe Asn Tyr Gly
165      170      175
Ser Ile Ile Lys Ala Ile Tyr Gln Ala Ser Gly Ser Thr Ile Asp Trp
180      185      190
Thr Tyr Ser Gln Gly Ile Lys Tyr Ser Phe Thr Phe Glu Leu Arg Asp
195      200      205
Thr Gly Arg Tyr Gly Phe Leu Leu Pro Ala Ser Gln Ile Ile Pro Thr
210      215      220
Ala Lys Glu Thr Trp Leu Ala Leu Leu Thr Ile Met Glu His Thr Leu
225      230      235      240
Asn His Pro Tyr

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<210> 139

<211> 538

<212> PRT

<213> Homo sapiens

<400> 139

```

Met Ala Leu Tyr Asp Glu Asp Leu Leu Lys Asn Pro Phe Tyr Leu Ala
 1      5      10      15
Leu Gln Lys Cys Arg Pro Asp Leu Cys Ser Lys Val Ala Gln Ile His
 20      25      30
Gly Ile Val Leu Val Pro Cys Lys Gly Ser Leu Ser Ser Ser Ile Gln
 35      40      45
Ser Thr Cys Gln Phe Glu Ser Tyr Ile Leu Ile Pro Val Glu Glu His
 50      55      60
Phe Gln Thr Leu Asn Gly Lys Asp Val Phe Ile Gln Gly Asn Arg Ile
 65      70      75      80
Lys Leu Gly Ala Gly Phe Ala Cys Leu Leu Ser Val Pro Ile Leu Phe
 85      90      95
Glu Glu Thr Phe Tyr Asn Glu Lys Glu Glu Ser Phe Ser Ile Leu Cys
100      105      110
Ile Ala His Pro Leu Glu Lys Arg Glu Ser Ser Glu Glu Pro Leu Ala

```

115	120	125
Pro Ser Asp Pro Phe Ser Leu Lys Thr Ile Glu Asp Val Arg Glu Phe		
130	135	140
Leu Gly Arg His Ser Glu Arg Phe Asp Arg Asn Ile Ala Ser Phe His		
145	150	155
Arg Thr Phe Arg Glu Cys Glu Arg Lys Ser Leu Arg His His Ile Asp		
160	165	170
Ser Ala Asn Ala Leu Tyr Thr Lys Cys Leu Gln Gln Leu Leu Arg Asp		
175	180	185
Ser His Leu Lys Met Leu Ala Lys Gln Glu Ala Gln Met Asn Leu Met		
190	195	200
Lys Gln Ala Val Glu Ile Tyr Val His His Glu Ile Tyr Asn Leu Ile		
205	210	215
Phe Lys Tyr Val Gly Thr Met Glu Ala Ser Glu Asp Ala Ala Phe Asn		
220	225	230
Lys Ile Thr Arg Ser Leu Gln Asp Leu Gln Gln Lys Asp Ile Gly Val		
235	240	245
Lys Pro Glu Phe Ser Phe Asn Ile Pro Arg Ala Lys Arg Glu Leu Ala		
250	255	260
Gln Leu Asn Lys Cys Thr Ser Pro Gln Gln Lys Leu Val Cys Leu Arg		
265	270	275
Lys Val Val Gln Leu Ile Thr Gln Ser Pro Ser Gln Arg Val Asn Leu		
280	285	290
Glu Thr Met Cys Ala Asp Asp Leu Leu Ser Val Leu Leu Tyr Leu Leu		
295	300	305
Val Lys Thr Glu Ile Pro Asn Trp Met Ala Asn Leu Ser Tyr Ile Lys		
310	315	320
Asn Phe Arg Phe Ser Ser Leu Ala Lys Asp Glu Leu Gly Tyr Cys Leu		
325	330	335
Thr Ser Phe Glu Ala Ala Ile Glu Tyr Ile Arg Gln Gly Ser Leu Ser		
340	345	350
Ala Lys Pro Pro Glu Ser Glu Gly Phe Gly Asp Arg Leu Phe Leu Lys		
355	360	365
Gln Arg Met Ser Leu Leu Ser Gln Met Thr Ser Ser Pro Thr Asp Cys		
370	375	380
Leu Phe Lys His Ile Ala Ser Gly Asn Gln Lys Glu Val Glu Arg Leu		
385	390	395
Leu Ser Gln Glu Asp His Asp Lys Asp Thr Val Gln Lys Met Cys His		
400	405	410
Pro Leu Cys Phe Cys Asp Asp Cys Glu Lys Leu Val Ser Gly Arg Leu		
415	420	425
Asn Asp Pro Ser Val Val Thr Pro Phe Ser Arg Asp Arg Gly His		
430	435	440
Thr Pro Leu His Val Ala Val Cys Gly Gln Ala Ser Leu Ile Asp		
445	450	455
Leu Leu Val Ser Lys Gly Ala Met Val Asn Ala Thr Asp Tyr His Gly		
460	465	470
Ala Thr Pro Leu His Leu Ala Cys Gln Lys Gly Tyr Gln Ser Val Thr		
475	480	485
Leu Leu Leu Leu His Tyr Lys Ala Ser Ala Glu Val Gln Asp Asn Asn		
490	495	500
Gly Asn Thr Pro His Val Leu Arg Pro Leu		
505	510	515
520	525	530
535		

<210> 140
 <211> 232
 <212> PRT
 <213> Homo sapiens

```

<400> 140
Met Ala Thr Gly Ile Arg Leu Pro Ala Leu Pro Ala Ser Pro Arg Val
1      5      10      15
Pro Ser Glu Gly Pro Gly Phe Ser Glu His Pro Glu Gly Pro Pro Ala
20      25      30
Leu Pro Pro Ala Ile Pro Phe Ser Phe Thr Leu Leu Val Gln Ala Val
35      40      45
Phe Phe Leu Tyr Gln Ala Trp Trp Leu Leu His Gly Ala Pro Gln Gly
50      55      60
Lys Gly Trp Pro Gln Ala Ser Gly Leu Glu Asp Arg Val Thr Arg Glu
65      70      75      80
Glu Gly Ser Pro Arg Gly Pro Ser Ile Ser Leu Asn Cys Gly Cys Pro
85      90      95
Ala Trp Val Pro Cys Glu Arg Pro Ala Cys Val Gly Trp Gly Gly Pro
100     105     110
Pro Gln Pro Pro Gly Ala Ile Cys Glu Ala Thr Ala Pro Pro Ser Ile
115     120     125
Phe Leu Pro Phe Pro Phe Gln Pro Leu Phe Gln Glu Pro Cys His Thr
130     135     140
His Thr Cys Ser Leu Pro Ser Pro Ala Leu Pro Pro Leu Leu Arg Arg
145     150     155     160
Gly Arg Pro Arg Pro Cys Ala Ala Leu Ala Leu Pro Ala Leu Ser Ser
165     170     175
Leu Phe Ser Pro Val Phe Ser Leu Leu Ser Leu Gln Leu Pro Ala Asp
180     185     190
Arg Val Arg Gln Val His Pro Val Leu Arg Ala Pro Gly Pro Pro Ser
195     200     205
Thr Ser Lys Gln Ile Pro Pro Leu Leu Gly Asp Leu Pro Phe Gln Ala
210     215     220
Cys Leu Asp Gly Cys Ser Val Thr
225     230

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```

<210> 141
<211> 105
<212> PRT
<213> Homo sapiens

```

```

<400> 141
Met Thr Ser Ile Ile Lys Leu Thr Thr Leu Ser Gly Val Gln Glu Glu
1      5      10      15
Ser Ala Leu Cys Tyr Leu Leu Gln Val Asp Glu Phe Arg Phe Leu Leu
20      25      30
Asp Cys Gly Trp Asp Glu His Phe Ser Met Asp Ile Ile Asp Ser Leu
35      40      45
Arg Lys His Val His Gln Ile Asp Ala Val Leu Leu Ser His Pro Asp
50      55      60
Pro Leu His Leu Gly Ala Leu Pro Tyr Ala Val Gly Lys Leu Gly Leu
65      70      75      80
Asn Cys Ala Ile Tyr Ala Thr Ile Pro Val Tyr Lys Met Gly Gln Met
85      90      95
Phe Met Tyr Asp Leu Tyr Gln Val Ile
100     105

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```

<210> 142
<211> 333

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<212> PRT
 <213> Homo sapiens

<400> 142
 Met Asn Leu Ser Leu Val Leu Ala Ala Phe Cys Leu Gly Ile Ala Ser
 1 5 10 15
 Ala Val Pro Lys Phe Asp Gln Asn Leu Asp Thr Lys Trp Tyr Gln Trp
 20 25 30
 Lys Ala Thr His Arg Arg Leu Tyr Gly Ala Asn Glu Glu Gly Trp Arg
 35 40 45
 Arg Ala Val Trp Glu Lys Asn Met Lys Met Ile Glu Leu His Asn Gly
 50 55 60
 Glu Tyr Ser Gln Gly Lys His Ser Phe Thr Met Ala Met Asn Ala Phe
 65 70 75 80
 Gly Asp Met Thr Asn Glu Glu Phe Arg Gln Val Met Asn Gly Phe Gln
 85 90 95
 Tyr Gln Lys His Arg Lys Gly Lys Gln Phe Gln Glu Arg Leu Leu Leu
 100 105 110
 Glu Ile Pro Thr Ser Val Asp Trp Arg Glu Lys Gly Tyr Met Thr Pro
 115 120 125
 Val Lys Asp Gln Gly Gln Cys Gly Ser Cys Trp Ala Phe Ser Ala Thr
 130 135 140
 Gly Ala Leu Glu Gly Gln Met Phe Trp Lys Thr Gly Lys Leu Ile Ser
 145 150 155 160
 Leu Asn Glu Gln Asn Leu Val Asp Cys Ser Gly Pro Gln Gly Asn Glu
 165 170 175
 Gly Cys Asn Gly Asp Phe Met Asp Asn Pro Phe Arg Tyr Val Gln Glu
 180 185 190
 Asn Gly Gly Leu Asp Ser Glu Glu Ser Tyr Pro Tyr Glu Ala Thr Glu
 195 200 205
 Glu Ser Cys Lys Tyr Asn Pro Lys Tyr Ser Val Ala Asn Asp Thr Gly
 210 215 220
 Phe Val Asp Ile Pro Lys Gln Glu Lys Ala Leu Met Lys Ala Val Ala
 225 230 235 240
 Thr Val Gly Pro Ile Ser Val Ala Ile Asp Ala Gly His Glu Ser Phe
 245 250 255
 Leu Phe Tyr Lys Glu Gly Ile Tyr Phe Glu Pro Asp Cys Ser Ser Glu
 260 265 270
 Asp Met Asp His Gly Val Leu Val Val Gly Tyr Gly Phe Glu Ser Thr
 275 280 285
 Glu Ser Asp Asn Asn Lys Tyr Trp Leu Val Lys Asn Ser Trp Gly Glu
 290 295 300
 Glu Trp Gly Met Gly Gly Tyr Val Lys Met Ala Lys Asp Arg Arg Asn
 305 310 315 320
 His Cys Gly Ile Ala Ser Ala Ala Ser Tyr Pro Thr Val
 325 330

<210> 143
 <211> 208
 <212> PRT
 <213> Homo sapiens

<400> 143
 Met Leu Gly Cys Gln Gly Arg Met Tyr Thr Leu Leu Ser Gly Leu Tyr
 1 5 10 15
 Lys Tyr Met Phe Gln Lys Asp Glu Tyr Cys Ile Leu Ile Leu Gly Leu
 20 25 30

```

Asp Asn Ala Gly Lys Thr Thr Phe Leu Glu Gln Ser Lys Thr Arg Phe
      35                      40                      45
Asn Lys Asn Tyr Lys Gly Met Ser Leu Ser Lys Ile Thr Thr Val
      50                      55                      60
Gly Leu Asn Ile Gly Thr Val Asp Val Gly Lys Ala Arg Leu Met Phe
      65                      70                      75                      80
Trp Asp Leu Gly Gly Gln Glu Glu Leu Gln Ser Leu Trp Asp Lys Tyr
      85                      90                      95
Tyr Ala Glu Cys His Gly Val Ile Tyr Val Ile Asp Ser Thr Asp Glu
      100                      105                      110
Glu Arg Leu Ala Glu Ser Lys Gln Ala Phe Glu Lys Val Val Thr Ser
      115                      120                      125
Glu Ala Leu Cys Gly Val Pro Val Leu Val Leu Ala Asn Lys Gln Asp
      130                      135                      140
Val Glu Thr Cys Leu Ser Ile Pro Asp Ile Lys Thr Ala Phe Ser Asp
      145                      150                      155                      160
Cys Thr Ser Lys Ile Gly Arg Arg Asp Cys Leu Thr Gln Ala Cys Ser
      165                      170                      175
Ala Leu Thr Gly Lys Gly Val Arg Glu Gly Ile Glu Trp Met Val Lys
      180                      185                      190
Cys Val Val Arg Asn Val His Arg Pro Pro Arg Gln Arg Asp Ile Thr
      195                      200                      205

```

<210> 144
 <211> 229
 <212> PRT
 <213> Homo sapiens

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<400> 144
Met Leu Ser Val Asp Ile Thr Ser Arg Tyr Arg Ala Pro Ser Thr Tyr
      1                      5                      10                      15
Leu Leu Asn Ser Leu Lys Glu Gly Leu Glu Gly Leu His Gly Glu Ser
      20                      25                      30
Cys Ser Ser Phe Leu Leu Gly Pro Ser Val Ala Met Asn Met Gln Thr
      35                      40                      45
Ala Gly Leu Glu Met Asp Ile Cys Asp Gly His Phe Arg Gln Asn Gly
      50                      55                      60
Gly Cys Gly Tyr Val Leu Lys Pro Asp Phe Leu Arg Asp Ile Gln Ser
      65                      70                      75                      80
Ser Phe His Pro Glu Lys Pro Ile Ser Pro Phe Lys Ala Gln Thr Leu
      85                      90                      95
Leu Ile Gln Val Ile Ser Gly Gln Gln Leu Pro Lys Val Asp Lys Thr
      100                      105                      110
Lys Glu Gly Ser Ile Val Asp Pro Leu Val Lys Val Gln Ile Phe Gly
      115                      120                      125
Val Arg Leu Asp Thr Ala Arg Gln Glu Thr Asn Tyr Val Glu Asn Asn
      130                      135                      140
Gly Phe Asn Pro Tyr Trp Gly Gln Thr Leu Cys Phe Arg Val Leu Val
      145                      150                      155                      160
Pro Glu Leu Ala Met Leu Arg Phe Val Val Met Asp Tyr Asp Trp Lys
      165                      170                      175
Ser Arg Asn Asp Phe Ile Gly Gln Tyr Thr Leu Pro Trp Thr Cys Met
      180                      185                      190
Gln Gln Gly Tyr Arg His Ile His Leu Leu Ser Lys Asp Gly Ile Ser
      195                      200                      205
Leu Arg Pro Ala Ser Ile Phe Val Tyr Ile Cys Ile Gln Glu Gly Leu

```

210
Glu Gly Asp Glu Ser
225

215

220

<210> 145
<211> 223
<212> PRT
<213> Homo sapiens

<400> 145
Met Arg Gly Pro Gly Gln Ala Asp Cys Ala Val Ala Ile Gly Arg Pro
1 5 10 15
Leu Gly Glu Val Val Thr Leu Arg Val Leu Glu Ser Ser Leu Asn Cys
20 25 30
Ser Ala Gly Asp Met Leu Leu Leu Trp Gly Arg Leu Thr Trp Arg Lys
35 40 45
Met Cys Arg Lys Leu Leu Asp Met Thr Phe Ser Ser Lys Thr Asn Thr
50 55 60
Leu Val Val Arg Gln Arg Cys Gly Arg Pro Gly Gly Gly Val Leu Leu
65 70 75 80
Arg Tyr Gly Ser Gln Leu Ala Pro Glu Thr Phe Tyr Arg Glu Cys Asp
85 90 95
Met Gln Leu Phe Gly Pro Trp Gly Glu Ile Val Ser Pro Ser Leu Ser
100 105 110
Pro Ala Thr Ser Asn Ala Gly Gly Cys Arg Leu Phe Ile Asn Val Ala
115 120 125
Pro His Ala Arg Ile Ala Ile His Ala Leu Ala Thr Asn Met Gly Ala
130 135 140
Gly Thr Glu Gly Ala Asn Ala Ser Tyr Ile Leu Ile Arg Asp Thr His
145 150 155 160
Ser Leu Arg Thr Thr Ala Phe His Gly Gln Gln Val Leu Tyr Trp Glu
165 170 175
Ser Glu Ser Ser Gln Ala Glu Met Glu Phe Ser Glu Gly Phe Leu Lys
180 185 190
Ala Gln Ala Ser Leu Arg Gly Gln Tyr Trp Thr Leu Gln Ser Trp Val
195 200 205
Pro Glu Met Gln Asp Pro Gln Ser Trp Lys Gly Lys Glu Gly Thr
210 215 220

<210> 146
<211> 73
<212> PRT
<213> Homo sapiens

<400> 146
Met Thr Asp Pro Asp Gly Asn Pro Lys Cys Leu Thr Lys Ile Asn Tyr
1 5 10 15
Gly Gly Glu Val Pro Lys Ser Tyr Tyr Leu Cys Lys Gln Val Arg Leu
20 25 30
Gln Tyr Glu His Thr Arg Ser Val Gly Arg Gly Ser Ser Leu Gln Val
35 40 45
Glu Asn Glu Ile Leu Phe Pro Gly Cys Val Leu Arg Cys Pro Glu Val
50 55 60
Leu Gln His Leu Gln Pro Gly Ser Phe
65 70

<210> 147
 <211> 202
 <212> PRT
 <213> Homo sapiens

<400> 147
 Met Ala Glu Tyr Leu Ala Ser Ile Phe Gly Thr Glu Lys Asp Lys Val
 1 5 10 15
 Asn Cys Ser Phe Tyr Phe Lys Ile Gly Val Cys Arg His Gly Asp Arg
 20 25 30
 Cys Ser Arg Leu His Asn Lys Pro Thr Phe Ser Gln Glu Val Phe Thr
 35 40 45
 Glu Leu Gln Glu Lys Tyr Gly Glu Ile Glu Glu Met Asn Val Cys Asp
 50 55 60
 Asn Leu Gly Asp His Leu Val Gly Asn Val Tyr Val Lys Phe Arg Arg
 65 70 75 80
 Glu Glu Asp Gly Glu Arg Ala Val Ala Glu Leu Ser Asn Arg Trp Phe
 85 90 95
 Asn Gly Gln Ala Val His Gly Asn Val Pro Glu Val Ala Ser Ala Thr
 100 105 110
 Ser Cys Ile Cys Gly Pro Phe Pro Arg Thr Ser Arg Gly Ser Ser Met
 115 120 125
 Gly Gly Asp Pro Gly Ala Gly His Pro Arg Gly Ser Ile Leu Ala Thr
 130 135 140
 Ile Pro Glu Arg Gly Thr Ile Gly Val Pro Leu Ile Thr Gly Met Ala
 145 150 155 160
 Ala Ser Glu Ala Leu Ala Pro Leu Pro Phe Thr Pro Asn Arg Asp Arg
 165 170 175
 Cys Ser Trp Gln Asp Leu Ser Ser Lys Pro Pro Ser Leu Ser Cys Pro
 180 185 190
 Ile Leu Pro Arg Leu Pro Gly Ser Ile Met
 195 200

<210> 148
 <211> 241
 <212> PRT
 <213> Homo sapiens

<400> 148
 Met Ala Glu Tyr Leu Ala Ser Ile Phe Gly Thr Glu Lys Asp Lys Val
 1 5 10 15
 Asn Cys Ser Phe Tyr Phe Lys Ile Gly Ala Cys Arg His Gly Asp Arg
 20 25 30
 Cys Ser Arg Leu His Asn Lys Pro Thr Phe Ser Gln Thr Ile Val Leu
 35 40 45
 Leu Asn Leu Tyr Arg Asn Pro Gln Asn Thr Ala Gln Thr Ala Asp Gly
 50 55 60
 Ser His Cys His Val Ser Asp Val Glu Val Gln Glu His Tyr Asp Ser
 65 70 75 80
 Phe Phe Glu Glu Val Phe Thr Glu Leu Gln Glu Lys Tyr Gly Glu Ile
 85 90 95
 Glu Glu Met Asn Val Cys Asp Asn Leu Gly Asp His Leu Val Gly Asn
 100 105 110
 Val Tyr Val Lys Phe Arg Arg Glu Glu Asp Gly Glu Arg Ala Val Ala

```

115      120      125
Glu Leu Ser Asn Arg Trp Phe Asn Gly Gln Ala Val His Gly Asn Val
130      135      140
Pro Glu Val Ala Ser Ala Thr Ser Cys Ile Cys Gly Pro Phe Pro Arg
145      150      155      160
Thr Ser Arg Gly Ser Ser Met Gly Gly Asp Pro Gly Ala Gly His Pro
165      170      175
Arg Gly Ser Ile Leu Ala Thr Ile Pro Glu Arg Gly Thr Ile Val Val
180      185      190
Pro Leu Ile Thr Gly Met Ala Ala Ser Glu Ala Leu Ala Pro Leu Pro
195      200      205
Phe Thr Pro Asn Arg Asp Arg Cys Ser Trp Gln Asp Leu Ser Ser Lys
210      215      220
Pro Pro Ser Leu Ser Cys Pro Ile Leu Pro Arg Leu Pro Gly Ser Ile
225      230      235      240
Met

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<210> 149
<211> 794
<212> PRT
<213> Homo sapiens

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<400> 149
Met Leu Cys Gly Arg Trp Arg Arg Cys Arg Arg Pro Pro Glu Glu Pro
1      5      10      15
Pro Val Ala Ala Gln Val Ala Ala Gln Val Ala Ala Pro Val Ala Leu
20      25      30
Pro Ser Pro Pro Thr Pro Ser Asp Gly Thr Lys Arg Pro Gly Leu
35      40      45
Arg Ala Leu Lys Lys Met Gly Leu Thr Glu Asp Glu Asp Val Arg Ala
50      55      60
Met Leu Arg Gly Ser Arg Leu Arg Lys Ile Arg Ser Arg Thr Trp His
65      70      75      80
Lys Glu Arg Leu Tyr Arg Leu Gln Glu Asp Gly Leu Ser Val Trp Phe
85      90      95
Gln Arg Arg Ile Pro Arg Ala Pro Ser Gln His Ile Phe Phe Val Gln
100      105      110
His Ile Glu Ala Val Arg Glu Gly His Gln Ser Glu Gly Leu Arg Arg
115      120      125
Phe Gly Gly Ala Phe Ala Pro Ala Arg Cys Leu Thr Ile Ala Phe Lys
130      135      140
Gly Arg Arg Lys Asn Leu Asp Leu Ala Ala Pro Thr Ala Glu Glu Ala
145      150      155      160
Gln Arg Trp Val Arg Gly Leu Thr Lys Leu Arg Ala Arg Leu Asp Ala
165      170      175
Met Ser Gln Arg Glu Arg Leu Asp His Trp Ile His Ser Tyr Leu His
180      185      190
Arg Ala Asp Ser Asn Gln Asp Ser Lys Met Ser Phe Lys Glu Ile Lys
195      200      205
Ser Leu Leu Arg Met Val Asn Val Asp Met Asn Asp Met Tyr Ala Tyr
210      215      220
Leu Leu Phe Lys Glu Cys Asp His Ser Asn Asn Asp Arg Leu Glu Gly
225      230      235      240
Ala Glu Ile Glu Glu Phe Leu Arg Arg Leu Leu Lys Arg Pro Glu Leu
245      250      255
Glu Glu Ile Phe His Gln Tyr Ser Gly Glu Asp Arg Val Leu Ser Ala
260      265      270

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Pro Glu Leu Leu Glu Phe Leu Glu Asp Gln Gly Glu Glu Gly Ala Thr
 275 280
 Leu Ala Arg Ala Gln Gln Leu Ile Gln Thr Tyr Glu Leu Asn Glu Thr
 290 295
 Ala Lys Gln His Glu Leu Met Thr Leu Asp Gly Phe Met Met Tyr Leu
 300 305
 Leu Ser Pro Glu Gly Ala Ala Leu Asp Asn Thr His Thr Cys Val Phe
 310 315
 Gln Asp Met Asn Gln Pro Leu Ala His Tyr Phe Ile Ser Ser Ser His
 320 325
 Asn Thr Tyr Leu Thr Asp Ser Gln Ile Gly Gly Pro Ser Ser Thr Glu
 330 335
 Ala Tyr Val Arg Tyr Cys Ser Arg Gly Ala Phe Ala Gln Gly Cys Arg
 340 345
 Cys Val Glu Leu Asp Cys Trp Glu Gly Pro Gly Glu Pro Val Ile
 350 355
 Tyr His Gly His Thr Leu Thr Ser Lys Ile Leu Phe Arg Asp Val Val
 360 365
 Gln Ala Val Arg Asp His Ala Phe Thr Leu Ser Pro Tyr Pro Val Ile
 370 375
 Leu Ser Leu Glu Asn His Cys Gly Leu Glu Gln Ala Ala Met Ala
 380 385
 Arg His Leu Cys Thr Ile Leu Gly Asp Met Leu Val Thr Gln Ala Leu
 390 395
 Asp Ser Pro Asn Pro Glu Glu Leu Pro Ser Pro Glu Gln Leu Lys Gly
 400 405
 Arg Val Leu Val Lys Gly Lys Lys Leu Pro Ala Ala Arg Ser Glu Asp
 410 415
 Gly Arg Ala Leu Ser Asp Arg Glu Glu Glu Glu Asp Asp Glu Glu
 420 425
 Glu Glu Glu Glu Val Glu Ala Ala Ala Gln Arg Arg Leu Ala Lys Gln
 430 435
 Ile Ser Pro Glu Leu Ser Ala Leu Ala Val Tyr Cys His Ala Thr Arg
 440 445
 Leu Arg Thr Leu His Pro Ala Pro Asn Ala Pro Gln Pro Cys Gln Val
 450 455
 Ser Ser Leu Ser Glu Arg Lys Ala Lys Lys Leu Ile Arg Glu Ala Gly
 460 465
 Asn Ser Phe Val Arg His Asn Ala Arg Gln Leu Thr Arg Val Tyr Pro
 470 475
 Leu Gly Leu Arg Met Asn Ser Ala Asn Tyr Ser Pro Gln Glu Met Trp
 480 485
 Asn Ser Gly Cys Gln Leu Val Ala Leu Asn Phe Gln Thr Pro Gly Tyr
 490 495
 Glu Met Asp Leu Asn Ala Gly Arg Phe Leu Val Asn Gly Gln Cys Gly
 500 505
 Tyr Val Leu Lys Pro Ala Cys Leu Arg Gln Pro Asp Ser Thr Phe Asp
 510 515
 Pro Glu Tyr Pro Gly Pro Pro Arg Thr Thr Leu Ser Ile Gln Val Leu
 520 525
 Thr Ala Gln Gln Leu Pro Lys Leu Asn Ala Glu Lys Pro His Ser Ile
 530 535
 Val Asp Pro Leu Val Arg Ile Glu Ile His Gly Val Pro Ala Asp Cys
 540 545
 Ala Arg Gln Glu Thr Asp Tyr Val Leu Asn Asn Gly Phe Asn Pro Arg
 550 555
 Trp Gly Gln Thr Leu Gln Phe Gln Leu Arg Ala Pro Glu Leu Ala Leu
 560 565
 Val Arg Phe Val Val Glu Asp Tyr Asp Ala Thr Ser Pro Asn Asp Phe
 570 575
 Val Gly Gln Phe Thr Leu Pro Leu Ser Ser Leu Lys Gln Gly Tyr Arg
 580 585
 590 595
 600 605
 610 615
 620 625
 630 635
 640 645
 650 655
 660 665
 670 675
 680 685
 690 695
 700 705
 710 715
 720 725
 730 735
 740 745
 750 755

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      755              760              765
His Ile His Leu Leu Ser Lys Asp Gly Ala Ser Leu Ser Pro Ala Thr
770              775              780
Leu Phe Ile Gln Ile Arg Ile Gln Arg Ser
785              790

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<210> 150
 <211> 115
 <212> PRT
 <213> Homo sapiens

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    <400> 150
Met Ala Ala Val Pro Met Val Leu Ser Ala Met Gly Phe Thr Ala Ala
1              5              10              15
Gly Ile Ala Ser Ser Ser Ile Ala Ala Lys Met Met Ser Ala Ala Ala
20              25              30
Ile Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu Val Ala Thr Leu
35              40              45
Gln Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser Asn Ile Leu Leu
50              55              60
Ala Ser Val Gly Ser Val Leu Gly Ala Cys Leu Gly Asn Ser Pro Ser
65              70              75              80
Ser Ser Leu Pro Ala Glu Pro Glu Ala Lys Glu Asp Glu Ala Arg Glu
85              90              95
Asn Val Pro Gln Gly Glu Pro Pro Lys Pro Pro Leu Lys Ser Glu Lys
100              105              110
His Glu Glu
115

```

<210> 151
 <211> 294
 <212> PRT
 <213> Homo sapiens

```

    <400> 151
Met Ala Gln Ala Pro Ala Asp Pro Gly Arg Glu Ala Lys Arg Pro Gln
1              5              10              15
Gln His Ala Ala Thr Ile Pro Glu Thr Pro Gly Pro Gln Phe Ser Gln
20              25              30
Gln Arg Glu Glu Asp Ile Tyr Arg Phe Leu Lys Asp Asn Gly Pro Gln
35              40              45
Arg Ala Leu Val Ile Ala Gln Ala Leu Gly Met Arg Thr Ala Lys Asp
50              55              60
Val Asn Arg Asp Leu Tyr Arg Met Lys Ser Arg His Leu Leu Asp Met
65              70              75              80
Asp Glu Gln Ser Lys Ala Trp Thr Ile Tyr Arg Pro Glu Asp Ser Gly
85              90              95
Arg Arg Ala Lys Ser Ala Ser Ile Ile Tyr Gln His Asn Pro Ile Asn
100              105              110
Met Ile Cys Gln Asn Gly Pro Asn Ser Trp Ile Ser Ile Ala Asn Ser
115              120              125
Glu Ala Ile Gln Ile Gly His Gly Asn Ile Ile Thr Arg Gln Thr Val
130              135              140
Ser Arg Glu Asp Gly Ser Ala Gly Pro Arg His Leu Pro Ser Met Ala
145              150              155              160

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Pro Gly Asp Ser Ser Thr Trp Gly Thr Leu Val Asp Pro Trp Gly Pro
 165 170 175
 Gln Asp Ile His Met Glu Arg Ser Ile Leu Arg Arg Val Gln Leu Gly
 180 185 190
 His Ser Asn Glu Met Arg Leu His Gly Val Pro Ser Glu Gly Pro Ala
 195 200 205
 His Ile Pro Pro Gly Ser Pro Pro Val Ser Ala Thr Ala Ala Gly Pro
 210 215 220
 Glu Ala Ser Phe Glu Ala Arg Ile Pro Ser Pro Gly Thr His Pro Glu
 225 230 235 240
 Gly Glu Ala Ala Gln Arg Ile His Met Lys Ser Cys Phe Leu Glu Asp
 245 250 255
 Ala Thr Ile Gly Asn Ser Asn Lys Met Ser Ile Gln Pro Arg Gly Gly
 260 265 270
 Trp Pro Arg Arg Ser Arg Arg Val Trp Arg Gly Gly Ala Arg Gly Gly
 275 280 285
 Arg Ser Cys Cys Leu His
 290

<210> 152

<211> 328

<212> PRT

<213> Homo sapiens

<400> 152

Met Ser Val Arg Ser Lys Leu Pro Asn Ser Pro Ala Ala Ser Ser His
 1 5 10 15
 Pro Lys Leu Lys Ser Ser Lys Gly Ile Thr Lys Lys Pro Gln Ala Pro
 20 25 30
 Ser Asn Asn Ala Ser Ser Ser Leu Ala Ser Leu Asn Pro Val Gly Lys
 35 40 45
 Asn Thr Ser Ser Pro Ala Leu Pro Arg Thr Ala Pro Cys Ile Ser Glu
 50 55 60
 Ser Pro Arg Lys Cys Ile Ser Ser Pro Asn Thr Pro Lys Ala Lys Val
 65 70 75 80
 Ile Pro Ala Gln Asn Ser Ala Asp Leu Pro Glu Ser Thr Leu Leu Pro
 85 90 95
 Asn Lys Cys Ser Gly Lys Thr Gln Pro Lys Tyr Leu Lys His Asn His
 100 105 110
 Ile Ser Ser Arg Asp Asn Ala Val Ser His Leu Ala Ala His Ser Asn
 115 120 125
 Ser Ser Ser Lys Cys Pro Lys Leu Pro Lys Ala Asn Ile Pro Val Arg
 130 135 140
 Pro Lys Pro Ser Phe Gln Ser Ser Ala Lys Met Thr Lys Thr Ser Ser
 145 150 155 160
 Lys Thr Ile Ala Thr Gly Leu Gly Thr Gln Ser Gln Pro Ser Asp Gly
 165 170 175
 Ala Pro Gln Ala Lys Pro Val Pro Ala Gln Lys Leu Lys Ser Ala Leu
 180 185 190
 Asn Leu Asn Gln Pro Val Ser Val Ser Ser Val Ser Pro Val Lys Ala
 195 200 205
 Thr Gln Lys Ser Lys Asp Lys Asn Ile Val Ser Ala Thr Lys Lys Gln
 210 215 220
 Pro Gln Asn Lys Ser Ala Phe Gln Lys Thr Gly Pro Ser Ser Leu Lys
 225 230 235 240
 Ser Pro Gly Arg Thr Pro Leu Ser Ile Val Ser Leu Pro Gln Ser Ser
 245 250 255
 Thr Lys Thr Gln Thr Ala Pro Lys Ser Ala Gln Thr Val Ala Lys Ser

260										265					270				
Gln	His	Ser	275	Thr	Lys	Gly	Pro	Pro	280	Arg	Ser	Gly	Lys	Thr	Pro	Ala	Ser		
Ile	Arg	Lys	Pro	Pro	Ser	Ser	285	Val	Lys	Asp	Asp	Ala	Asp	Ser	Gly	Asp	Lys		
290										300									
Lys	Pro	Thr	Ala	Lys	Lys	Lys	295	Glu	Asp	Asp	Asp	Asp	His	Tyr	Phe	Val	Met		
35					310							315					320		
Thr	Gly	Ser	Lys	Lys	Pro	Arg	Lys												

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<210> 153
<211> 1651
<212> PRT
<213> Homo sapiens
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<400> 153																	
Met	Ala	Pro	Thr	Leu	Phe	Gln	Lys	Leu	Phe	Ser	Lys	Arg	Thr	Gly	Leu		
1				5				10						15			
Gly	Ala	Pro	Gly	Arg	Asp	Ala	Arg	Asp	Pro	Asp	Cys	Gly	Phe	Ser	Trp		
			20					25					30				
Pro	Leu	Pro	Glu	Phe	Asp	Pro	Ser	Gln	Ile	Arg	Leu	Ile	Val	Tyr	Gln		
		35					40					45					
Asp	Cys	Glu	Arg	Arg	Gly	Arg	Asn	Val	Leu	Phe	Asp	Ser	Ser	Val	Lys		
	50					55				60							
Arg	Arg	Asn	Glu	Asp	Ile	Ser	Val	Ser	Asp	Leu	Asn	Thr	Ile	Tyr	Ser		
65					70					75				80			
Tyr	Leu	His	Gly	Met	Glu	Ile	Leu	Ser	Asn	Leu	Arg	Glu	His	Gln	Leu		
				85					90				95				
Arg	Leu	Met	Ser	Ala	Arg	Ala	Arg	Tyr	Glu	Arg	Tyr	Ser	Gly	Asn	Gln		
		100						105					110				
Val	Leu	Phe	Cys	Ser	Glu	Thr	Ile	Ala	Arg	Cys	Trp	Tyr	Ile	Leu	Leu		
		115					120					125					
Ser	Gly	Ser	Val	Leu	Val	Lys	Gly	Ser	Met	Val	Leu	Pro	Pro	Cys	Ser		
	130					135				140							
Phe	Gly	Lys	Gln	Phe	Gly	Gly	Lys	Arg	Gly	Cys	Asp	Cys	Leu	Val	Leu		
145					150					155					160		
Glu	Pro	Ser	Glu	Met	Ile	Val	Val	Glu	Asn	Ala	Lys	Asp	Asn	Glu	Asp		
				165				170					175				
Ser	Ile	Leu	Gln	Arg	Glu	Ile	Pro	Ala	Arg	Gln	Ser	Arg	Arg	Arg	Phe		
		180						185					190				
Arg	Lys	Ile	Asn	Tyr	Lys	Gly	Glu	Arg	Gln	Thr	Ile	Thr	Asp	Asp	Val		
		195					200					205					
Glu	Val	Asn	Ser	Tyr	Leu	Ser	Leu	Pro	Ala	Asp	Leu	Thr	Lys	Met	His		
	210					215					220						
Leu	Thr	Glu	Asn	Pro	His	Pro	Gln	Val	Thr	His	Val	Ser	Ser	Ser	Gln		
225					230					235					240		
Ser	Gly	Cys	Ser	Ile	Ala	Ser	Asp	Ser	Gly	Ser	Ser	Ser	Leu	Ser	Asp		
				245					250					255			
Ile	Tyr	Gln	Ala	Thr	Glu	Ser	Glu	Val	Gly	Asp	Val	Asp	Leu	Thr	Arg		
		260						265					270				
Leu	Pro	Glu	Gly	Pro	Val	Asp	Ser	Glu	Asp	Asp	Glu	Glu	Glu	Asp	Glu		
		275					280					285					
Glu	Ile	Asp	Arg	Thr	Asp	Pro	Leu	Gln	Gly	Arg	Asp	Leu	Val	Arg	Glu		
	290					295				300							
Cys	Leu	Glu	Lys	Glu	Pro	Ala	Asp	Lys	Thr	Asp	Asp	Asp	Ile	Glu	Gln		
305					310					315					320		
Leu	Leu	Glu	Phe	Met	His	Gln	Leu	Pro	Ala	Phe							

Ser Val Arg Arg Glu Leu Cys Ser Val Met Ile Phe Glu Val Val Glu
 340 345 350
 Gln Ala Gly Ala Ile Ile Leu Glu Asp Gly Gln Glu Leu Asp Ser Trp
 355 360 365
 Tyr Val Ile Leu Asn Gly Thr Val Glu Ile Ser His Pro Asp Gly Lys
 370 375 380
 Val Glu Asn Leu Phe Met Gly Asn Ser Phe Gly Ile Thr Pro Thr Leu
 385 390 395 400
 Asp Lys Gln Tyr Met His Gly Ile Val Arg Thr Lys Val Asp Asp Cys
 405 410 415
 Gln Phe Val Cys Ile Ala Gln Gln Asp Tyr Trp Arg Ile Leu Asn His
 420 425 430
 Val Glu Lys Asn Thr His Lys Val Glu Glu Gly Glu Ile Val Met
 435 440 445
 Val His Glu His Arg Glu Leu Asp Arg Ser Gly Thr Arg Lys Gly His
 450 455 460
 Ile Val Ile Lys Ala Thr Pro Glu Arg Leu Ile Met His Leu Ile Glu
 465 470 475 480
 Glu His Ser Ile Val Asp Pro Thr Tyr Ile Glu Asp Phe Leu Leu Thr
 485 490 495
 Tyr Arg Thr Phe Leu Glu Ser Pro Leu Asp Val Gly Ile Lys Leu Leu
 500 505 510
 Glu Trp Phe Lys Ile Asp Ser Leu Arg Asp Lys Val Thr Arg Ile Val
 515 520 525
 Leu Leu Trp Val Asn Asn His Phe Asn Asp Phe Glu Gly Asp Pro Ala
 530 535 540
 Met Thr Arg Phe Leu Glu Glu Phe Glu Lys Asn Leu Glu Asp Thr Lys
 545 550 555 560
 Met Asn Gly His Leu Arg Leu Leu Asn Ile Ala Cys Ala Ala Lys Ala
 565 570 575
 Lys Trp Arg Gln Val Val Leu Gln Lys Ala Ser Arg Glu Ser Pro Leu
 580 585 590
 Gln Phe Ser Leu Asn Gly Gly Ser Glu Lys Gly Phe Gly Ile Phe Val
 595 600 605
 Glu Gly Val Glu Pro Gly Ser Lys Ala Ala Asp Ser Gly Leu Lys Arg
 610 615 620
 Gly Asp Gln Ile Met Glu Val Asn Gly Gln Asn Phe Glu Asn Ile Thr
 625 630 635 640
 Phe Met Lys Ala Val Glu Ile Leu Arg Asn Asn Thr His Leu Ala Leu
 645 650 655
 Thr Val Lys Thr Asn Ile Phe Val Phe Lys Glu Leu Leu Phe Arg Thr
 660 665 670
 Glu Gln Glu Lys Ser Gly Val Pro His Ile Pro Lys Ile Ala Glu Lys
 675 680 685
 Lys Ser Asn Arg His Ser Ile Gln His Val Pro Gly Asp Ile Glu Gln
 690 695 700
 Thr Ser Gln Glu Lys Gly Ser Lys Lys Val Lys Ala Asn Thr Val Ser
 705 710 715 720
 Gly Gly Arg Asn Lys Ile Arg Lys Ile Leu Asp Lys Thr Arg Phe Ser
 725 730 735
 Ile Leu Pro Pro Lys Leu Phe Ser Asp Gly Gly Leu Ser Gln Ser Gln
 740 745 750
 Asp Asp Ser Ile Val Gly Thr Arg His Cys Arg His Ser Leu Ala Ile
 755 760 765
 Met Pro Ile Pro Gly Thr Leu Ser Ser Ser Pro Asp Leu Leu Gln
 770 775 780
 Pro Thr Thr Ser Met Leu Asp Phe Ser Asn Pro Ser Asp Ile Pro Asp
 785 790 795 800
 Gln Val Ile Arg Val Phe Lys Val Asp Gln Gln Ser Cys Tyr Ile Ile
 805 810 815
 Ile Ser Lys Asp Thr Thr Ala Lys Glu Val Val Phe His Ala Val His

820
 Glu Phe Gly 835 Leu Thr Gly Ala Ser 840 Asp Thr Tyr Ser 845 Leu Cys Glu Val
 Ser Val Thr Pro Glu Gly Val Ile Lys Gln Arg Arg 860 Leu Pro Asp Gln
 850
 Phe Ser Lys Leu Ala Asp Arg Ile Gln Leu Asn Gly Arg Tyr Tyr Leu
 865
 Lys Asn Asn Met Glu Thr Glu Thr Leu Cys Ser Asp Glu Asp Ala Gln
 885
 Glu Leu Val Lys Glu Ser Gln Leu Ser Met Leu Gln Leu Ser Thr Ile
 900
 Glu Val Ala Thr Gln Leu Ser Met Arg Asp Phe Asp Leu Phe Arg Asn
 915
 Ile Glu Pro Thr Glu Tyr Ile Asp Asp Leu Phe Lys Leu Asn Ser Lys
 930
 Thr Gly Asn Thr His Leu Lys Arg Phe Glu Asp Ile Val Asn Gln Glu
 945
 Thr Phe Trp Val Ala Ser Glu Ile Leu Thr Glu Ala Asn Gln Leu Lys
 965
 Arg Met Lys Ile Ile Lys His Phe Ile Lys Ile Ala Leu His Cys Arg
 980
 Glu Cys Lys Asn Phe Asn Ser Met Phe Ala Ile Ile Ser Gly Leu Asn
 995
 Leu Ala Ser Val Ala Arg Leu Arg Gly Thr Trp Glu Lys Leu Pro Ser
 1010
 Lys Tyr Glu Lys His Leu Gln Asp Leu Gln Asp Ile Phe Asp Pro Ser
 1025
 Arg Asn Met Ala Lys Tyr Arg Asn Ile Leu Ser Ser Gln Ser Met Gln
 1045
 Pro Pro Ile Ile Pro Leu Phe Pro Val Val Lys Lys Asp Met Thr Phe
 1060
 Leu His Glu Gly Asn Asp Ser Lys Val Asp Gly Leu Val Asn Phe Glu
 1075
 Lys Leu Arg Met Ile Ser Lys Glu Ile Arg Gln Val Val Arg Met Thr
 1090
 Ser Ala Asn Met Asp Pro Ala Met Met Phe Arg Gln Arg Ser Leu Ser
 1105
 Gln Gly Ser Thr Asn Ser Asn Met Leu Asp Val Gln Gly Gly Ala His
 1125
 Lys Lys Arg Ala Arg Arg Ser Ser Leu Leu Asn Ala Lys Lys Leu Tyr
 1140
 Glu Asp Ala Gln Met Ala Arg Lys Val Lys Gln Tyr Leu Ser Ser Leu
 1155
 Asp Val Glu Thr Asp Glu Glu Lys Phe Gln Met Met Ser Leu Gln Trp
 1170
 Glu Pro Ala Tyr Gly Thr Leu Thr Lys Asn Leu Ser Glu Lys Arg Ser
 1185
 Ala Lys Ser Ser Glu Met Ser Pro Val Pro Met Arg Ser Ala Gly Gln
 1205
 Thr Thr Lys Ala His Leu His Gln Pro His Arg Val Ser Gln Val Leu
 1220
 Gln Val Pro Ala Val Asn Leu His Pro Ile Arg Lys Lys Gly Gln Thr
 1235
 Lys Asp Pro Ala Leu Asn Thr Ser Leu Pro Gln Lys Val Leu Gly Thr
 1250
 Thr Glu Glu Ile Ser Gly Lys Lys His Thr Glu Asp Thr Ile Ser Val
 1265
 Ala Ser Ser Leu His Ser Ser Pro Pro Ala Ser Pro Gln Gly Ser Pro
 1285
 His Lys Gly Tyr Thr Leu Ile Pro Ser Ala Lys Ser Asp Asn Leu Ser
 1300
 1305
 1310

Asp Ser Ser His Ser Glu Ile Ser Ser Arg Ser Ser Ile Val Ser Asn
 1315 1320 1325
 Cys Ser Val Asp Ser Met Ser Ala Ala Leu Gln Asp Glu Arg Cys Ser
 1330 1335 1340
 Ser Gln Ala Leu Ala Val Pro Glu Ser Thr Gly Ala Leu Glu Lys Thr
 1345 1350 1355 1360
 Glu His Ala Ser Gly Ile Gly Asp His Ser Gln His Gly Pro Gly Trp
 1365 1370 1375
 Thr Leu Leu Lys Pro Ser Leu Ile Lys Cys Leu Ala Val Ser Ser Ser
 1380 1385 1390
 Val Ser Asn Glu Glu Ile Ser Gln Glu His Ile Ile Ile Glu Ala Ala
 1395 1400 1405
 Asp Ser Gly Arg Gly Ser Trp Thr Ser Cys Ser Ser Ser Ser His Asp
 1410 1415 1420
 Asn Phe Gln Ser Leu Pro Asn Pro Lys Ser Trp Asp Phe Leu Asn Ser
 1425 1430 1435 1440
 Tyr Arg His Thr His Leu Asp Asp Pro Ile Ala Glu Val Glu Pro Thr
 1445 1450 1455
 Asp Ser Glu Pro Tyr Ser Cys Ser Lys Ser Cys Ser Arg Thr Cys Gly
 1460 1465 1470
 Gln Cys Lys Gly Ser Leu Glu Arg Lys Ser Trp Thr Ser Ser Ser Ser
 1475 1480 1485
 Leu Ser Asp Thr Tyr Glu Pro Asn Tyr Gly Thr Val Lys Arg Arg Val
 1490 1495 1500
 Leu Glu Ser Thr Pro Ala Glu Ser Ser Glu Gly Leu Asp Pro Lys Asp
 1505 1510 1515 1520
 Ala Thr Asp Pro Val Tyr Lys Thr Val Thr Ser Ser Thr Glu Lys Gly
 1525 1530 1535
 Leu Ile Val Tyr Cys Val Thr Ser Pro Lys Lys Asp Asp Arg Tyr Arg
 1540 1545 1550
 Glu Pro Pro Pro Thr Pro Pro Gly Tyr Leu Gly Ile Ser Leu Ala Asp
 1555 1560 1565
 Leu Lys Glu Gly Pro His Thr His Leu Lys Pro Pro Asp Tyr Ser Val
 1570 1575 1580
 Ala Val Gln Arg Ser Lys Met Met His Asn Ser Leu Ser Arg Leu Pro
 1585 1590 1595 1600
 Pro Ala Ser Leu Ser Ser Asn Leu Val Ala Cys Val Pro Ser Lys Ile
 1605 1610 1615
 Val Thr Gln Pro Gln Arg His Asn Leu Gln Pro Phe His Pro Lys Leu
 1620 1625 1630
 Gly Asp Val Thr Asp Ala Asp Ser Glu Ala Asp Glu Asn Glu Gln Val
 1635 1640 1645
 Ser Ala Val
 1650

<210> 154
 <211> 1424
 <212> PRT
 <213> Homo sapiens

<400> 154
 Met Ser Asp Ser Trp Val Pro Asn Ser Ala Ser Gly Gln Asp Pro Gly
 1 5 10 15
 Gly Arg Arg Ala Trp Ala Glu Leu Leu Ala Gly Arg Val Lys Arg
 20 25 30
 Glu Lys Tyr Asn Pro Glu Arg Ala Gln Lys Leu Lys Glu Ser Ala Val
 35 40 45
 Arg Leu Leu Arg Ser His Gln Asp Leu Asn Ala Leu Leu Leu Val

50	55	60
Glu Gly Pro Leu Cys Lys Lys Leu Ser Leu Ser Lys Val Ile Asp Cys	70	75
65 Asp Ser Ser Glu Ala Tyr Ala Asn His Ser Ser Ser Phe Ile Gly Ser	85	90
Ala Leu Gln Asp Gln Ala Ser Arg Leu Gly Val Pro Val Gly Ile Leu	100	105
Ser Ala Gly Met Val Ala Ser Ser Val Gly Gln Ile Cys Thr Ala Pro	115	120
Ala Glu Thr Ser His Pro Val Leu Leu Thr Val Glu Gln Arg Lys Lys	130	135
Leu Ser Ser Leu Leu Glu Phe Ala Gln Tyr Leu Leu Ala His Ser Met	145	150
Phe Ser Arg Leu Ser Phe Cys Gln Glu Leu Trp Lys Ile Gln Ser Ser	165	170
Leu Leu Leu Glu Ala Val Trp His Leu His Val Gln Gly Ile Val Ser	180	185
Leu Gln Glu Leu Leu Glu Ser His Pro Asp Met His Ala Val Gly Ser	195	200
Trp Leu Phe Arg Asn Leu Cys Cys Leu Cys Glu Gln Met Glu Ala Ser	210	215
Cys Gln His Ala Asp Val Ala Arg Ala Met Leu Ser Asp Phe Val Gln	225	230
Met Phe Val Leu Arg Gly Phe Gln Lys Asn Ser Asp Leu Arg Arg Thr	245	250
Val Glu Pro Glu Lys Met Pro Gln Val Thr Val Asp Val Leu Gln Arg	260	265
Met Leu Ile Phe Ala Leu Asp Ala Leu Ala Gly Val Gln Glu Glu	275	280
Ser Ser Thr His Lys Ile Val Arg Cys Trp Phe Gly Val Phe Ser Gly	290	295
His Thr Leu Gly Ser Val Ile Ser Thr Asp Pro Leu Lys Arg Phe Phe	305	310
Ser His Thr Leu Thr Gln Ile Leu Thr His Ser Pro Val Leu Lys Ala	315	320
Ser Asp Ala Val Gln Met Gln Arg Glu Trp Ser Phe Ala Arg Thr His	325	330
Pro Leu Leu Thr Ser Leu Tyr Arg Arg Leu Phe Val Met Leu Ser Ala	335	340
Glu Glu Leu Val Gly His Leu Gln Glu Val Leu Glu Thr Gln Glu Val	345	350
His Trp Gln Arg Val Leu Ser Phe Val Ser Ala Leu Val Val Cys Phe	355	360
365 Pro Glu Ala Gln Gln Leu Leu Glu Asp Trp Val Ala Arg Leu Met Ala	370	375
Gln Ala Phe Glu Ser Cys Gln Leu Asp Ser Met Val Thr Ala Phe Leu	380	385
Val Val Arg Gln Ala Ala Leu Glu Gly Pro Ser Ala Phe Leu Ser Tyr	390	395
Ala Asp Trp Phe Lys Ala Ser Phe Gly Ser Thr Arg Gly Tyr His Gly	400	405
Cys Ser Lys Lys Ala Leu Val Phe Leu Phe Thr Phe Leu Ser Glu Leu	410	415
Val Pro Phe Glu Ser Pro Arg Tyr Leu Gln Val His Ile Leu His Pro	420	425
Pro Leu Val Pro Ser Lys Tyr Arg Ser Leu Leu Thr Asp Tyr Ile Ser	430	435
Leu Ala Lys Thr Arg Leu Ala Ser Asp Leu Lys Val Ser Ile Glu Asn Met	440	445
Gly Leu Tyr Glu Asp Leu Ser Ser Ala Gly Asp Ile Thr Glu Pro His	450	455

Ser Gln Ala Leu Gln Asp Val Glu Lys Ala Ile Met Val Phe Glu His
 545 550 555 560
 Thr Gly Asn Ile Pro Val Thr Val Met Glu Ala Ser Ile Phe Arg Arg
 565 570 575
 Pro Tyr Tyr Val Ser His Phe Leu Pro Ala Leu Leu Thr Pro Arg Val
 580 585 590
 Leu Pro Lys Val Pro Asp Ser Arg Val Ala Phe Ile Glu Ser Leu Lys
 595 600 605
 Arg Ala Asp Lys Ile Pro Pro Ser Leu Tyr Ser Thr Tyr Cys Gln Ala
 610 615 620
 Cys Ser Ala Ala Glu Glu Lys Pro Glu Asp Ala Ala Leu Gly Val Arg
 625 630 635 640
 Ala Glu Pro Asn Ser Ala Glu Glu Pro Leu Gly Gln Leu Thr Ala Ala
 645 650 655
 Leu Gly Glu Leu Arg Ala Ser Met Thr Asp Pro Ser Gln Arg Asp Val
 660 665 670
 Ile Ser Ala Gln Val Ala Val Ile Ser Glu Arg Leu Arg Ala Val Leu
 675 680 685
 Gly His Asn Glu Asp Asp Ser Ser Val Glu Ile Ser Lys Ile Gln Leu
 690 695 700
 Ser Ile Asn Thr Pro Arg Leu Glu Pro Arg Glu His Ile Ala Val Asp
 705 710 715 720
 Leu Leu Leu Thr Ser Phe Cys Gln Asn Leu Met Ala Ala Ser Ser Val
 725 730 735
 Ala Pro Pro Glu Arg Gln Gly Pro Trp Ala Ala Leu Phe Val Arg Thr
 740 745 750
 Met Cys Gly Arg Val Leu Pro Ala Val Leu Thr Arg Leu Cys Gln Leu
 755 760 765
 Leu Arg His Gln Gly Pro Ser Leu Ser Ala Pro His Val Leu Gly Leu
 770 775 780
 Ala Ala Leu Ala Val His Leu Gly Glu Ser Arg Ser Ala Leu Pro Glu
 785 790 795 800
 Val Asp Val Gly Pro Pro Ala Pro Gly Ala Gly Leu Pro Val Pro Ala
 805 810 815
 Leu Phe Asp Ser Leu Leu Thr Cys Arg Thr Arg Asp Ser Leu Phe Phe
 820 825 830
 Cys Leu Lys Phe Cys Thr Ala Ala Ile Ser Tyr Ser Leu Cys Lys Phe
 835 840 845
 Ser Ser Gln Ser Arg Asp Thr Leu Cys Ser Cys Leu Ser Pro Gly Leu
 850 855 860
 Ile Lys Lys Phe Gln Phe Leu Met Phe Arg Leu Phe Ser Glu Ala Arg
 865 870 875 880
 Gln Pro Leu Ser Glu Glu Asp Val Ala Ser Leu Ser Trp Arg Pro Leu
 885 890 895
 His Leu Pro Ser Ala Asp Trp Gln Arg Ala Ala Leu Ser Leu Trp Thr
 900 905 910
 His Arg Thr Phe Arg Glu Val Leu Lys Glu Glu Asp Val His Leu Thr
 915 920 925
 Tyr Gln Asp Trp Leu His Leu Glu Leu Glu Ile Gln Pro Glu Ala Asp
 930 935 940
 Ala Leu Ser Asp Thr Glu Arg Gln Asp Phe His Gln Trp Ala Ile His
 945 950 955 960
 Glu His Phe Leu Pro Glu Ser Ser Ala Ser Gly Gly Cys Asp Gly Asp
 965 970 975
 Leu Gln Ala Ala Cys Thr Ile Leu Val Asn Ala Leu Met Asp Phe His
 980 985 990
 Gln Ser Ser Arg Ser Tyr Asp His Ser Glu Asn Ser Asp Leu Val Phe
 995 1000 1005
 Gly Gly Arg Thr Gly Asn Glu Asp Ile Ile Ser Arg Leu Gln Glu Met
 1010 1015 1020
 Val Ala Asp Leu Glu Leu Gln Gln Asp Leu Ile Val Pro Leu Gly His

1025 1030 1035 1040
 Thr Pro Ser Gln Glu His Phe Leu Phe Glu Ile Phe Arg Arg Arg Leu
 1045 1050 1055
 Gln Ala Leu Thr Ser Gly Trp Ser Val Ala Ala Ser Leu Gln Arg Gln
 1060 1065 1070
 Arg Glu Leu Leu Met Tyr Lys Arg Ile Leu Leu Arg Leu Pro Ser Ser
 1075 1080 1085
 Val Leu Cys Gly Ser Ser Phe Gln Ala Glu Gln Pro Ile Thr Ala Arg
 1090 1095 1100
 Cys Glu Gln Phe Phe His Leu Val Asn Ser Glu Met Arg Asn Phe Cys
 1105 1110 1115 1120
 Ser His Gly Gly Ala Leu Thr Gln Asp Ile Thr Ala His Phe Phe Arg
 1125 1130 1135
 Gly Leu Leu Asn Ala Cys Leu Arg Ser Arg Asp Pro Ser Leu Met Val
 1140 1145 1150
 Asp Phe Ile Leu Ala Lys Cys Gln Thr Lys Cys Pro Leu Ile Leu Thr
 1155 1160 1165
 Ser Ala Leu Val Trp Trp Pro Ser Leu Glu Pro Val Leu Leu Cys Arg
 1170 1175 1180
 Trp Arg Arg His Cys Gln Ser Pro Leu Pro Arg Glu Leu Gln Lys Leu
 1185 1190 1195 1200
 Gln Glu Gly Arg Gln Phe Ala Ser Asp Phe Leu Ser Pro Glu Ala Ala
 1205 1210 1215
 Ser Pro Ala Pro Asn Pro Asp Trp Leu Ser Ala Ala Ala Leu His Phe
 1220 1225 1230
 Ala Ile Gln Gln Val Arg Glu Glu Asn Ile Arg Lys Gln Leu Lys Lys
 1235 1240 1245
 Leu Asp Cys Glu Arg Glu Glu Leu Leu Val Phe Leu Phe Phe Ser
 1250 1255 1260
 Leu Met Gly Leu Leu Ser Ser His Leu Thr Ser Asn Ser Thr Thr Asp
 1265 1270 1275 1280
 Leu Pro Lys Ala Phe His Val Cys Ala Ala Ile Leu Glu Cys Leu Glu
 1285 1290 1295
 Lys Arg Lys Ile Ser Trp Leu Ala Leu Phe Gln Leu Thr Glu Ser Asp
 1300 1305 1310
 Leu Arg Leu Gly Arg Leu Leu Leu Arg Val Ala Pro Asp Gln His Thr
 1315 1320 1325
 Arg Leu Leu Pro Phe Ala Phe Tyr Ser Leu Leu Ser Tyr Phe His Glu
 1330 1335 1340
 Asp Ala Ala Ile Arg Glu Glu Ala Phe Leu His Val Ala Val Asp Met
 1345 1350 1355 1360
 Tyr Leu Lys Leu Val Gln Leu Phe Val Ala Gly Asp Thr Ser Thr Val
 1365 1370 1375
 Ser Pro Pro Ala Gly Arg Ser Leu Glu Leu Lys Gly Gln Ala Gly Gln
 1380 1385 1390
 Pro Arg Gly Thr Asp Asn Lys Ser Ser Phe Ser Ala Ala Val Asn
 1395 1400 1405
 Thr Ser Val Pro Glu Lys Glu Leu Leu Thr Arg Gly Arg Ala Ala Gly
 1410 1415 1420

<210> 155
 <211> 1381
 <212> PRT
 <213> Homo sapiens

<400> 155

Met Ser Asp Ser Trp Val Pro Asn Ser Ala Ser Gly Gln Asp Pro Gly
 1 5 10 15
 Gly Arg Arg Arg Ala Trp Ala Glu Leu Leu Ala Gly Arg Val Lys Arg
 20 25 30
 Glu Lys Tyr Asn Pro Glu Arg Ala Gln Lys Leu Lys Glu Ser Ala Val
 35 40 45
 Arg Leu Leu Arg Ser His Gln Asp Leu Asn Ala Leu Leu Leu Glu Val
 50 55 60
 Glu Gly Pro Leu Cys Lys Lys Leu Ser Leu Ser Lys Val Ile Asp Cys
 65 70 75 80
 Asp Ser Ser Glu Ala Tyr Ala Asn His Ser Ser Ser Phe Ile Gly Ser
 85 90 95
 Ala Leu Gln Asp Gln Ala Ser Arg Leu Gly Val Pro Val Gly Ile Leu
 100 105 110
 Ser Ala Gly Met Val Ala Ser Ser Val Gly Gln Ile Cys Thr Ala Pro
 115 120 125
 Ala Glu Thr Ser His Pro Val Leu Leu Thr Val Glu Gln Arg Lys Lys
 130 135 140
 Leu Ser Ser Leu Leu Glu Phe Ala Gln Tyr Leu Leu Ala His Ser Met
 145 150 155 160
 Phe Ser Arg Leu Ser Phe Cys Gln Glu Leu Trp Lys Ile Gln Ser Ser
 165 170 175
 Leu Leu Leu Glu Ala Val Trp His Leu His Val Gln Gly Ile Val Ser
 180 185 190
 Leu Gln Glu Leu Leu Glu Ser His Pro Asp Met His Ala Val Gly Ser
 195 200 205
 Trp Leu Phe Arg Asn Leu Cys Cys Leu Cys Glu Gln Met Glu Ala Ser
 210 215 220
 Cys Gln His Ala Asp Val Ala Arg Ala Met Leu Ser Asp Phe Val Gln
 225 230 235 240
 Met Phe Val Leu Arg Gly Phe Gln Lys Asn Ser Asp Leu Arg Arg Thr
 245 250 255
 Val Glu Pro Glu Lys Met Pro Gln Val Thr Val Asp Val Leu Gln Arg
 260 265 270
 Met Leu Ile Phe Ala Leu Asp Ala Leu Ala Ala Gly Val Gln Glu Glu
 275 280 285
 Ser Ser Thr His Lys Ile Val Arg Cys Trp Phe Gly Val Phe Ser Gly
 290 295 300
 His Thr Leu Gly Ser Val Ile Ser Thr Asp Pro Leu Lys Arg Phe Phe
 305 310 315 320
 Ser His Thr Leu Thr Gln Ile Leu Thr His Ser Pro Val Leu Lys Ala
 325 330 335
 Ser Asp Ala Val Gln Met Gln Arg Glu Trp Ser Phe Ala Arg Thr His
 340 345 350
 Pro Leu Leu Thr Ser Leu Tyr Arg Arg Leu Phe Val Met Leu Ser Ala
 355 360 365
 Glu Glu Leu Val Gly His Leu Gln Glu Val Leu Glu Thr Gln Glu Val
 370 375 380
 His Trp Gln Arg Val Leu Ser Phe Val Ser Ala Leu Val Val Cys Phe
 385 390 395 400
 Pro Glu Ala Gln Gln Leu Leu Glu Asp Trp Val Ala Arg Leu Met Ala
 405 410 415
 Gln Ala Phe Glu Ser Cys Gln Leu Asp Ser Met Val Thr Ala Phe Leu
 420 425 430
 Val Val Arg Gln Ala Ala Leu Glu Gly Pro Ser Ala Phe Leu Ser Tyr
 435 440 445
 Ala Asp Trp Phe Lys Ala Ser Phe Gly Ser Thr Arg Gly Tyr His Gly
 450 455 460
 Cys Ser Lys Lys Ala Leu Val Phe Leu Phe Thr Phe Leu Ser Glu Leu
 465 470 475 480
 Val Pro Phe Glu Ser Pro Arg Tyr Leu Gln Val His Ile Leu His Pro

										485				490				495			
Pro	Leu	Val	Pro	Ser	Lys	Tyr	Arg	Ser	Leu	Leu	Thr	Asp	Tyr	Ile	Ser						
			500					505					510								
Leu	Ala	Lys	Thr	Arg	Leu	Ala	Asp	Leu	Lys	Val	Ser	Ile	Glu	Asn	Met						
		515					520					525									
Gly	Leu	Tyr	Glu	Asp	Leu	Ser	Ser	Ala	Gly	Asp	Ile	Thr	Glu	Pro	His						
	530				535					540											
Ser	Gln	Ala	Leu	Gln	Asp	Val	Glu	Lys	Ala	Ile	Met	Val	Phe	Glu	His						
	545			550					555					560							
Thr	Gly	Asn	Ile	Pro	Val	Thr	Val	Met	Glu	Ala	Ser	Ile	Phe	Arg	Arg						
			565					570						575							
Pro	Tyr	Tyr	Val	Ser	His	Phe	Leu	Pro	Ala	Leu	Leu	Thr	Pro	Arg	Val						
		580					585						590								
Leu	Pro	Lys	Val	Pro	Asp	Ser	Arg	Val	Ala	Phe	Ile	Glu	Ser	Leu	Lys						
		595					600					605									
Arg	Ala	Asp	Lys	Ile	Pro	Pro	Ser	Leu	Tyr	Ser	Thr	Tyr	Cys	Gln	Ala						
	610				615						620										
Cys	Ser	Ala	Ala	Glu	Glu	Lys	Pro	Glu	Asp	Ala	Ala	Leu	Gly	Val	Arg						
	625				630				635					640							
Ala	Glu	Pro	Asn	Ser	Ala	Glu	Glu	Pro	Leu	Gly	Gln	Leu	Thr	Ala	Ala						
			645					650						655							
Leu	Gly	Glu	Leu	Arg	Ala	Ser	Met	Thr	Asp	Pro	Ser	Gln	Arg	Asp	Val						
		660					665						670								
Ile	Ser	Ala	Gln	Val	Ala	Val	Ile	Ser	Glu	Arg	Leu	Arg	Ala	Val	Leu						
		675					680					685									
Gly	His	Asn	Glu	Asp	Asp	Ser	Ser	Val	Glu	Ile	Ser	Lys	Ile	Gln	Leu						
		690			695						700										
Ser	Ile	Asn	Thr	Pro	Arg	Leu	Glu	Pro	Arg	Glu	His	Ile	Ala	Val	Asp						
	705			710					715					720							
Leu	Leu	Leu	Thr	Ser	Phe	Cys	Gln	Asn	Leu	Met	Ala	Ala	Ser	Ser	Val						
			725					730					735								
Ala	Pro	Pro	Glu	Arg	Gln	Gly	Pro	Trp	Ala	Ala	Leu	Phe	Val	Arg	Thr						
		740					745						750								
Met	Cys	Gly	Arg	Val	Leu	Pro	Ala	Val	Leu	Thr	Arg	Leu	Cys	Gln	Leu						
		755				760						765									
Leu	Arg	His	Gln	Gly	Pro	Ser	Leu	Ser	Ala	Pro	His	Val	Leu	Gly	Leu						
	770				775						780										
Ala	Ala	Leu	Ala	Val	His	Leu	Gly	Glu	Ser	Arg	Ser	Ala	Leu	Pro	Glu						
	785			790					795					800							
Val	Asp	Val	Gly	Pro	Pro	Ala	Pro	Gly	Ala	Gly	Leu	Pro	Val	Pro	Ala						
			805					810						815							
Leu	Phe	Asp	Ser	Leu	Leu	Thr	Cys	Arg	Thr	Arg	Asp	Ser	Leu	Phe	Phe						
		820					825						830								
Cys	Leu	Lys	Phe	Cys	Thr	Ala	Ala	Ile	Ser	Tyr	Ser	Leu	Cys	Lys	Phe						
	835						840					845									
Ser	Ser	Gln	Ser	Arg	Asp	Thr	Leu	Cys	Ser	Cys	Leu	Ser	Pro	Gly	Leu						
	850				855						860										
Ile	Lys	Lys	Phe	Gln	Phe	Leu	Met	Phe	Arg	Leu	Phe	Ser	Glu	Ala	Arg						
	865			870					875					880							
Gln	Pro	Leu	Ser	Glu	Glu	Asp	Val	Ala	Ser	Leu	Ser	Trp	Arg	Pro	Leu						
			885					890						895							
His	Leu	Pro	Ser	Ala	Asp	Trp	Gln	Arg	Ala	Ala	Leu	Ser	Leu	Trp	Thr						
		900					905						910								
His	Arg	Thr	Phe	Arg	Glu	Val	Leu	Lys	Glu	Glu	Asp	Val	His	Leu	Thr						
		915					920					925									
Tyr	Gln	Asp	Trp	Leu	His	Leu	Glu	Leu	Glu	Ile	Gln	Pro	Glu	Ala	Asp						
	930				935						940										
Ala	Leu	Ser	Asp	Thr	Glu	Arg	Ser	Arg	Ser	Tyr	Asp	His	Ser	Glu	Asn						
	945				950				955					960							
Ser	Asp	Leu	Val	Phe	Gly	Gly	Arg	Thr	Gly	Asn	Glu	Asp	Ile	Ile	Ser						
			965						970					975							

Arg Leu Gln Glu Met Val Ala Asp Leu Glu Leu Gln Gln Asp Leu Ile
 980 985 990
 Val Pro Leu Gly His Thr Pro Ser Gln Glu His Phe Leu Phe Glu Ile
 995 1000 1005
 Phe Arg Arg Arg Leu Gln Ala Leu Thr Ser Gly Trp Ser Val Ala Ala
 1010 1015 1020
 Ser Leu Gln Arg Gln Arg Glu Leu Leu Met Tyr Lys Arg Ile Leu Leu
 1025 1030 1035 1040
 Arg Leu Pro Ser Ser Val Leu Cys Gly Ser Ser Phe Gln Ala Glu Gln
 1045 1050 1055
 Pro Ile Thr Ala Arg Cys Glu Gln Phe Phe His Leu Val Asn Ser Glu
 1060 1065 1070
 Met Arg Asn Phe Cys Ser His Gly Gly Ala Leu Thr Gln Asp Ile Thr
 1075 1080 1085
 Ala His Phe Phe Arg Gly Leu Leu Asn Ala Cys Leu Arg Ser Arg Asp
 1090 1095 1100
 Pro Ser Leu Met Val Asp Phe Ile Leu Ala Lys Cys Gln Thr Lys Cys
 1105 1110 1115 1120
 Pro Leu Ile Leu Thr Ser Ala Leu Val Trp Trp Pro Ser Leu Glu Pro
 1125 1130 1135
 Val Leu Leu Cys Arg Trp Arg Arg His Cys Gln Ser Pro Leu Pro Arg
 1140 1145 1150
 Glu Leu Gln Lys Leu Gln Glu Gly Arg Gln Phe Ala Ser Asp Phe Leu
 1155 1160 1165
 Ser Pro Glu Ala Ala Ser Pro Ala Pro Asn Pro Asp Trp Leu Ser Ala
 1170 1175 1180
 Ala Ala Leu His Phe Ala Ile Gln Gln Val Arg Glu Glu Asn Ile Arg
 1185 1190 1195 1200
 Lys Gln Leu Lys Lys Leu Asp Cys Glu Arg Glu Glu Leu Leu Val Phe
 1205 1210 1215
 Leu Phe Phe Phe Ser Leu Met Gly Leu Leu Ser Ser His Leu Thr Ser
 1220 1225 1230
 Asn Ser Thr Thr Asp Leu Pro Lys Ala Phe His Val Cys Ala Ala Ile
 1235 1240 1245
 Leu Glu Cys Leu Glu Lys Arg Lys Ile Ser Trp Leu Ala Leu Phe Gln
 1250 1255 1260
 Leu Thr Glu Ser Asp Leu Arg Leu Gly Arg Leu Leu Leu Arg Val Ala
 1265 1270 1275 1280
 Pro Asp Gln His Thr Arg Leu Leu Pro Phe Ala Phe Tyr Ser Leu Leu
 1285 1290 1295
 Ser Tyr Phe His Glu Asp Ala Ala Ile Arg Glu Glu Ala Phe Leu His
 1300 1305 1310
 Val Ala Val Asp Met Tyr Leu Lys Leu Val Gln Leu Phe Val Ala Gly
 1315 1320 1325
 Asp Thr Ser Thr Val Ser Pro Pro Ala Gly Arg Ser Leu Glu Leu Lys
 1330 1335 1340
 Gly Gln Ala Gly Gln Pro Arg Gly Thr Asp Asn Lys Ser Ser Ser Phe
 1345 1350 1355 1360
 Ser Ala Ala Val Asn Thr Ser Val Pro Glu Lys Glu Leu Leu Thr Arg
 1365 1370 1375
 Gly Arg Ala Ala Gly
 1380

<210> 156
 <211> 162
 <212> PRT
 <213> Homo sapiens

```

<400> 156
Met Leu Arg Ala Val Gly Ser Leu Leu Arg Leu Gly Arg Gly Leu Thr
 1          5          10          15
Val Arg Cys Gly Pro Gly Ala Pro Leu Glu Ala Thr Arg Arg Pro Ala
          20          25          30
Pro Ala Leu Pro Pro Arg Gly Leu Pro Cys Tyr Ser Ser Gly Gly Ala
          35          40          45
Pro Ser Asn Ser Gly Pro Gln Gly His Gly Glu Ile His Arg Val Pro
          50          55          60
Thr Gln Arg Arg Pro Ser Gln Phe Asp Lys Lys Ile Leu Leu Trp Thr
          65          70          75          80
Gly Arg Phe Lys Ser Met Glu Glu Ile Pro Pro Arg Ile Pro Pro Glu
          85          90          95
Met Ile Asp Thr Ala Arg Asn Lys Ala Arg Val Lys Ala Cys Tyr Ile
          100          105          110
Met Ile Gly Leu Thr Ile Ile Ala Cys Phe Ala Val Ile Val Ser Ala
          115          120          125
Lys Arg Ala Val Glu Arg His Glu Ser Leu Thr Ser Trp Asn Leu Ala
          130          135          140
Lys Lys Ala Lys Trp Arg Glu Glu Ala Ala Leu Ala Ala Gln Ala Lys
          145          150          155          160
Ala Lys

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<210> 157
<211> 311
<212> PRT
<213> Homo sapiens

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```

<400> 157
Met His Ala Ala Arg His Gly Trp Asp Val Glu Lys Asp Ala Pro Leu
 1          5          10          15
Phe Arg Asn Trp Ala Ile His Thr Gly Lys His Gln Pro Gly Val Asp
          20          25          30
Lys Pro Asp Pro Lys Thr Trp Lys Ala Asn Phe Arg Cys Ala Met Asn
          35          40          45
Ser Leu Pro Asp Ile Glu Glu Val Lys Asp Lys Ser Ile Lys Lys Gly
          50          55          60
Asn Asn Ala Phe Arg Val Tyr Arg Met Leu Pro Leu Ser Glu Arg Pro
          65          70          75          80
Ser Lys Lys Gly Lys Lys Pro Lys Thr Glu Lys Glu Asp Lys Val Lys
          85          90          95
His Ile Lys Gln Glu Pro Val Glu Ser Ser Leu Gly Leu Ser Asn Gly
          100          105          110
Val Ser Asp Leu Ser Pro Glu Tyr Ala Val Leu Thr Ser Thr Ile Lys
          115          120          125
Asn Glu Val Asp Ser Thr Val Asn Ile Ile Val Val Gly Gln Ser His
          130          135          140
Leu Asp Ser Asn Ile Glu Asn Gln Glu Ile Val Thr Asn Pro Pro Asp
          145          150          155          160
Ile Cys Gln Val Val Glu Val Thr Thr Glu Ser Asp Glu Gln Pro Val
          165          170          175
Ser Met Ser Glu Leu Tyr Pro Leu Gln Ile Ser Pro Val Ser Ser Tyr
          180          185          190
Ala Glu Ser Glu Thr Thr Asp Ser Val Pro Ser Asp Glu Glu Ser Ala
          195          200          205
Glu Gly Arg Pro His Trp Arg Lys Arg Asn Ile Glu Gly Lys Gln Tyr
          210          215          220

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Leu Ser Asn Met Gly Thr Arg Gly Ser Tyr Leu Leu Pro Gly Met Ala
225      230      235      240
Ser Phe Val Thr Ser Asn Lys Pro Asp Leu Gln Val Thr Ile Lys Glu
      245      250      255
Glu Ser Asn Pro Val Pro Tyr Asn Ser Ser Trp Pro Pro Phe Gln Asp
      260      265      270
Leu Pro Leu Ser Ser Ser Met Thr Pro Ala Ser Ser Ser Ser Arg Pro
      275      280      285
Asp Arg Glu Thr Arg Ala Ser Val Ile Lys Lys Thr Ser Asp Ile Thr
      290      295      300
Gln Ala Arg Val Lys Ser Cys
305      310

```

```

<210> 158
<211> 210
<212> PRT
<213> Homo sapiens

```

```

<400> 158
Met Asn Ser Leu Pro Asp Ile Glu Glu Val Lys Asp Lys Ser Ile Lys
1      5      10      15
Lys Gly Asn Asn Ala Phe Arg Val Tyr Arg Met Leu Pro Leu Ser Glu
      20      25      30
Arg Pro Ser Lys Lys Val Val Gly Gln Ser His Leu Asp Ser Asn Ile
      35      40      45
Glu Asn Gln Glu Ile Val Thr Asn Pro Pro Asp Ile Cys Gln Val Val
      50      55      60
Glu Val Thr Thr Glu Ser Asp Glu Gln Pro Val Ser Met Ser Glu Leu
      65      70      75      80
Tyr Pro Leu Gln Ile Ser Pro Val Ser Ser Tyr Ala Glu Ser Glu Thr
      85      90      95
Thr Asp Ser Val Pro Ser Asp Glu Glu Ser Ala Glu Gly Arg Pro His
      100      105      110
Trp Arg Lys Arg Asn Ile Glu Gly Lys Gln Tyr Leu Ser Asn Met Gly
      115      120      125
Thr Arg Gly Ser Tyr Leu Leu Pro Gly Met Ala Ser Phe Val Thr Ser
      130      135      140
Asn Lys Pro Asp Leu Gln Val Thr Ile Lys Glu Glu Ser Asn Pro Val
      145      150      155      160
Pro Tyr Asn Ser Ser Trp Pro Pro Phe Gln Asp Leu Pro Leu Ser Ser
      165      170      175
Ser Met Thr Pro Ala Ser Ser Ser Ser Arg Pro Asp Arg Glu Thr Arg
      180      185      190
Ala Ser Val Ile Lys Lys Thr Ser Asp Ile Thr Gln Ala Arg Val Lys
      195      200      205
Ser Cys
210

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<210> 159
<211> 529
<212> PRT
<213> Homo sapiens

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<400> 159
Met Tyr Lys Arg Asn Gly Leu Met Ala Ser Val Leu Val Thr Ser Ala

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1	5	10	15
Thr Pro Gln Gly Ser Ser Ser Ser Asp Ser Leu Glu Gly Gln Ser Cys			
20		25	30
Asp Tyr Ala Ser Lys Ser Tyr Asp Ala Val Val Phe Asp Val Leu Lys			
35		40	45
Val Thr Pro Glu Glu Phe Ala Ser Gln Ile Thr Leu Met Asp Ile Pro			
50		55	60
Val Phe Lys Ala Ile Gln Pro Glu Glu Leu Ala Ser Cys Gly Trp Ser			
65		70	75
Lys Lys Glu Lys His Ser Leu Ala Pro Asn Val Val Ala Phe Thr Arg			
85		90	95
Arg Phe Asn Gln Val Ser Phe Trp Val Val Arg Glu Ile Leu Thr Ala			
100		105	110
Gln Thr Leu Lys Ile Arg Ala Glu Ile Leu Ser His Phe Val Lys Ile			
115		120	125
Ala Lys Lys Leu Leu Glu Leu Asn Asn Leu His Ser Leu Met Ser Val			
130		135	140
Val Ser Ala Leu Gln Ser Ala Pro Ile Phe Arg Leu Thr Lys Thr Trp			
145		150	155
Ala Leu Leu Asn Arg Lys Asp Lys Thr Thr Phe Glu Lys Leu Asp Tyr			
165		170	175
Leu Met Ser Lys Glu Asp Asn Tyr Lys Arg Thr Arg Glu Tyr Ile Arg			
180		185	190
Ser Leu Lys Met Val Pro Ser Ile Pro Tyr Leu Gly Ile Tyr Leu Leu			
195		200	205
Asp Leu Ile Tyr Ile Asp Ser Ala Tyr Pro Ala Ser Gly Ser Ile Met			
210		215	220
Glu Asn Glu Gln Arg Ser Asn Gln Met Asn Asn Ile Leu Arg Ile Ile			
225		230	235
Ala Asp Leu Gln Val Ser Cys Ser Tyr Asp His Leu Thr Thr Leu Pro			
245		250	255
His Val Gln Lys Tyr Leu Lys Ser Val Arg Tyr Ile Glu Glu Leu Gln			
260		265	270
Lys Phe Val Glu Asp Asp Asn Tyr Lys Leu Ser Leu Arg Ile Glu Pro			
275		280	285
Gly Ser Ser Ser Pro Arg Leu Val Ser Ser Lys Glu Asp Leu Ala Gly			
290		295	300
Pro Ser Ala Gly Ser Gly Ser Ala Arg Phe Ser Arg Arg Pro Thr Cys			
305		310	315
Pro Asp Thr Ser Val Ala Gly Ser Leu Pro Thr Pro Pro Val Pro Arg			
325		330	335
His Arg Lys Ser His Ser Leu Gly Asn Asn Arg Gly Arg Leu Tyr Ala			
340		345	350
Thr Leu Gly Pro Asn Trp Arg Val Pro Val Arg Asn Ser Pro Arg Thr			
355		360	365
Arg Ser Cys Val Tyr Ser Pro Thr Gly Pro Cys Ile Cys Ser Leu Gly			
370		375	380
Asn Ser Ala Ala Val Pro Thr Met Glu Gly Pro Leu Arg Arg Lys Thr			
385		390	395
Leu Leu Lys Glu Gly Arg Lys Pro Ala Leu Ser Ser Trp Thr Arg Tyr			
405		410	415
Trp Val Ile Leu Ser Gly Ser Thr Leu Leu Tyr Tyr Gly Ala Lys Ser			
420		425	430
Leu Arg Gly Thr Asp Arg Lys His Val Ser Ile Val Gly Trp Met Val			
435		440	445
Gln Leu Pro Asp Asp Pro Glu His Pro Asp Ile Phe Gln Leu Asn Asn			
450		455	460
Pro Asp Lys Gly Asn Val Tyr Lys Phe Gln Thr Gly Ser Arg Phe His			
465		470	475
Ala Ile Leu Trp His Lys His Leu Asp Asp Ala Cys Lys Ser Asn Arg			
485		490	495

Pro Gln Glu Ala Gly Ala Ala Pro Gly Pro Thr Gly Thr Asp Ser His
 500 505
 Glu Val Asp His Leu Glu Gly Gly Ala Gly Lys Glu Ala Gly Pro Cys
 515 520 525
 Ala

<210> 160
 <211> 404
 <212> PRT
 <213> Homo sapiens

<400> 160
 Met Ala Glu Glu Gln Gln Gln Pro Pro Pro Gln Gln Pro Asp Ala His
 1 5 10 15
 Gln Gln Leu Pro Pro Ser Ala Pro Asn Ser Gly Val Ala Leu Pro Ala
 20 25 30
 Leu Val Pro Gly Leu Pro Gly Thr Glu Ala Ser Ala Leu Gln His Lys
 35 40 45
 Ile Lys Asn Ser Ile Cys Lys Thr Val Gln Ser Lys Val Asp Cys Ile
 50 55 60
 Leu Gln Glu Val Glu Lys Phe Thr Asp Leu Glu Lys Leu Tyr Leu Tyr
 65 70 75 80
 Leu Gln Leu Pro Ser Gly Leu Ser Asn Gly Glu Lys Ser Asp Gln Asn
 85 90 95
 Ala Met Ser Ser Ser Arg Ala Gln Gln Met His Ala Phe Ser Trp Ile
 100 105 110
 Arg Asn Thr Leu Glu Glu His Pro Glu Thr Ser Leu Pro Lys Gln Glu
 115 120 125
 Val Tyr Asp Glu Tyr Lys Ser Tyr Cys Asp Asn Leu Gly Tyr His Pro
 130 135 140
 Leu Ser Ala Ala Asp Phe Gly Lys Ile Met Lys Asn Val Phe Pro Asn
 145 150 155 160
 Met Lys Ala Arg Arg Leu Gly Thr Arg Gly Lys Ser Lys Tyr Cys Tyr
 165 170 175
 Ser Gly Leu Arg Lys Lys Ala Phe Val His Met Pro Thr Leu Pro Asn
 180 185 190
 Leu Asp Phe His Lys Thr Gly Asn Gly Leu Glu Gly Ala Glu Pro Ser
 195 200 205
 Gly Gln Leu Gln Asn Ile Asp Glu Glu Val Ile Ser Ser Ala Cys Arg
 210 215 220
 Leu Val Cys Glu Trp Ala Gln Lys Val Leu Ser Gln Pro Phe Asp Thr
 225 230 235 240
 Val Leu Glu Leu Ala Arg Phe Leu Val Lys Ser His Tyr Ile Gly Thr
 245 250 255
 Lys Ser Met Ala Ala Leu Thr Val Met Ala Ala Ala Pro Ala Gly Met
 260 265 270
 Lys Gly Ile Thr Gln Pro Ser Ala Phe Ile Pro Thr Ala Glu Ser Asn
 275 280 285
 Ser Phe Gln Pro Gln Val Lys Thr Leu Pro Ser Pro Ile Asp Ala Lys
 290 295 300
 Gln Gln Leu Gln Arg Lys Ile Gln Lys Lys Gln Gln Glu Gln Lys Leu
 305 310 315 320
 Gln Ser Pro Leu Pro Gly Glu Ser Ala Ala Lys Lys Ser Glu Ser Ala
 325 330 335
 Thr Ser Asn Gly Val Thr Asn Leu Pro Asn Gly Asn Pro Ser Ile Leu
 340 345 350
 Ser Pro Gln Pro Ile Gly Ile Val Met Ala Ala Val Pro Ser Pro Ile

355				360				365							
Pro	Val	Gln	Arg	Thr	Arg	His	Leu	Val	Thr	Ser	Pro	Ser	Pro	Met	Ser
370				375				380							
Ser	Ser	Asp	Gly	Lys	Val	Leu	Pro	Leu	Asn	Val	Gln	Val	Ser	Leu	Ser
385				390				395				400			
Thr	Cys	Ser	Leu												

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<210> 161
<211> 157
<212> PRT
<213> Homo sapiens
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<400> 161														
Met	Ser	Glu	Gly	Val	Asp	Leu	Ile	Asp	Ile	Tyr	Ala	Asp	Glu	Phe
1				5				10					15	
Asn	Gln	Asp	Pro	Glu	Phe	Asn	Asn	Thr	Asp	Gln	Ile	Asp	Leu	Tyr
			20					25					30	
Asp	Val	Leu	Thr	Ala	Thr	Ser	Gln	Pro	Ser	Asp	Asp	Arg	Ser	Ser
			35				40					45		
Thr	Glu	Pro	Pro	Pro	Pro	Val	Arg	Gln	Glu	Pro	Ser	Pro	Lys	Pro
			50			55					60			
Asn	Lys	Thr	Pro	Ala	Ile	Leu	Tyr	Thr	Tyr	Ser	Gly	Leu	Arg	Asn
65					70				75					80
Arg	Ala	Ala	Val	Tyr	Val	Gly	Ser	Phe	Ser	Trp	Trp	Thr	Thr	Asp
				85					90					95
Gln	Leu	Ile	Gln	Val	Ile	Arg	Ser	Ile	Gly	Val	Tyr	Asp	Val	Glu
			100					105				110		
Leu	Lys	Phe	Ala	Glu	Asn	Arg	Ala	Asn	Gly	Gln	Ser	Lys	Gly	Tyr
		115				120						125		Ala
Glu	Val	Val	Val	Ala	Ser	Glu	Asn	Ser	Val	His	Lys	Lys	Leu	Leu
		130				135					140			
Leu	Pro	Gly	Lys	Val	Leu	Asn	Trp	Gln	Lys	Lys	Trp	Thr		
145					150					155				

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<210> 162
<211> 354
<212> PRT
<213> Homo sapiens
```

<400> 162																	
Met	Gln	Glu	Ala	Ile	Ile	Leu	Leu	Ala	Leu	Leu	Gly	Ala	Met	Ser	Gly		
1				5					10					15			
Gly	Glu	Ala	Leu	His	Leu	Ile	Leu	Leu	Pro	Ala	Thr	Gly	Asn	Val	Ala		
			20					25					30				
Glu	Asn	Ser	Pro	Pro	Gly	Thr	Ser	Val	His	Lys	Phe	Ser	Val	Lys	Leu		
			35				40					45					
Ser	Ala	Ser	Leu	Ser	Pro	Val	Ile	Pro	Gly	Phe	Pro	Gln	Ile	Val	Asn		
	50					55				60							
Ser	Asn	Pro	Leu	Thr	Glu	Ala	Phe	Arg	Val	Asn	Trp	Leu	Ser	Gly	Thr		
65					70					75					80		
Tyr	Phe	Glu	Val	Val	Thr	Thr	Gly	Met	Glu	Gln	Leu	Asp	Phe	Glu	Thr		
				85					90					95			
Gly	Pro	Asn	Ile	Phe	Asp	Leu	Gln	Ile	Tyr	Val	Lys	Asp	Glu	Val	Gly		
			100					105					110				

Val Thr Asp Leu Gln Val Leu Thr Val Gln Val Thr Asp Val Asn Glu
 115 120 125
 Pro Pro Gln Phe Gln Gly Asn Leu Ala Glu Gly Leu His Leu Tyr Ile
 130 135 140
 Val Glu Arg Ala Asn Pro Gly Phe Ile Tyr Gln Val Glu Ala Phe Asp
 145 150 155 160
 Pro Glu Asp Thr Ser Arg Asn Ile Pro Leu Ser Tyr Phe Leu Ile Ser
 165 170 175
 Pro Pro Lys Ser Phe Arg Met Ser Ala Asn Gly Thr Leu Phe Ser Thr
 180 185 190
 Thr Glu Leu Asp Phe Glu Ala Gly His Arg Ser Phe His Leu Ile Val
 195 200 205
 Glu Val Arg Asp Ser Gly Gly Leu Lys Ala Ser Thr Glu Leu Gln Val
 210 215 220
 Asn Ile Val Asn Leu Asn Asp Glu Val Pro Arg Phe Thr Ser Pro Thr
 225 230 235 240
 Arg Val Tyr Thr Val Leu Glu Glu Leu Ser Pro Gly Thr Ile Val Ala
 245 250 255
 Asn Ile Thr Ala Glu Asp Pro Asp Asp Glu Gly Phe Pro Ser His Leu
 260 265 270
 Leu Tyr Ser Ile Thr Thr Val Ser Lys Tyr Phe Met Ile Asn Gln Leu
 275 280 285
 Thr Gly Thr Ile Gln Val Ala Gln Arg Ile Asp Arg Asp Ala Gly Glu
 290 295 300
 Leu Arg Gln Asn Pro Thr Ile Ser Leu Glu Val Leu Val Lys Asp Arg
 305 310 315 320
 Pro Tyr Gly Gly Gln Glu Asn Arg Ile Gln Ile Thr Phe Ile Val Glu
 325 330 335
 Asp Val Asn Asp Asn Pro Ala Thr Cys Gln Lys Phe Thr Phe Arg Trp
 340 345 350
 Arg Asn

<210> 163
 <211> 1579
 <212> PRT
 <213> Homo sapiens

<400> 163
 Met Lys Leu Cys Pro Arg Tyr Asn Ser Gln Glu Glu Thr Leu Glu Phe
 1 5 10 15
 Val Ala Asp Tyr Ser Gly Gln Asp Asn Phe Leu Gln Arg Val Gly Gln
 20 25 30
 Asn Gly Leu Lys Asn Ser Glu Lys Glu Ser Thr Val Asn Ser Ile Phe
 35 40 45
 Gln Val Ile Arg Ser Cys Asn Arg Ser Leu Glu Thr Asp Glu Glu Asp
 50 55 60
 Ser Pro Ser Glu Gly Asn Ser Ser Arg Lys Ser Ser Leu Lys Asp Lys
 65 70 75 80
 Ser Arg Trp Gln Phe Ile Ile Gly Asp Leu Leu Asp Ser Asp Asn Asp
 85 90 95
 Ile Phe Glu Gln Ser Lys Glu Tyr Asp Ser His Gly Ser Glu Asp Ser
 100 105 110
 Gln Lys Ala Phe Asp His Gly Thr Glu Leu Ile Pro Trp Tyr Val Leu
 115 120 125
 Ser Ile Gln Ala Asp Val His Gln Phe Leu Leu Gln Gly Ala Thr Val
 130 135 140
 Ile His Tyr Asp Gln Asp Thr His Leu Ser Ala Arg Cys Phe Leu Gln


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145          150          155          160
Leu Gln Pro Asp Asn Ser Thr Leu Thr Trp Val Lys Pro Thr Thr Ala
165          170          175
Ser Pro Ala Ser Ser Lys Ala Lys Leu Gly Val Leu Asn Asn Thr Ala
180          185          190
Glu Pro Gly Lys Phe Pro Leu Leu Gly Asn Ala Gly Leu Ser Ser Leu
195          200          205
Thr Glu Gly Val Leu Asp Leu Phe Ala Val Lys Ala Val Tyr Met Gly
210          215          220
His Pro Gly Ile Asp Ile His Thr Val Cys Val Gln Asn Lys Leu Gly
225          230          235          240
Ser Met Phe Leu Ser Glu Thr Gly Val Thr Leu Leu Tyr Gly Leu Gln
245          250          255
Thr Thr Asp Asn Arg Leu Leu His Phe Val Ala Pro Lys His Thr Ala
260          265          270
Lys Met Leu Phe Ser Gly Leu Leu Glu Leu Thr Arg Ala Val Arg Lys
275          280          285
Met Arg Lys Phe Pro Asp Gln Arg Gln Gln Trp Leu Arg Lys Gln Tyr
290          295          300
Val Ser Leu Tyr Gln Glu Asp Gly Arg Tyr Glu Gly Pro Thr Leu Ala
305          310          315          320
His Ala Val Glu Leu Phe Gly Gly Arg Arg Trp Ser Ala Arg Asn Pro
325          330          335
Ser Pro Gly Thr Ser Ala Lys Asn Ala Glu Lys Pro Asn Met Gln Arg
340          345          350
Asn Asn Thr Leu Gly Ile Ser Thr Thr Lys Lys Lys Lys Lys Ile Leu
355          360          365
Met Arg Gly Glu Ser Gly Glu Val Thr Asp Asp Glu Met Ala Thr Arg
370          375          380
Lys Ala Lys Met His Lys Glu Cys Arg Ser Arg Ser Gly Ser Asp Pro
385          390          395          400
Gln Asp Ile Asn Glu Gln Glu Glu Ser Glu Val Asn Ala Ile Ala Asn
405          410          415
Pro Pro Asn Pro Leu Pro Ser Arg Arg Ala His Ser Leu Thr Thr Ala
420          425          430
Gly Ser Pro Asn Leu Ala Ala Gly Thr Ser Ser Pro Ile Arg Pro Val
435          440          445
Ser Ser Pro Val Leu Ser Ser Ser Asn Lys Ser Pro Ser Ser Ala Trp
450          455          460
Ser Ser Ser Ser Trp His Gly Arg Ile Lys Gly Gly Met Lys Gly Phe
465          470          475          480
Gln Ser Phe Met Val Ser Asp Ser Asn Met Ser Phe Val Glu Phe Val
485          490          495
Glu Leu Phe Lys Ser Phe Ser Val Arg Gln Ala Lys Asp Leu Lys Asp
500          505          510
Leu Phe Asp Val Tyr Ala Val Pro Cys Asn Arg Ser Gly Ser Glu Ser
515          520          525
Ala Pro Leu Tyr Thr Asn Leu Thr Ile Asp Glu Asn Thr Ser Asp Leu
530          535          540
Gln Pro Asp Leu Asp Leu Leu Thr Arg Asn Val Ser Asp Leu Gly Leu
545          550          555          560
Phe Ile Lys Ser Lys Gln Gln Leu Ser Asp Asn Gln Arg Gln Ile Ser
565          570          575
Asp Ala Ile Ala Ala Ala Ser Ile Val Thr Asn Gly Thr Gly Ile Glu
580          585          590
Ser Thr Ser Leu Gly Ile Phe Gly Val Gly Ile Leu Gln Leu Asn Asp
595          600          605
Phe Leu Val Asn Cys Gln Gly Glu His Cys Thr Tyr Asp Glu Ile Leu
610          615          620
Ser Ile Ile Gln Lys Phe Glu Pro Ser Ile Ser Met Cys His Gln Gly
625          630          635          640

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Leu Met Ser Phe Glu Gly Phe Ala Arg Phe Leu Met Asp Lys Glu Asn
 645 650 655
 Phe Ala Ser Lys Asn Asp Glu Ser Gln Glu Asn Ile Lys Glu Leu Gln
 660 665 670
 Leu Pro Leu Ser Tyr Tyr Tyr Ile Glu Ser Ser His Asn Thr Tyr Leu
 675 680 685
 Thr Gly His Gln Leu Lys Gly Glu Ser Ser Val Glu Leu Tyr Ser Gln
 690 695 700
 Val Leu Leu Gln Gly Cys Arg Ser Val Glu Leu Asp Cys Trp Asp Gly
 705 710 715 720
 Asp Asp Gly Met Pro Ile Ile Tyr His Gly His Thr Leu Thr Thr Lys
 725 730 735
 Ile Pro Phe Lys Glu Val Val Glu Ala Ile Asp Arg Ser Ala Phe Ile
 740 745 750
 Asn Ser Asp Leu Pro Ile Ile Ile Ser Ile Glu Asn His Cys Ser Leu
 755 760 765
 Pro Gln Gln Arg Lys Met Ala Glu Ile Phe Lys Thr Val Phe Gly Glu
 770 775 780
 Lys Leu Val Thr Lys Phe Leu Phe Glu Thr Asp Phe Ser Asp Asp Pro
 785 790 795 800
 Met Leu Pro Ser Pro Asp Gln Leu Arg Lys Lys Val Leu Leu Lys Asn
 805 810 815
 Lys Lys Leu Lys Ala His Gln Thr Pro Val Asp Ile Leu Lys Gln Lys
 820 825 830
 Ala His Gln Leu Ala Ser Met Gln Val Gln Ala Tyr Asn Gly Gly Asn
 835 840 845
 Ala Asn Pro Arg Pro Ala Asn Asn Glu Glu Glu Glu Asp Glu Glu Asp
 850 855 860
 Glu Tyr Asp Tyr Asp Tyr Glu Ser Leu Ser Asp Asp Asn Ile Leu Glu
 865 870 875 880
 Asp Arg Pro Glu Asn Lys Ser Cys Asn Asp Lys Leu Gln Phe Glu Tyr
 885 890 895
 Asn Glu Glu Ile Pro Lys Arg Ile Lys Lys Ala Asp Asn Ser Ala Cys
 900 905 910
 Asn Lys Gly Lys Val Tyr Asp Met Glu Leu Gly Glu Glu Phe Tyr Leu
 915 920 925
 Asp Gln Asn Lys Lys Glu Ser Arg Gln Ile Ala Pro Glu Leu Ser Asp
 930 935 940
 Leu Val Ile Tyr Cys Gln Ala Val Lys Phe Pro Gly Leu Ser Thr Leu
 945 950 955 960
 Asn Ala Ser Gly Ser Ser Arg Gly Lys Glu Arg Lys Ser Arg Lys Ser
 965 970 975
 Ile Phe Gly Asn Asn Pro Gly Arg Met Ser Pro Gly Glu Thr Ala Ser
 980 985 990
 Phe Asn Lys Thr Ser Gly Lys Ser Ser Cys Glu Gly Ile Arg Gln Thr
 995 1000 1005
 Trp Glu Glu Ser Ser Ser Pro Leu Asn Pro Thr Thr Ser Leu Ser Ala
 1010 1015 1020
 Ile Ile Arg Thr Pro Lys Cys Tyr His Ile Ser Ser Leu Asn Glu Asn
 1025 1030 1035 1040
 Ala Ala Lys Arg Leu Cys Arg Arg Tyr Ser Gln Lys Leu Thr Gln His
 1045 1050 1055
 Thr Ala Cys Gln Leu Leu Arg Thr Tyr Pro Ala Ala Thr Arg Ile Asp
 1060 1065 1070
 Ser Ser Asn Pro Asn Pro Leu Met Phe Trp Leu His Gly Ile Gln Leu
 1075 1080 1085
 Val Ala Leu Asn Tyr Gln Thr Asp Asp Leu Pro Leu His Leu Asn Ala
 1090 1095 1100
 Ala Met Phe Glu Ala Asn Gly Gly Cys Gly Tyr Val Leu Lys Pro Pro
 1105 1110 1115 1120
 Val Leu Trp Asp Lys Asn Cys Pro Met Tyr Gln Lys Phe Ser Pro Leu

1125 1130 1135
 Glu Arg Asp Leu Asp Ser Met Asp Pro Ala Val Tyr Ser Leu Thr Ile
 1140 1145 1150
 Val Ser Gly Gln Asn Val Cys Pro Ser Asn Ser Met Gly Ser Pro Cys
 1155 1160 1165
 Ile Glu Val Asp Val Leu Gly Met Pro Leu Asp Ser Cys His Phe Arg
 1170 1175 1180
 Thr Lys Pro Ile His Arg Asn Thr Leu Asn Pro Met Trp Asn Glu Gln
 1185 1190 1195 1200
 Phe Leu Phe Arg Val His Phe Glu Asp Leu Val Phe Leu Arg Phe Ala
 1205 1210 1215
 Val Val Glu Asn Asn Ser Ser Ala Val Thr Ala Gln Arg Ile Ile Pro
 1220 1225 1230
 Leu Lys Ala Leu Lys Arg Gly Tyr Arg His Leu Gln Leu Arg Asn Leu
 1235 1240 1245
 His Asn Glu Val Leu Glu Ile Ser Ser Leu Phe Ile Asn Ser Arg Arg
 1250 1255 1260
 Met Glu Glu Asn Ser Ser Gly Asn Thr Met Ser Ala Ser Ser Met Phe
 1265 1270 1275 1280
 Asn Thr Glu Glu Arg Lys Cys Leu Gln Thr His Arg Val Thr Val His
 1285 1290 1295
 Gly Val Pro Gly Pro Glu Pro Phe Thr Val Phe Thr Ile Asn Gly Gly
 1300 1305 1310
 Thr Lys Ala Lys Gln Leu Leu Gln Gln Ile Leu Thr Asn Glu Gln Asp
 1315 1320 1325
 Ile Lys Pro Val Thr Thr Asp Tyr Phe Leu Met Glu Glu Lys Tyr Phe
 1330 1335 1340
 Ile Ser Lys Glu Lys Asn Glu Cys Arg Lys Gln Pro Phe Gln Arg Ala
 1345 1350 1355 1360
 Ile Gly Pro Glu Glu Glu Ile Met Gln Ile Leu Ser Ser Trp Phe Pro
 1365 1370 1375
 Glu Glu Gly Tyr Met Gly Arg Ile Val Leu Lys Thr Gln Gln Glu Asn
 1380 1385 1390
 Leu Glu Glu Lys Asn Ile Val Gln Asp Asp Lys Glu Val Ile Leu Ser
 1395 1400 1405
 Ser Glu Glu Glu Ser Phe Phe Val Gln Val His Asp Val Ser Pro Glu
 1410 1415 1420
 Gln Pro Arg Thr Val Ile Lys Ala Pro Arg Val Ser Thr Ala Gln Asp
 1425 1430 1435 1440
 Val Ile Gln Gln Thr Leu Cys Lys Ala Lys Tyr Ser Tyr Ser Ile Leu
 1445 1450 1455
 Ser Asn Pro Asn Pro Ser Asp Tyr Val Leu Leu Glu Val Val Lys
 1460 1465 1470
 Asp Thr Thr Asn Lys Lys Thr Thr Thr Pro Lys Ser Ser Gln Arg Val
 1475 1480 1485
 Leu Leu Asp Gln Glu Cys Val Phe Gln Ala Gln Ser Lys Trp Lys Gly
 1490 1495 1500
 Ala Gly Lys Phe Ile Leu Lys Leu Lys Glu Gln Val Gln Ala Ser Arg
 1505 1510 1515 1520
 Glu Asp Lys Lys Lys Gly Ile Ser Phe Ala Ser Glu Leu Lys Lys Leu
 1525 1530 1535
 Thr Lys Ser Thr Lys Gln Pro Arg Gly Leu Thr Ser Pro Ser Gln Leu
 1540 1545 1550
 Leu Thr Ser Glu Ser Ile Gln Thr Lys Glu Glu Lys Pro Val Gly Gly
 1555 1560 1565
 Leu Ser Ser Ser Asp Thr Met Asp Tyr Arg Gln
 1570 1575

<210> 164

<211> 407

<212> PRT

<213> Homo sapiens

<400> 164

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Met Asp Gly Leu Pro Gly Arg Ala Leu Gly Ala Ala Cys Leu Leu Leu
 1          5          10          15
Leu Ala Ala Gly Trp Leu Gly Pro Glu Ala Trp Gly Ser Pro Thr Pro
          20          25          30
Pro Pro Thr Pro Ala Ala Pro Pro Pro Pro Pro Gly Ala Pro
          35          40          45
Gly Gly Ser Gln Asp Thr Cys Thr Ser Cys Gly Gly Phe Arg Arg Pro
          50          55          60
Glu Glu Leu Gly Arg Val Asp Gly Asp Phe Leu Glu Ala Val Lys Arg
65          70          75          80
His Ile Leu Ser Arg Leu Gln Met Arg Gly Arg Pro Asn Ile Thr His
          85          90          95
Ala Val Pro Lys Ala Ala Met Val Thr Ala Leu Arg Lys Leu His Ala
          100          105          110
Gly Lys Val Arg Glu Asp Gly Arg Val Glu Ile Pro His Leu Asp Gly
          115          120          125
His Ala Ser Pro Gly Ala Asp Gly Gln Glu Arg Val Ser Glu Ile Ile
          130          135          140
Ser Phe Ala Glu Thr Asp Gly Leu Ala Ser Ser Arg Val Arg Leu Tyr
145          150          155          160
Phe Phe Ile Ser Asn Glu Gly Asn Gln Asn Leu Phe Val Val Gln Ala
          165          170          175
Ser Leu Trp Leu Tyr Leu Lys Leu Leu Pro Tyr Val Leu Glu Lys Gly
          180          185          190
Ser Arg Arg Lys Val Arg Val Lys Val Tyr Phe Gln Glu Gln Gly His
          195          200          205
Gly Asp Arg Trp Asn Met Val Glu Lys Arg Val Asp Leu Lys Arg Ser
          210          215          220
Gly Trp His Thr Phe Pro Leu Thr Glu Ala Ile Gln Ala Leu Phe Glu
225          230          235          240
Arg Gly Glu Arg Arg Leu Asn Leu Asp Val Gln Cys Asp Ser Cys Gln
          245          250          255
Glu Leu Ala Val Val Pro Val Phe Val Asp Pro Gly Glu Glu Ser His
          260          265          270
Arg Pro Phe Val Val Val Gln Ala Arg Leu Gly Asp Ser Arg His Arg
          275          280          285
Ile Arg Lys Arg Gly Leu Glu Cys Asp Gly Arg Thr Asn Leu Cys Cys
          290          295          300
Arg Gln Gln Phe Phe Ile Asp Phe Arg Leu Ile Gly Trp Asn Asp Trp
          305          310          315
Ile Ile Ala Pro Thr Gly Tyr Tyr Gly Asn Tyr Cys Glu Gly Ser Cys
          320          325          330
Pro Ala Tyr Leu Ala Gly Val Pro Gly Ser Ala Ser Ser Phe His Thr
          335          340          345
Ala Val Val Asn Gln Tyr Arg Met Arg Gly Leu Asn Pro Gly Thr Val
          350          355          360
Asn Ser Cys Cys Ile Pro Thr Lys Leu Ser Thr Met Ser Met Leu Tyr
          365          370          375
Phe Asp Asp Glu Tyr Asn Ile Val Lys Arg Asp Val Pro Asn Met Ile
          380          385          390
Val Glu Glu Cys Gly Cys Ala
          395          400
          405

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<210> 165
 <211> 407
 <212> PRT
 <213> Homo sapiens

<400> 165
 Met Ala Leu Gly Val Gly Arg Ala Arg Pro Gly Leu Ser Cys Gly Val
 1 5 10 15
 Ile Ser Pro Pro Cys Ala Pro Thr Arg Asn Ser His Pro Gly Pro Gly
 20 25 30
 Cys Thr Ala Ser Pro Pro Ala Pro Gly Trp Pro Phe Ser Gln Arg
 35 40 45
 Gly Pro Gly Arg Trp Ser Thr Thr Glu Leu Arg Lys Glu Lys Ser Arg
 50 55 60
 Asp Ala Ala Arg Ser Arg Arg Ser Gln Glu Thr Glu Val Leu Tyr Gln
 65 70 75 80
 Leu Ala His Thr Leu Pro Phe Ala Arg Gly Val Ser Ala His Leu Asp
 85 90 95
 Lys Ala Ser Ile Met Arg Leu Thr Ile Ser Tyr Leu Arg Met His Arg
 100 105 110
 Leu Cys Ala Ala Gly Glu Trp Asn Gln Val Gly Ala Gly Gly Glu Pro
 115 120 125
 Leu Asp Ala Cys Tyr Leu Lys Ala Leu Glu Gly Phe Val Met Val Leu
 130 135 140
 Thr Ala Glu Gly Asp Met Ala Tyr Leu Ser Glu Asn Val Ser Lys His
 145 150 155 160
 Leu Gly Leu Ser Gln Leu Glu Leu Ile Gly His Ser Ile Phe Asp Phe
 165 170 175
 Ile His Pro Cys Asp Gln Glu Glu Leu Gln Asp Ala Leu Thr Pro Gln
 180 185 190
 Gln Thr Leu Ser Arg Arg Lys Val Glu Ala Pro Thr Glu Arg Cys Phe
 195 200 205
 Ser Leu Arg Met Lys Ser Thr Leu Thr Ser Arg Gly Arg Thr Leu Asn
 210 215 220
 Leu Lys Ala Ala Thr Trp Lys Val Leu Asn Cys Ser Gly His Met Arg
 225 230 235 240
 Ala Tyr Lys Pro Pro Ala Gln Thr Ser Pro Ala Gly Ser Pro Asp Ser
 245 250 255
 Glu Pro Pro Leu Gln Cys Leu Val Leu Ile Cys Glu Ala Ile Pro His
 260 265 270
 Pro Gly Ser Leu Glu Pro Pro Leu Gly Arg Gly Ala Phe Leu Ser Arg
 275 280 285
 His Ser Leu Asp Met Lys Phe Thr Tyr Cys Asp Asp Arg Ile Ala Glu
 290 295 300
 Val Ala Gly Tyr Ser Pro Asp Asp Leu Ile Gly Cys Ser Ala Tyr Glu
 305 310 315 320
 Tyr Ile His Ala Leu Asp Ser Asp Ala Val Ser Lys Ser Ile His Thr
 325 330 335
 Cys Met Tyr Pro Ile Ser Pro Gly Ala Lys Pro Ala Ala Thr Trp Pro
 340 345 350
 Pro Ala Asp Thr Arg Thr Pro Gln Leu Pro Ile Pro Gln Asp Ala Leu
 355 360 365
 Pro Pro His Leu Asn Thr Ser Ser Leu Leu Pro Lys Pro Gln Gly Thr
 370 375 380
 Val Ser Phe Leu Ala Pro Ser Tyr Pro Val Pro Arg Ser Phe Ser Pro
 385 390 395 400
 His Leu Pro Pro Trp Trp Pro
 405

<210> 166
 <211> 418
 <212> PRT
 <213> Homo sapiens

<400> 166
 Met Ser Glu Gly Val Asp Leu Ile Asp Ile Tyr Ala Asp Glu Glu Phe
 1 5 10 15
 Asn Gln Asp Pro Glu Phe Asn Asn Thr Asp Gln Ile Asp Leu Tyr Asp
 20 25 30
 Asp Val Leu Thr Ala Thr Ser Gln Pro Ser Asp Asp Arg Ser Ser
 35 40 45
 Thr Glu Pro Pro Pro Val Arg Gln Glu Pro Ser Gly Lys Pro Asn
 50 55 60
 Asn Lys Thr Pro Ala Ile Leu Tyr Thr Tyr Ser Gly Leu Arg Asn Arg
 65 70 75 80
 Arg Ala Ala Val Tyr Val Gly Ser Phe Ser Trp Trp Thr Thr Asp Gln
 85 90 95
 Gln Leu Ile Gln Val Ile Arg Ser Ile Gly Val Tyr Asp Val Val Glu
 100 105 110
 Leu Lys Phe Ala Glu Asn Arg Ala Asn Gly Gln Ser Lys Gly Tyr Ala
 115 120 125
 Glu Val Val Val Ala Ser Glu Asn Ser Val His Lys Leu Leu Glu Leu
 130 135 140
 Leu Pro Gly Lys Val Leu Asn Gly Glu Lys Val Asp Val Arg Pro Ala
 145 150 155 160
 Thr Arg Gln Asn Leu Ser Gln Phe Glu Ala Gln Ala Arg Lys Arg Glu
 165 170 175
 Cys Val Arg Val Pro Arg Gly Gly Ile Pro Pro Arg Ala His Ser Arg
 180 185 190
 Asp Ser Ser Asp Ser Ala Asp Gly Arg Ala Thr Pro Ser Glu Asn Leu
 195 200 205
 Val Pro Ser Ser Ala Arg Val Asp Lys Pro Pro Ser Val Leu Pro Tyr
 210 215 220
 Phe Asn Arg Pro Pro Ser Ala Leu Pro Leu Met Gly Leu Pro Pro Pro
 225 230 235 240
 Pro Ile Pro Pro Pro Pro Pro Leu Ser Ser Ser Phe Gly Val Pro Pro
 245 250 255
 Pro Pro Pro Gly Ile His Tyr Gln His Leu Met Pro Pro Pro Pro Arg
 260 265 270
 Leu Pro Pro His Leu Ala Val Pro Pro Pro Gly Ala Ile Pro Pro Ala
 275 280 285
 Leu His Leu Asn Pro Ala Phe Leu Pro Pro Pro Asn Ala Thr Val Gly
 290 295 300
 Pro Pro Pro Asp Thr Tyr Met Lys Ala Ser Ala Pro Tyr Asn His His
 305 310 315 320
 Gly Ser Arg Asp Ser Gly Pro Pro Pro Ser Thr Val Ser Glu Ala Glu
 325 330 335
 Phe Glu Asp Ile Met Lys Arg Asn Arg Ala Ile Ser Ser Ser Ala Ile
 340 345 350
 Ser Lys Ala Val Ser Gly Ala Ser Ala Gly Asp Tyr Ser Asp Ala Ile
 355 360 365
 Glu Thr Leu Leu Thr Ala Ile Ala Val Ile Lys Gln Ser Arg Val Ala
 370 375 380
 Asn Asp Glu Arg Cys Arg Val Leu Ile Ser Ser Leu Lys Asp Cys Leu
 385 390 395 400
 His Gly Ile Glu Ala Lys Ser Tyr Ser Val Gly Ala Ser Gly Ser Ser
 405 410 415
 Ser Arg

<210> 167
 <211> 694
 <212> PRT
 <213> Homo sapiens

<400> 167
 Met Gly Ala Pro Ala Cys Ala Leu Ala Leu Cys Val Ala Val Ala Ile
 1 5 10 15
 Val Ala Gly Ala Ser Ser Glu Ser Leu Gly Thr Glu Gln Arg Val Val
 20 25 30
 Gly Arg Ala Ala Glu Val Pro Gly Pro Glu Pro Gly Gln Gln Glu Gln
 35 40 45
 Leu Val Phe Gly Ser Gly Asp Ala Val Glu Leu Ser Cys Pro Pro Pro
 50 55 60
 Gly Gly Gly Pro Met Gly Pro Thr Val Trp Val Lys Asp Gly Thr Gly
 65 70 75 80
 Leu Val Pro Ser Glu Arg Val Leu Val Gly Pro Gln Arg Leu Gln Val
 85 90 95
 Leu Asn Ala Ser His Glu Asp Ser Gly Ala Tyr Ser Cys Arg Gln Arg
 100 105 110
 Leu Thr Gln Arg Val Leu Cys His Phe Ser Val Arg Val Thr Asp Ala
 115 120 125
 Pro Ser Ser Gly Asp Asp Glu Asp Gly Glu Asp Glu Ala Glu Asp Thr
 130 135 140
 Gly Val Asp Thr Gly Ala Pro Tyr Trp Thr Arg Pro Glu Arg Met Asp
 145 150 155 160
 Lys Lys Leu Leu Ala Val Pro Ala Ala Asn Thr Val Arg Phe Arg Cys
 165 170 175
 Pro Ala Ala Gly Asn Pro Thr Pro Ser Ile Ser Trp Leu Lys Asn Gly
 180 185 190
 Arg Glu Phe Arg Gly Glu His Arg Ile Gly Gly Ile Lys Leu Arg His
 195 200 205
 Gln Gln Trp Ser Leu Val Met Glu Ser Val Val Pro Ser Asp Arg Gly
 210 215 220
 Asn Tyr Thr Cys Val Val Glu Asn Lys Phe Gly Ser Ile Arg Gln Thr
 225 230 235 240
 Tyr Thr Leu Asp Val Leu Glu Arg Ser Pro His Arg Pro Ile Leu Gln
 245 250 255
 Ala Gly Leu Pro Ala Asn Gln Thr Ala Val Leu Gly Ser Asp Val Glu
 260 265 270
 Phe His Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Leu
 275 280 285
 Lys His Val Glu Val Asn Gly Ser Lys Val Gly Pro Asp Gly Thr Pro
 290 295 300
 Tyr Val Thr Val Leu Lys Val Ser Leu Glu Ser Asn Ala Ser Met Ser
 305 310 315 320
 Ser Asn Thr Pro Leu Val Arg Ile Ala Arg Leu Ser Ser Gly Glu Gly
 325 330 335
 Pro Thr Leu Ala Asn Val Ser Glu Leu Glu Leu Pro Ala Asp Pro Lys
 340 345 350
 Trp Glu Leu Ser Arg Ala Arg Leu Thr Leu Gly Lys Pro Leu Gly Glu
 355 360 365
 Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Ile Gly Ile Asp Lys
 370 375 380
 Asp Arg Ala Ala Lys Pro Val Thr Val Ala Val Lys Met Leu Lys Asp
 385 390 395 400

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Asp Ala Thr Asp Lys Asp Leu Ser Asp Leu Val Ser Glu Met Glu Met
              405              410              415
Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly Ala
              420              425              430
Cys Thr Gln Gly Gly Pro Leu Tyr Val Leu Val Glu Tyr Ala Ala Lys
              435              440              445
Gly Asn Leu Arg Glu Phe Leu Arg Ala Arg Arg Pro Gly Leu Asp
              450              455              460
Tyr Ser Phe Asp Thr Cys Lys Pro Pro Glu Glu Gln Leu Thr Phe Lys
              465              470              475              480
Asp Leu Val Ser Cys Ala Tyr Gln Val Ala Arg Gly Met Glu Tyr Leu
              485              490              495
Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu
              500              505              510
Val Thr Glu Asp Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg
              515              520              525
Asp Val His Asn Leu Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu
              530              535              540
Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr
              545              550              555              560
His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe
              565              570              575
Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe
              580              585              590
Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn Cys Thr
              595              600              605
His Asp Leu Tyr Met Ile Met Arg Glu Cys Trp His Ala Ala Pro Ser
              610              615              620
Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg Val Leu
              625              630              635              640
Thr Val Thr Ser Thr Asp Glu Tyr Leu Asp Leu Ser Ala Pro Phe Glu
              645              650              655
Gln Tyr Ser Pro Gly Gly Gln Asp Thr Pro Ser Ser Ser Ser Gly
              660              665              670
Asp Asp Ser Val Phe Ala His Asp Leu Leu Pro Pro Ala Pro Pro Ser
              675              680              685
Ser Gly Gly Ser Arg Thr
              690

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<210> 168
<211> 53
<212> PRT
<213> Homo sapiens

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<400> 168
Met Met Glu Thr Met Gln Leu Lys Val Asn Arg His Pro Phe Cys Phe
  1              5              10              15
Ser Val Lys Gly Gln Val Lys Met Leu Gln Leu Met Arg Leu Gly Leu
              20              25              30
Arg Val Arg Gly Val Val Glu Ser Ala Cys Gly Arg Glu Met Trp Leu
              35              40              45
Cys Gly Tyr Lys Gly
  50

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<210> 169
<211> 42

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<212> PRT
 <213> Homo sapiens

<400> 169
 Met Ser Ser Phe Ser Thr Thr Thr Val Ser Phe Leu Leu Leu Leu Ala
 1 5 10 15
 Phe Gln Leu Leu Gly Gln Thr Arg Ala Asn Pro Met Tyr Asn Ala Val
 20 25 30
 Ser Asn Ala Asp Leu Leu Leu Lys Val Val
 35 40

<210> 170
 <211> 289
 <212> PRT
 <213> Homo sapiens

<400> 170
 Met Phe Val Leu Leu Tyr Val Thr Ser Phe Ala Ile Cys Ala Ser Gly
 1 5 10 15
 Gln Pro Arg Gly Asn Gln Leu Lys Gly Glu Asn Tyr Ser Pro Arg Tyr
 20 25 30
 Ile Cys Ser Ile Pro Gly Leu Pro Gly Pro Pro Gly Pro Pro Gly Ala
 35 40 45
 Asn Gly Ser Pro Gly Pro His Gly Arg Ile Gly Leu Pro Gly Arg Asp
 50 55 60
 Gly Arg Asp Gly Arg Lys Gly Glu Lys Gly Glu Lys Gly Thr Ala Gly
 65 70 75 80
 Leu Arg Gly Lys Thr Gly Pro Leu Gly Leu Ala Gly Glu Lys Gly Asp
 85 90 95
 Gln Gly Glu Thr Gly Lys Lys Gly Pro Ile Gly Pro Glu Gly Glu Lys
 100 105 110
 Gly Glu Val Gly Pro Ile Gly Pro Pro Lys Gly Asp Arg Gly
 115 120 125
 Glu Gln Gly Asp Pro Gly Leu Pro Gly Val Cys Arg Cys Gly Ser Ile
 130 135 140
 Val Leu Lys Ser Ala Phe Ser Val Gly Ile Thr Thr Ser Tyr Pro Glu
 145 150 155 160
 Glu Arg Leu Pro Ile Ile Phe Asn Lys Val Leu Phe Asn Glu Gly Glu
 165 170 175
 His Tyr Asn Pro Ala Thr Gly Lys Phe Ile Cys Ala Phe Pro Gly Ile
 180 185 190
 Tyr Tyr Phe Ser Tyr Asp Ile Thr Leu Ala Asn Lys His Leu Ala Ile
 195 200 205
 Gly Leu Val His Asn Gly Gln Tyr Arg Ile Lys Thr Phe Asp Ala Asn
 210 215 220
 Thr Gly Asn His Asp Val Ala Ser Gly Ser Thr Val Ile Tyr Leu Gln
 225 230 235 240
 Pro Glu Asp Glu Val Trp Leu Glu Ile Phe Phe Thr Asp Gln Asn Gly
 245 250 255
 Leu Phe Ser Asp Pro Gly Trp Ala Asp Ser Leu Phe Ser Gly Phe Leu
 260 265 270
 Leu Tyr Val Asp Thr Asp Tyr Leu Asp Ser Ile Ser Glu Asp Asp Glu
 275 280 285
 Leu

<210> 171
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 171
 Met Asp Ala Leu Ser Glu Ala Asn Gly Thr Phe Ala Leu Asn Leu Leu
 1 5 10 15
 Lys Lys Leu Gly Glu Asn Asn Ser Asn Asn Leu Phe Phe Ser Pro Leu
 20 25 30
 Ser Ile Ser Ser Ala Leu Ala Met Val Phe Met Gly Ala Lys Gly Asn
 35 40 45
 Thr Ala Ala Gln Met Ser Gln Ala Leu Cys Phe Ser Lys Ile Gly Gly
 50 55 60
 Glu Asp Gly Asp Ile His Arg Gly Phe Gln Ser Leu Val Ala Ile
 65 70 75 80
 Asn Arg Thr Asp Thr Glu Tyr Val Leu Arg Thr Ala Asn Gly Leu Phe
 85 90 95
 Gly Glu Lys Ser Tyr Asp Phe Leu Thr Gly Phe Thr Asp Ser Cys Gly
 100 105 110
 Lys Phe Tyr Gln Ala Thr Ile Lys Gln Leu Asp Phe Val Asn Asp Thr
 115 120 125
 Glu Lys Ser Thr Thr Arg Val Asn Ser Trp Val Ala Asp Lys Thr Lys
 130 135 140
 Gly Glu Asn Ile Leu Leu Phe Tyr Phe Asp Asn Ile Leu Asn Ser Phe
 145 150 155 160
 Ile Val Ser Ser Leu Gln Asn Cys Gln Ile
 165 170

<210> 172
 <211> 212
 <212> PRT
 <213> Homo sapiens

<400> 172
 Met Leu Ser Ser Val Val Phe Trp Gly Leu Ile Ala Leu Ile Gly Thr
 1 5 10 15
 Ser Arg Gly Ser Tyr Pro Phe Ser His Ser Met Lys Pro His Leu His
 20 25 30
 Pro Arg Leu Tyr His Gly Cys Tyr Gly Asp Ile Met Thr Met Lys Thr
 35 40 45
 Ser Gly Ala Thr Cys Asp Ala Asn Ser Val Met Asn Cys Gly Ile Arg
 50 55 60
 Gly Ser Glu Met Phe Ala Glu Met Asp Leu Arg Ala Ile Lys Pro Tyr
 65 70 75 80
 Gln Thr Leu Ile Lys Glu Val Gly Gln Arg His Cys Val Asp Pro Ala
 85 90 95
 Val Ile Ala Ala Ile Ile Ser Arg Glu Ser His Gly Gly Ser Val Leu
 100 105 110
 Gln Asp Gly Trp Asp His Arg Gly Leu Lys Phe Gly Leu Met Gln Leu
 115 120 125
 Asp Lys Gln Thr Tyr His Pro Val Gly Ala Trp Asp Ser Lys Glu His
 130 135 140
 Leu Ser Gln Ala Thr Gly Ile Leu Thr Glu Arg Ile Lys Ala Ile Gln
 145 150 155 160
 Lys Lys Phe Pro Thr Trp Ser Val Ala Gln His Leu Lys Gly Gly Leu

Ser	Ala	Phe	Lys	165	Ser	Gly	Ile	Glu	170	Ala	Ile	Ala	Thr	Pro	Ser	Asp	Ile	175
Asp	Asn	Asp	Phe	180	Val	Asn	Asp	Ile	185	Ile	Ala	Arg	Ala	Lys	Phe	Tyr	Lys	190
Arg	Gln	Ser	Phe	195				200						205				
				210														

<210> 173
 <211> 581
 <212> PRT
 <213> Homo sapiens

<400> 173

Met	Val	Phe	Arg	Asn	Val	Gly	Arg	Pro	Pro	Glu	Glu	Glu	Asp	Val	Glu			
1				5					10					15				
Ala	Ala	Pro	Glu	Pro	Gly	Pro	Ser	Glu	Leu	Leu	Cys	Pro	Arg	His	Arg			
			20					25					30					
Cys	Ala	Leu	Asp	Pro	Lys	Ala	Leu	Pro	Pro	Gly	Leu	Ala	Leu	Glu	Arg			
		35					40					45						
Thr	Trp	Gly	Pro	Ala	Ala	Gly	Leu	Glu	Ala	Gln	Leu	Ala	Ala	Leu	Gly			
	50					55					60							
Leu	Gly	Gln	Pro	Ala	Gly	Pro	Gly	Val	Lys	Thr	Val	Gly	Gly	Gly	Cys			
	65				70				75					80				
Cys	Pro	Cys	Pro	Cys	Pro	Pro	Gln	Pro	Pro	Pro	Pro	Gln	Pro	Gln	Pro			
				85					90				95					
Pro	Ala	Ala	Ala	Pro	Gln	Ala	Gly	Glu	Asp	Pro	Thr	Glu	Thr	Ser	Asp			
	100						105					110						
Ala	Leu	Leu	Val	Leu	Glu	Gly	Leu	Glu	Ser	Glu	Ala	Glu	Ser	Leu	Glu			
	115					120						125						
Thr	Asn	Ser	Cys	Ser	Glu	Glu	Glu	Leu	Ser	Ser	Pro	Gly	Arg	Gly	Gly			
	130				135						140							
Gly	Gly	Gly	Gly	Arg	Leu	Leu	Leu	Gln	Pro	Pro	Gly	Pro	Glu	Leu	Pro			
	145			150					155					160				
Pro	Val	Pro	Phe	Pro	Leu	Gln	Asp	Leu	Val	Pro	Leu	Gly	Arg	Leu	Ser			
			165					170					175					
Arg	Gly	Glu	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Pro	Pro	Pro	Pro	Pro			
	180						185					190						
Pro	Pro	Pro	Gly	Pro	Leu	Arg	Pro	Leu	Ala	Gly	Pro	Ser	Arg	Lys	Gly			
	195					200					205							
Ser	Phe	Lys	Ile	Arg	Leu	Ser	Arg	Leu	Phe	Arg	Thr	Lys	Ser	Cys	Asn			
	210			215						220								
Gly	Gly	Ser	Gly	Gly	Asp	Gly	Thr	Gly	Lys	Arg	Pro	Ser	Gly	Glu				
	225			230				235					240					
Leu	Ala	Ala	Ser	Ala	Ser	Leu	Thr	Asp	Met	Gly	Gly	Ser	Ala	Gly				
		245				250						255						
Arg	Glu	Leu	Asp	Ala	Gly	Arg	Lys	Pro	Lys	Leu	Thr	Arg	Thr	Gln	Ser			
	260					265						270						
Ala	Phe	Ser	Pro	Val	Ser	Phe	Ser	Pro	Leu	Phe	Thr	Gly	Glu	Thr	Val			
	275					280						285						
Ser	Leu	Val	Asp	Val	Asp	Ile	Ser	Gln	Arg	Gly	Leu	Thr	Ser	Pro	His			
	290				295					300								
Pro	Pro	Thr	Pro	Pro	Pro	Pro	Pro	Arg	Arg	Ser	Leu	Ser	Leu	Leu	Asp			
	305				310				315					320				
Asp	Ile	Ser	Gly	Thr	Leu	Pro	Thr	Ser	Val	Leu	Val	Ala	Pro	Met	Gly			
			325					330					335					
Ser	Ser	Leu	Gln	Ser	Phe	Pro	Leu	Pro	Pro	Pro	Pro	Pro	Pro	His	Ala			
			340					345					350					

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Pro Asp Ala Phe Pro Arg Ile Ala Pro Ile Arg Ala Ala Glu Ser Leu
      355                               360                               365
His Ser Gln Pro Pro Gln His Leu Gln Cys Pro Leu Tyr Arg Pro Asp
      370                               375                               380
Ser Ser Ser Phe Ala Ala Ser Leu Arg Glu Leu Glu Lys Cys Gly Trp
      385                               390                               395                               400
Tyr Trp Gly Pro Met Asn Trp Glu Asp Ala Glu Met Lys Leu Lys Gly
      405                               410                               415
Lys Pro Asp Gly Ser Phe Leu Val Arg Asp Ser Ser Asp Pro Arg Tyr
      420                               425                               430
Ile Leu Ser Leu Ser Phe Arg Ser Gln Gly Ile Thr His His Thr Arg
      435                               440                               445
Met Glu His Tyr Arg Gly Thr Phe Ser Leu Trp Cys His Pro Lys Phe
      450                               455                               460
Glu Asp Arg Cys Gln Ser Val Val Glu Phe Ile Lys Arg Ala Ile Met
      465                               470                               475                               480
His Ser Lys Asn Gly Lys Phe Leu Tyr Phe Leu Arg Ser Arg Val Pro
      485                               490                               495
Gly Leu Pro Pro Thr Pro Val Gln Leu Tyr Pro Val Ser Arg Phe
      500                               505                               510
Ser Asn Val Lys Ser Leu Gln His Leu Cys Arg Phe Arg Ile Arg Gln
      515                               520                               525
Leu Val Arg Ile Asp His Ile Pro Asp Leu Pro Leu Pro Lys Pro Leu
      530                               535                               540
Ile Ser Tyr Ile Arg Lys Phe Tyr Tyr Tyr Asp Pro Gln Glu Glu Val
      545                               550                               555                               560
Tyr Leu Ser Leu Lys Glu Ala Gln Leu Ile Ser Lys Gln Lys Gln Glu
      565                               570                               575
Val Glu Pro Ser Thr
      580

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<210> 174
 <211> 87
 <212> PRT
 <213> Homo sapiens

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<400> 174
Met His Ser Tyr Pro Gly Ile Phe Phe Phe Pro Leu Ala Val Phe Gln
  1      5      10      15
Ile Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr
      20      25      30
Leu His Asp Asn Pro Ala Val Asn Tyr Ile Tyr Asn Trp Ala Tyr Gly
      35      40      45
Phe Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly Cys Ser Phe Phe Phe
      50      55      60
Cys Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly Ala Ala Lys Pro
      65      70      75      80
Arg Tyr Phe Tyr Pro Pro Ala
      85

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<210> 175
 <211> 193
 <212> PRT
 <213> Homo sapiens

<400> 175
 Met Leu Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro
 1 5 10 15
 Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly
 20 25 30
 Arg Gly Trp Leu Gln Ser Ser Asn His Ile Gln Thr Ser Ser Leu Trp
 35 40 45
 Trp Arg Cys Phe Asp Glu Gly Gly Ser Gly Ser Tyr Asp Asp Gly
 50 55 60
 Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Thr
 65 70 75 80
 Leu Phe Cys Gly Phe Ile Ile Leu Cys Ile Cys Phe Ile Leu Ser Phe
 85 90 95
 Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly
 100 105 110
 Gly Leu Leu Ala Leu Ala Ala Ile Phe Gln Ile Ile Ser Leu Val Ile
 115 120 125
 Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu His Asp Asn Pro Ala
 130 135 140
 Val Asn Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr
 145 150 155 160
 Ile Ile Leu Ile Gly Cys Ser Phe Phe Phe Cys Cys Leu Pro Asn Tyr
 165 170 175
 Glu Asp Asp Leu Leu Gly Ala Ala Lys Pro Arg Tyr Phe Tyr Pro Pro
 180 185 190
 Ala

<210> 176
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 176
 Met Gly Leu Met Phe Leu Pro Cys Leu Ile Asn Leu Phe Gln Arg Phe
 1 5 10 15
 Phe Lys Leu Thr Gly Ser Trp Pro Phe His Arg Gln Leu Pro Lys Asn
 20 25 30
 Ile Tyr Arg Arg His Cys Ser Tyr Gln His Asp Thr Arg Glu Leu Ser
 35 40 45
 Val Pro Ser Ser Ala Gly Ser Ser Gln Lys Glu His Ala Ala Pro Arg
 50 55 60
 Pro Phe Tyr Asn Tyr Glu Val Trp Ile Asp Arg Ala Glu Ala Ser Pro
 65 70 75 80
 Leu Trp Ile Ser Ala Ser Phe
 85

<210> 177
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 177
 Met Ser Leu Leu Arg Leu His Arg Leu Ser Ile Ile Trp Lys Asn Leu
 1 5 10 15

```

Ile Phe His Gln Glu Tyr Glu His Val Phe Gln Val Glu Asn Ala Lys
      20      25      30
Asp Asn Glu Asp Ser Ile Leu Gln Arg Glu Ile Pro Ala Arg Gln Ser
      35      40      45
Arg Arg Arg Phe Arg Lys Ile Asn Tyr Lys Gly Glu Arg Gln Thr Ile
      50      55      60
Thr Asp Asp Val Glu Val Asn Ser Tyr Leu Ser Val Ser Ile Phe Arg
      65      70      75      80
Asn Thr Ser

```

<210> 178

<211> 662

<212> PRT

<213> Homo sapiens

<400> 178

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Met Lys Glu Val Thr Phe His Cys His Glu Gly Tyr Ile Leu His Gly
  1      5      10      15
Ala Pro Lys Leu Thr Cys Gln Ser Asp Gly Asn Trp Asp Ala Glu Ile
      20      25      30
Pro Leu Cys Lys Pro Val Asn Cys Gly Pro Pro Glu Asp Leu Ala His
      35      40      45
Gly Phe Pro Asn Gly Phe Ser Phe Ile His Gly Gly His Ile Gln Tyr
      50      55      60
Gln Cys Phe Pro Gly Tyr Lys Leu His Gly Asn Ser Ser Arg Arg Cys
      65      70      75      80
Leu Ser Asn Gly Ser Trp Ser Gly Ser Ser Pro Ser Cys Leu Pro Cys
      85      90      95
Arg Cys Ser Thr Pro Val Ile Glu Tyr Gly Thr Val Asn Gly Thr Asp
      100      105      110
Phe Asp Cys Gly Lys Ala Ala Arg Ile Gln Cys Phe Lys Gly Phe Lys
      115      120      125
Leu Leu Gly Leu Ser Glu Ile Thr Cys Glu Ala Asp Gly Gln Trp Ser
      130      135      140
Ser Gly Phe His His Phe Glu His Thr Ser Cys Gly Ser Leu Pro Met
      145      150      155      160
Ile Pro Asn Ala Phe Ile Ser Glu Thr Ser Ser Trp Lys Glu Asn Val
      165      170      175
Ile Thr Tyr Ser Cys Arg Ser Gly Tyr Val Ile Gln Gly Ser Ser Asp
      180      185      190
Leu Ile Cys Thr Glu Lys Gly Val Trp Ser Gln Pro Tyr Pro Val Cys
      195      200      205
Glu Pro Leu Ser Cys Gly Ser Pro Pro Ser Val Ala Asn Ala Val Ala
      210      215      220
Thr Gly Glu Ala His Thr Tyr Glu Ser Glu Val Lys Leu Arg Cys Leu
      225      230      235      240
Glu Gly Tyr Thr Met Asp Thr Asp Thr Arg Ser Ile Thr Cys Gln Lys
      245      250      255
Asp Gly Arg Trp Phe Pro Glu Arg Ile Ser Cys Ser Pro Lys Lys Cys
      260      265      270
Pro Leu Pro Glu Asn Ile Thr His Ile Leu Val His Gly Asp Asp Phe
      275      280      285
Ser Val Asn Arg Gln Val Ser Val Ser Cys Ala Glu Gly Tyr Thr Phe
      290      295      300
Glu Gly Val Asn Ile Ser Val Cys Gln Leu Asp Gly Thr Trp Glu Pro
      305      310      315      320
Pro Phe Ser Asp Glu Ser Cys Ser Pro Val Ser Cys Gly Lys Pro Glu

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325 330 335
 Ser Pro Glu His Gly Phe Val Val Gly Ser Lys Tyr Thr Phe Glu Ser
 340 345 350
 Thr Ile Ile Tyr Gln Cys Glu Pro Gly Tyr Glu Leu Gly Asn Arg
 355 360 365
 Glu Arg Val Cys Gln Glu Asn Arg Gln Trp Ser Gly Val Ala Ile
 370 375 380
 Cys Lys Glu Thr Arg Cys Glu Thr Pro Leu Glu Phe Leu Asn Gly Lys
 385 390 395 400
 Ala Asp Ile Glu Asn Arg Thr Thr Gly Pro Asn Val Val Tyr Ser Cys
 405 410 415
 Asn Arg Gly Tyr Ser Leu Glu Gly Pro Ser Glu Ala His Cys Thr Glu
 420 425 430
 Asn Gly Thr Trp Ser His Pro Val Pro Leu Cys Lys Pro Asn Pro Cys
 435 440 445
 Pro Val Pro Phe Val Ile Pro Glu Asn Ala Leu Leu Ser Glu Lys Glu
 450 455 460
 Phe Tyr Val Asp Gln Asn Val Ser Ile Lys Cys Arg Glu Gly Phe Leu
 465 470 475 480
 Leu Gln Gly His Gly Ile Ile Thr Cys Asn Pro Asp Glu Thr Trp Thr
 485 490 495
 Gln Thr Ser Ala Lys Cys Glu Lys Ile Ser Cys Gly Pro Pro Ala His
 500 505 510
 Val Glu Asn Ala Ile Ala Arg Gly Val His Tyr Gln Tyr Gly Asp Met
 515 520 525
 Ile Thr Tyr Ser Cys Tyr Ser Gly Tyr Met Leu Glu Gly Phe Leu Arg
 530 535 540
 Ser Val Cys Leu Glu Asn Gly Thr Trp Thr Ser Pro Ile Cys Arg
 545 550 555 560
 Ala Val Cys Arg Phe Pro Cys Gln Asn Gly Gly Ile Cys Gln Arg Pro
 565 570 575
 Asn Ala Cys Ser Cys Pro Glu Gly Trp Met Gly Arg Leu Cys Glu Glu
 580 585 590
 Leu Ile Cys Ile Leu Pro Cys Leu Asn Gly Gly Arg Cys Val Ala Pro
 595 600 605
 Tyr Gln Cys Asp Cys Pro Pro Gly Trp Thr Gly Ser Arg Cys His Thr
 610 615 620
 Ala Val Cys Gln Ser Pro Cys Leu Asn Gly Gly Lys Cys Val Arg Pro
 625 630 635 640
 Asn Arg Cys His Cys Leu Ser Ser Trp Thr Gly His Asn Cys Ser Arg
 645 650 655
 Lys Arg Arg Thr Gly Phe
 660

<210> 179
 <211> 1867
 <212> PRT
 <213> Homo sapiens

<400> 179
 Met Ala Arg Leu Ala Asp Tyr Phe Val Leu Val Ala Phe Gly Pro His
 1 5 10 15
 Pro Arg Gly Ser Gly Glu Gly Gln Gly Gln Ile Leu Gln Arg Phe Pro
 20 25 30
 Glu Lys Asp Trp Glu Asp Asn Pro Phe Pro Gln Gly Ile Glu Leu Phe
 35 40 45
 Cys Gln Pro Ser Gly Trp Gln Leu Cys Pro Glu Arg Asn Pro Pro Thr
 50 55 60

Phe Phe Val Ala Val Leu Thr Asp Ile Asn Ser Glu Arg His Tyr Cys
 65 70 75 80
 Ala Cys Leu Thr Phe Trp Glu Pro Ala Glu Pro Ser Gln Glu Thr Thr
 85 90 95
 Arg Val Glu Asp Ala Thr Glu Arg Glu Glu Gly Asp Glu Gly Gly
 100 105 110
 Gln Thr His Leu Ser Pro Thr Ala Pro Ala Pro Ser Ala Gln Leu Phe
 115 120 125
 Ala Pro Lys Thr Leu Val Leu Val Ser Arg Leu Asp His Thr Glu Val
 130 135 140
 Phe Arg Asn Ser Leu Gly Leu Ile Tyr Ala Ile His Val Glu Gly Leu
 145 150 155 160
 Asn Val Cys Leu Glu Asn Val Ile Gly Asn Leu Leu Thr Cys Thr Val
 165 170 175
 Pro Leu Ala Gly Ser Gln Arg Thr Ile Ser Leu Gly Ala Gly Asp
 180 185 190
 Arg Gln Val Ile Gln Thr Pro Leu Ala Asp Ser Leu Pro Val Ser Arg
 195 200 205
 Cys Ser Val Ala Leu Leu Phe Arg Gln Leu Gly Ile Thr Asn Val Leu
 210 215 220
 Ser Leu Phe Cys Ala Ala Leu Thr Glu His Lys Val Leu Phe Leu Ser
 225 230 235 240
 Arg Ser Tyr Gln Arg Leu Ala Asp Ala Cys Arg Gly Leu Leu Ala Leu
 245 250 255
 Leu Phe Pro Leu Arg Tyr Ser Phe Thr Tyr Val Pro Ile Leu Pro Ala
 260 265 270
 Gln Leu Leu Glu Val Leu Ser Thr Pro Thr Pro Phe Ile Ile Gly Val
 275 280 285
 Asn Ala Ala Phe Gln Ala Glu Thr Gln Glu Leu Leu Asp Val Ile Val
 290 295 300
 Ala Asp Leu Asp Gly Gly Thr Val Thr Ile Pro Glu Cys Val His Ile
 305 310 315 320
 Pro Pro Leu Pro Glu Pro Leu Gln Ser Gln Thr His Ser Val Leu Ser
 325 330 335
 Met Val Leu Asp Pro Glu Leu Glu Leu Ala Asp Leu Ala Phe Pro Pro
 340 345 350
 Pro Thr Thr Ser Thr Ser Ser Leu Lys Met Gln Asp Lys Glu Leu Arg
 355 360 365
 Ala Val Phe Leu Arg Leu Phe Ala Gln Leu Leu Gln Gly Tyr Arg Trp
 370 375 380
 Cys Leu His Val Val Arg Ile His Pro Glu Pro Val Ile Arg Phe His
 385 390 395 400
 Lys Ala Ala Phe Leu Gly Gln Arg Gly Leu Val Glu Asp Asp Phe Leu
 405 410 415
 Met Lys Val Leu Glu Gly Met Ala Phe Ala Gly Phe Val Ser Glu Arg
 420 425 430
 Gly Val Pro Tyr Arg Pro Thr Asp Leu Phe Asp Glu Leu Val Ala His
 435 440 445
 Glu Val Ala Arg Met Arg Ala Asp Glu Asn His Pro Gln Arg Val Leu
 450 455 460
 Arg His Val Gln Glu Leu Ala Glu Gln Leu Tyr Lys Asn Glu Asn Pro
 465 470 475 480
 Tyr Pro Ala Val Ala Met His Lys Val Gln Arg Pro Gly Glu Ser Ser
 485 490 495
 His Leu Arg Arg Val Pro Arg Pro Phe Pro Arg Leu Asp Glu Gly Thr
 500 505 510
 Val Gln Trp Ile Val Asp Gln Ala Ala Lys Met Gln Gly Ala Pro
 515 520 525
 Pro Ala Val Lys Ala Glu Arg Arg Thr Thr Val Pro Ser Gly Pro Pro
 530 535 540
 Met Thr Ala Ile Leu Glu Arg Cys Ser Gly Leu His Val Asn Ser Ala

545	Arg	Arg	Leu	Glu	Val	Val	Arg	Asn	Cys	Ile	555	Ser	Tyr	Val	Phe	Glu	560
					565						570					Gly	575
Lys	Met	Leu	Glu	Ala	Lys	Lys	Leu	Leu	Pro	Ala	Val	Leu	Arg	Ala	Leu		
			580														590
Lys	Gly	Arg	Val	Ala	Arg	Arg	Cys	Leu	Ala	Gln	Glu	Leu	His	Leu	His		
		595					600										
Val	Gln	Gln	Asn	Arg	Ala	Val	Leu	Asp	His	Gln	Gln	Phe	Asp	Phe	Val		
		610					615										
Val	Arg	Met	Met	Asn	Cys	Cys	Leu	Gln	Asp	Cys	Thr	Ser	Leu	Asp	Glu		
		625					630										640
His	Gly	Ile	Ala	Ala	Ala	Leu	Leu	Pro	Leu	Val	Thr	Ala	Phe	Cys	Arg		
				645													655
Lys	Leu	Ser	Pro	Gly	Val	Thr	Gln	Phe	Ala	Tyr	Ser	Cys	Val	Gln	Glu		
			660					665									
His	Val	Val	Trp	Ser	Thr	Pro	Gln	Phe	Trp	Glu	Ala	Met	Phe	Tyr	Gly		
			675					680									
Asp	Val	Gln	Thr	His	Ile	Arg	Ala	Leu	Tyr	Leu	Glu	Pro	Thr	Glu	Asp		
			690				695										
Leu	Ala	Pro	Ala	Gln	Glu	Val	Gly	Glu	Ala	Pro	Ser	Gln	Glu	Asp	Glu		
			705				710										720
Arg	Ser	Ala	Leu	Asp	Val	Ala	Ser	Glu	Gln	Arg	Leu	Trp	Pro	Thr			
			725														
Leu	Ser	Arg	Glu	Lys	Gln	Gln	Glu	Leu	Val	Gln	Lys	Glu	Glu	Ser	Thr		
			740					745									
Val	Phe	Ser	Gln	Ala	Ile	His	Tyr	Ala	Asn	Arg	Met	Ser	Tyr	Leu	Leu		
			755				760										
Leu	Pro	Leu	Asp	Ser	Ser	Lys	Ser	Arg	Leu	Leu	Arg	Glu	Arg	Ala	Gly		
			770				775										
Leu	Gly	Asp	Leu	Glu	Ser	Ala	Ser	Asn	Ser	Leu	Val	Thr	Asn	Ser	Met		
			785				790										800
Ala	Gly	Ser	Val	Ala	Glu	Ser	Tyr	Asp	Thr	Glu	Ser	Gly	Phe	Glu	Asp		
			805														815
Ala	Glu	Thr	Cys	Asp	Val	Ala	Gly	Ala	Val	Val	Arg	Phe	Ile	Asn	Arg		
			820					825									
Phe	Val	Asp	Lys	Val	Cys	Thr	Glu	Ser	Gly	Val	Thr	Ser	Asp	His	Leu		
			835					840									
Lys	Gly	Leu	His	Val	Met	Val	Pro	Asp	Ile	Val	Gln	Met	His	Ile	Glu		
			850				855										
Thr	Leu	Glu	Ala	Val	Gln	Arg	Glu	Ser	Arg	Arg	Leu	Pro	Pro	Ile	Gln		
			865				870										880
Lys	Pro	Lys	Leu	Leu	Arg	Pro	Arg	Leu	Leu	Pro	Gly	Glu	Glu	Cys	Val		
			885														895
Leu	Asp	Gly	Leu	Arg	Val	Tyr	Leu	Leu	Pro	Asp	Gly	Arg	Glu	Glu	Gly		
			900					905									
Ala	Gly	Gly	Ser	Ala	Gly	Gly	Pro	Ala	Leu	Leu	Pro	Ala	Glu	Gly	Ala		
			915					920									
Val	Phe	Leu	Thr	Thr	Tyr	Arg	Val	Ile	Phe	Thr	Gly	Met	Pro	Thr	Asp		
			930				935										
Pro	Leu	Val	Gly	Glu	Gln	Val	Val	Val	Arg	Ser	Phe	Pro	Val	Ala	Ala		
			945				950										960
Leu	Thr	Lys	Glu	Lys	Arg	Ile	Ser	Val	Gln	Thr	Pro	Val	Asp	Gln	Leu		
			965														975
Leu	Gln	Asp	Gly	Leu	Gln	Leu	Arg	Ser	Cys	Thr	Phe	Gln	Leu	Leu	Lys		
			980														
Met	Ala	Phe	Asp	Glu	Glu	Val	Gly	Ser	Asp	Ser	Ala	Glu	Leu	Phe	Arg		
			995				1000										
Lys	Gln	Leu	His	Lys	Leu	Arg	Tyr	Pro	Pro	Asp	Ile	Arg	Ala	Thr	Phe		
			1010				1015										
Ala	Phe	Thr	Leu	Gly	Ser	Ala	His	Thr	Pro	Gly	Arg	Pro	Pro	Arg	Val		
			1025				1030										1040

Thr Lys Asp Lys Gly Pro Ser Leu Arg Thr Leu Ser Arg Asn Leu Val
 1045 1050 1055
 Lys Asn Ala Lys Lys Thr Ile Gly Arg Gln His Val Thr Arg Lys Lys
 1060 1065 1070
 Tyr Asn Pro Pro Ser Trp Glu His Arg Gly Gln Pro Pro Glu Asp
 1075 1080 1085
 Gln Glu Asp Glu Ile Ser Val Ser Glu Glu Leu Glu Pro Ser Thr Leu
 1090 1095 1100
 Thr Pro Ser Ser Ala Leu Lys Pro Ser Asp Arg Met Thr Met Ser Ser
 1105 1110 1115
 Leu Val Glu Arg Ala Cys Cys Arg Asp Tyr Gln Arg Leu Gly Leu Gly
 1125 1130 1135
 Thr Leu Ser Ser Leu Ser Arg Ala Lys Ser Glu Pro Phe Arg Ile
 1140 1145 1150
 Ser Pro Val Asn Arg Met Tyr Ala Ile Cys Arg Ser Tyr Pro Gly Leu
 1155 1160 1165
 Leu Ile Val Arg Gln Ser Val Gln Asp Asn Ala Leu Gln Arg Val Ser
 1170 1175 1180
 Arg Cys Tyr Arg Gln Asn Arg Phe Pro Val Val Cys Trp Arg Ser Gly
 1185 1190 1195
 Arg Ser Lys Ala Val Leu Leu Arg Ser Gly Gly Leu His Gly Lys Gly
 1205 1210 1215
 Val Val Gly Leu Phe Lys Ala Gln Asn Ala Pro Ser Pro Gly Gln Ser
 1220 1225 1230
 Gln Ala Asp Ser Ser Ser Leu Glu Gln Glu Lys Tyr Leu Gln Ala Val
 1235 1240 1245
 Val Ser Ser Met Pro Arg Tyr Ala Asp Ala Ser Gly Arg Asn Thr Leu
 1250 1255 1260
 Ser Gly Phe Ser Ser Ala His Met Gly Ser His Gly Lys Trp Gly Ser
 1265 1270 1275
 Val Arg Thr Ser Gly Arg Ser Ser Gly Leu Gly Thr Asp Val Gly Ser
 1285 1290 1295
 Arg Leu Ala Gly Arg Asp Ala Leu Ala Pro Pro Gln Ala Asn Gly Gly
 1300 1305 1310
 Pro Pro Asp Pro Gly Phe Leu Arg Pro Gln Arg Ala Ala Leu Tyr Ile
 1315 1320 1325
 Leu Gly Asp Lys Ala Gln Leu Lys Gly Val Arg Ser Asp Pro Leu Gln
 1330 1335 1340
 Gln Trp Glu Leu Val Pro Ile Glu Val Phe Glu Ala Arg Gln Val Lys
 1345 1350 1355
 Ala Ser Phe Lys Lys Leu Leu Lys Ala Cys Val Pro Gly Cys Pro Ala
 1365 1370 1375
 Ala Glu Pro Ser Pro Ala Ser Phe Leu Arg Ser Leu Glu Asp Ser Glu
 1380 1385 1390
 Trp Leu Ile Gln Ile His Lys Leu Leu Gln Val Ser Val Leu Val Val
 1395 1400 1405
 Glu Leu Leu Asp Ser Gly Ser Ser Val Leu Val Gly Leu Glu Asp Gly
 1410 1415 1420
 Trp Asp Ile Thr Thr Gln Val Val Ser Leu Val Gln Leu Leu Ser Asp
 1425 1430 1435
 Pro Phe Tyr Arg Thr Leu Glu Gly Phe Arg Leu Leu Val Glu Lys Glu
 1445 1450 1455
 Trp Leu Ser Phe Gly His Arg Phe Ser His Arg Gly Ala His Thr Leu
 1460 1465 1470
 Ala Gly Gln Ser Ser Gly Phe Thr Pro Val Phe Leu Gln Phe Leu Asp
 1475 1480 1485
 Cys Val His Gln Val His Leu Gln Phe Pro Met Glu Phe Glu Phe Ser
 1490 1495 1500
 Gln Phe Tyr Leu Lys Phe Leu Gly Tyr His His Val Ser Arg Arg Phe
 1505 1510 1515
 Arg Thr Phe Leu Leu Asp Ser Asp Tyr Glu Arg Ile Glu Leu Gly Leu

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<210> 180
<211> 495
<212> PRT
<213> Homo sapiens
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Met																<400> 180																Met																															
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Met	Asp	Ile	Leu	Cys	Asp	Leu	Lys	Arg	His	Glu	Leu	Cys	Gly	Asp	Tyr	Ile	Met	Asp	Ile	Leu	Cys	Asp	Leu	Lys	Arg	His	Glu	Leu	Cys	Gly	Asp	Tyr	Ile	Met	Asp	Ile	Leu	Cys	Asp	Leu	Lys	Arg	His	Glu	Leu	Cys	Gly	Asp	Tyr	Ile													
Lys	Asp	Ile	Leu	Cys	Gln	Glu	Cys	Ser	Pro	Tyr	Ala	Ala	His	Leu	Tyr		Lys	Asp	Ile	Leu	Cys	Gln	Glu	Cys	Ser	Pro	Tyr	Ala	Ala	His	Leu	Tyr		Lys	Asp	Ile	Leu	Cys	Gln	Glu	Cys	Ser	Pro	Tyr	Ala	Ala	His	Leu	Tyr														
20																25																30																															
Asp	Ala	Glu	Asn	Thr	Gln	Thr	Pro	Leu	Arg	Asn	Leu	Pro	Gly	Leu	Cys		Asp	Ala	Glu	Asn	Thr	Gln	Thr	Pro	Leu	Arg	Asn	Leu	Pro	Gly	Leu	Cys		Asp	Ala	Glu	Asn	Thr	Gln	Thr	Pro	Leu	Arg	Asn	Leu	Pro	Gly	Leu	Cys														
35																40																45																															
Ser	Asp	Tyr	Cys	Ser	Ala	Phe	His	Ser	Asn	Cys	His	Ser	Ala	Ile	Ser		Ser	Asp	Tyr	Cys	Ser	Ala	Phe	His	Ser	Asn	Cys	His	Ser	Ala	Ile	Ser		Ser	Asp	Tyr	Cys	Ser	Ala	Phe	His	Ser	Asn	Cys	His	Ser	Ala	Ile	Ser														
50																55																60																															

Leu Leu Thr Asn Asp Arg Gly Leu Gln Glu Ser His Gly Arg Asp Gly
 65 70 75 80
 Thr Arg Phe Cys His Leu Leu Asp Leu Pro Asp Lys Asp Tyr Cys Phe
 85 90 95
 Pro Asn Val Leu Arg Asn Asp Tyr Leu Asn Arg His Leu Gly Met Val
 100 105 110
 Ala Gln Asp Pro Gln Gly Cys Leu Gln Leu Cys Leu Ser Glu Val Ala
 115 120 125
 Asn Gly Leu Arg Asn Pro Val Ser Met Val His Ala Gly Asp Gly Thr
 130 135 140
 His Arg Phe Phe Val Ala Glu Gln Val Gly Val Val Trp Val Tyr Leu
 145 150 155 160
 Pro Asp Gly Ser Arg Leu Glu Gln Pro Phe Leu Asp Leu Lys Asn Ile
 165 170 175
 Val Leu Thr Thr Pro Trp Ile Gly Asp Glu Arg Gly Phe Leu Gly Leu
 180 185 190
 Ala Phe His Pro Lys Phe Arg His Asn Arg Lys Phe Tyr Ile Tyr Tyr
 195 200 205
 Ser Cys Leu Asp Lys Lys Lys Val Glu Lys Ile Arg Ile Ser Glu Met
 210 215 220
 Lys Val Ser Arg Ala Asp Pro Asn Lys Ala Asp Leu Lys Ser Glu Arg
 225 230 235 240
 Val Ile Leu Glu Ile Glu Glu Pro Ala Ser Asn His Asn Gly Gly Gln
 245 250 255
 Leu Leu Phe Gly Leu Asp Gly Tyr Met Tyr Ile Phe Thr Gly Asp Gly
 260 265 270
 Gly Gln Ala Gly Asp Pro Phe Gly Leu Phe Gly Asn Ala Gln Asn Lys
 275 280 285
 Ser Ser Leu Leu Gly Lys Val Leu Arg Ile Asp Val Asn Arg Ala Gly
 290 295 300
 Ser His Gly Lys Arg Tyr Arg Val Pro Ser Asp Asn Pro Phe Val Ser
 305 310 315 320
 Glu Pro Gly Ala His Pro Ala Ile Tyr Ala Tyr Gly Ile Arg Asn Met
 325 330 335
 Trp Arg Cys Ala Val Asp Arg Gly Asp Pro Ile Thr Arg Gln Gly Arg
 340 345 350
 Gly Arg Ile Phe Cys Gly Asp Val Gly Gln Asn Arg Phe Glu Glu Val
 355 360 365
 Asp Leu Ile Leu Lys Gly Gly Asn Tyr Gly Trp Arg Ala Lys Glu Gly
 370 375 380
 Phe Ala Cys Tyr Asp Lys Lys Leu Cys His Asn Ala Ser Leu Glu Glu
 385 390 395 400
 Gln Ala Thr Glu Asp Gly Ser Pro Glu Ser Leu Gly Arg Pro Ala Ser
 405 410 415
 Gly Val Pro Ile Ser Gly Val Val Leu Asp Thr Gly Val Ser Gly Arg
 420 425 430
 Gly Glu Ala Pro Pro Pro Pro Ala Ala Phe Thr Lys Gly Asp Asp Glu
 435 440 445
 Leu Ala Met Gly Ala Asp Gln Pro Trp Glu Gly Thr Gly Arg Gly Ala
 450 455 460
 Ala Gln Ala Lys Ile Leu Leu Leu Pro Phe Leu Val Phe Ser Ile Phe
 465 470 475 480
 Leu Gln Ser His Lys Ser Thr Arg Gln Lys Ile Asn Pro Tyr Val
 485 490 495

<210> 181

<211> 217

<212> PRT

<213> Homo sapiens

<400> 181

Met	Ile	Thr	Ile	Ala	Lys	Glu	Thr	Gly	Leu	Gly	Leu	Lys	Val	Leu	Gly
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Gly	Ile	Asn	Arg	Asn	Glu	Gly	Pro	Leu	Val	Tyr	Ile	Gln	Glu	Ile	Ile
		20						25					30		
Pro	Gly	Gly	Asp	Cys	Tyr	Lys	Asp	Gly	Arg	Leu	Lys	Pro	Gly	Asp	Gln
		35					40					45			
Leu	Val	Ser	Val	Asn	Lys	Glu	Ser	Met	Ile	Gly	Val	Ser	Phe	Glu	Glu
		50				55					60				
Ala	Lys	Ser	Ile	Ile	Thr	Arg	Ala	Lys	Leu	Arg	Leu	Glu	Ser	Ala	Trp
65					70					75					80
Glu	Ile	Ala	Phe	Ile	Arg	Gln	Lys	Ser	Asp	Asn	Ile	Gln	Pro	Glu	Asn
			85						90					95	
Leu	Ser	Cys	Thr	Ser	Leu	Ile	Glu	Ala	Ser	Gly	Glu	Tyr	Gly	Pro	Gln
			100					105					110		
Ala	Ser	Thr	Leu	Ser	Leu	Phe	Ser	Ser	Pro	Pro	Glu	Ile	Leu	Ile	Pro
		115					120					125			
Lys	Thr	Ser	Ser	Thr	Pro	Lys	Thr	Asn	Asn	Asp	Ile	Leu	Ser	Ser	Cys
		130				135					140				
Glu	Ile	Lys	Thr	Gly	Tyr	Asn	Lys	Thr	Val	Gln	Ile	Pro	Ile	Thr	Ser
145					150					155					160
Glu	Asn	Ser	Thr	Val	Gly	Leu	Ser	Asn	Thr	Gly	Ser	Lys	Leu	Ser	Trp
			165						170					175	
Tyr	Ser	Ala	His	Lys	Gly	Thr	Thr	Pro	Ser	Pro	Glu	Thr	Ala	Ser	Thr
			180					185						190	
Ser	Arg	Leu	Lys	Arg	Asp	Ser	Val	Phe	Trp	Arg	Phe	Cys	Pro	Gly	Cys
		195					200					205			
Gln	Lys	Leu	Val	Leu	Leu	Ala	Val	Gly							
210						215									

<210> 182

<211> 179

<212> PRT

<213> Homo sapiens

<400> 182

Met	Gly	Leu	Ile	Phe	Ala	Lys	Leu	Trp	Ser	Leu	Phe	Cys	Asn	Gln	Glu
1				5					10					15	
His	Lys	Val	Ile	Ile	Val	Gly	Leu	Asp	Asn	Ala	Gly	Lys	Thr	Thr	Ile
		20						25					30		
Leu	Tyr	Gln	Phe	Leu	Met	Asn	Glu	Val	Val	His	Thr	Ser	Pro	Thr	Ile
		35					40					45			
Gly	Ser	Asn	Val	Glu	Glu	Ile	Val	Val	Lys	Asn	Thr	His	Phe	Leu	Met
		50				55					60				
Trp	Asp	Ile	Gly	Gly	Gln	Glu	Ser	Leu	Arg	Ser	Ser	Trp	Asn	Thr	Tyr
65					70				75						80
Tyr	Ser	Asn	Thr	Glu	Phe	Ile	Ile	Leu	Val	Val	Asp	Ser	Ile	Asp	Arg
			85						90				95		
Glu	Arg	Leu	Ala	Ile	Thr	Lys	Glu	Glu	Leu	Tyr	Arg	Met	Leu	Ala	His
			100					105					110		
Glu	Asp	Leu	Arg	Lys	Ala	Ala	Val	Leu	Ile	Phe	Ala	Asn	Lys	Gln	Asp
		115					120					125			
Met	Lys	Gly	Cys	Met	Thr	Ala	Ala	Glu	Ile	Ser	Lys	Tyr	Leu	Thr	Leu
		130				135					140				
Ser	Ser	Ile	Lys	Asp	His	Pro	Trp	His	Ile	Gln	Ser	Cys	Cys	Ala	Leu
145					150					155					160

Thr Gly Glu Gly Leu Cys Gln Gly Leu Glu Trp Met Thr Ser Arg Ile
 165 170 175
 Gly Val Arg

<210> 183
 <211> 1364
 <212> PRT
 <213> Homo sapiens

<400> 183
 Met Gly Pro Asp Glu Ala Thr Pro Pro Asp Leu Val Leu Pro Ala Trp
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 Arg Leu Arg His Gly Ala Phe Arg Thr Leu Val Thr Arg Glu Pro Gly
 20 25 30
 Ala Pro Arg Met Gly Ala Pro Ser Ala Cys Arg Thr Leu Val Leu Ala
 35 40 45
 Leu Ala Ala Met Leu Val Val Pro Gln Ala Glu Thr Gln Gly Pro Val
 50 55 60
 Glu Pro Ser Trp Glu Asn Ala Gly His Thr Met Asp Gly Gly Ala Pro
 65 70 75 80
 Thr Ser Ser Pro Thr Arg Arg Val Ser Phe Val Pro Pro Val Thr Val
 85 90 95
 Phe Pro Ser Leu Ser Pro Leu Asn Pro Ala His Asn Gly Arg Val Cys
 100 105 110
 Ser Thr Trp Gly Asp Phe His Tyr Lys Thr Phe Asp Gly Asp Val Phe
 115 120 125
 Arg Phe Pro Gly Leu Cys Asn Tyr Val Phe Ser Glu His Cys Arg Ala
 130 135 140
 Ala Tyr Glu Asp Phe Asn Val Gln Leu Arg Arg Gly Leu Val Gly Ser
 145 150 155 160
 Arg Pro Val Val Thr Arg Val Val Ile Lys Ala Gln Gly Leu Val Leu
 165 170 175
 Glu Ala Ser Asn Gly Ser Val Leu Ile Asn Gly Gln Arg Glu Glu Leu
 180 185 190
 Pro Tyr Ser Arg Thr Gly Leu Leu Val Glu Gln Ser Gly Asp Tyr Ile
 195 200 205
 Lys Val Ser Ile Arg Leu Val Leu Thr Phe Leu Trp Asn Gly Glu Asp
 210 215 220
 Ser Ala Leu Leu Glu Leu Asp Pro Lys Tyr Ala Asn Gln Thr Cys Gly
 225 230 235 240
 Leu Cys Gly Asp Phe Asn Gly Leu Pro Ala Phe Asn Glu Phe Tyr Ala
 245 250 255
 His Ser Glu Cys His Leu Asp Ala Arg Leu Thr Pro Leu Gln Phe Gly
 260 265 270
 Asn Leu Gln Lys Leu Asp Gly Pro Thr Glu Gln Cys Pro Asp Pro Leu
 275 280 285
 Pro Leu Pro Ala Gly Asn Cys Thr Asp Glu Glu Gly Ile Cys His Arg
 290 295 300
 Thr Leu Leu Gly Pro Ala Phe Ala Glu Cys His Ala Leu Val Asp Ser
 305 310 315 320
 Thr Ala Tyr Leu Ala Ala Cys Ala Gln Asp Leu Cys Arg Cys Pro Thr
 325 330 335
 Cys Pro Cys Ala Thr Phe Val Glu Tyr Ser Arg Gln Cys Ala His Ala
 340 345 350
 Gly Gly Gln Pro Arg Asn Trp Arg Cys Pro Glu Leu Cys Pro Arg Thr
 355 360 365
 Cys Pro Leu Asn Met Gln His Gln Glu Cys Gly Ser Pro Cys Thr Asp

	370					375				380									
Thr	Cys	Ser	Asn	Pro	Gln	Arg	Ala	Gln	Leu	Cys	Glu	Asp	His	Cys	Val				
385					390					395					400				
Asp	Gly	Cys	Phe	Cys	Pro	Pro	Gly	Thr	Val	Leu	Asp	Asp	Ile	Thr	His				
				405					410						415				
Ser	Gly	Cys	Leu	Pro	Leu	Gly	Gln	Cys	Pro	Cys	Thr	His	Gly	Gly	Arg				
				420					425					430					
Thr	Tyr	Ser	Pro	Gly	Thr	Ser	Phe	Asn	Thr	Thr	Cys	Ser	Ser	Cys	Thr				
				435					440					445					
Cys	Ser	Gly	Gly	Leu	Trp	Gln	Cys	Gln	Asp	Leu	Pro	Cys	Pro	Gly	Thr				
				450					455					460					
Cys	Ser	Val	Gln	Gly	Gly	Ala	His	Ile	Ser	Thr	Tyr	Asp	Glu	Lys	Leu				
465					470					475				480					
Tyr	Asp	Leu	His	Gly	Asp	Cys	Ser	Tyr	Val	Leu	Ser	Lys	Lys	Cys	Ala				
				485					490					495					
Asp	Ser	Ser	Phe	Thr	Val	Leu	Ala	Glu	Leu	Arg	Lys	Cys	Gly	Leu	Thr				
				500					505					510					
Asp	Asn	Glu	Asn	Cys	Leu	Lys	Ala	Val	Thr	Leu	Ser	Leu	Asp	Gly	Gly				
				515					520					525					
Asp	Thr	Ala	Ile	Arg	Val	Gln	Ala	Asp	Gly	Gly	Val	Phe	Leu	Asn	Ser				
				530					535					540					
Ile	Tyr	Thr	Gln	Leu	Pro	Leu	Ser	Ala	Ala	Asn	Ile	Thr	Leu	Phe	Thr				
545					550					555				560					
Pro	Ser	Ser	Phe	Phe	Ile	Val	Val	Gln	Thr	Gly	Leu	Gly	Leu	Gln	Leu				
				565					570					575					
Leu	Val	Gln	Leu	Val	Pro	Leu	Met	Gln	Val	Phe	Val	Arg	Leu	Asp	Pro				
				580					585					590					
Ala	His	Gln	Gly	Gln	Met	Cys	Gly	Leu	Cys	Gly	Asn	Phe	Asn	Gln	Asn				
				595					600					605					
Gln	Ala	Asp	Asp	Phe	Thr	Ala	Leu	Ser	Gly	Val	Val	Glu	Ala	Thr	Gly				
				610					615					620					
Ala	Ala	Phe	Ala	Asn	Thr	Trp	Lys	Ala	Gln	Ala	Cys	Ala	Asn	Ala	Ala				
625					630					635				640					
Arg	Asn	Ser	Phe	Glu	Asp	Pro	Cys	Ser	Leu	Ser	Val	Glu	Asn	Glu	Asn				
				645					650					655					
Tyr	Ala	Arg	His	Trp	Cys	Ser	Arg	Leu	Thr	Asp	Pro	Asn	Ser	Ala	Phe				
				660					665					670					
Ser	Arg	Cys	His	Ser	Ile	Ile	Asn	Pro	Lys	Pro	Phe								

Gly Cys Phe Ser Thr His Cys Val Ser Gly Cys Val Cys Pro Pro Gly
 865 870 875 880
 Leu Val Ser Asp Gly Ser Gly Gly Cys Ile Ala Glu Glu Asp Cys Pro
 885 890 895
 Cys Val His Asn Glu Ala Thr Tyr Lys Pro Gly Glu Thr Ile Arg Val
 900 905 910
 Asp Cys Asn Thr Cys Thr Cys Arg Asn Arg Arg Trp Glu Cys Ser His
 915 920 925
 Arg Leu Cys Leu Gly Thr Cys Val Ala Tyr Gly Asp Gly His Phe Ile
 930 935 940
 Thr Phe Asp Gly Asp Arg Tyr Ser Phe Glu Gly Ser Cys Glu Tyr Ile
 945 950 955 960
 Leu Ala Gln Asp Tyr Cys Gly Asp Asn Thr Thr His Gly Thr Phe Arg
 965 970 975
 Ile Val Thr Glu Asn Ile Pro Cys Gly Thr Thr Gly Thr Thr Cys Ser
 980 985 990
 Lys Ala Ile Lys Leu Phe Val Glu Ser Tyr Glu Leu Ile Leu Gln Glu
 995 1000 1005
 Gly Thr Phe Lys Ala Val Ala Arg Gly Pro Gly Gly Asp Pro Pro Tyr
 1010 1015 1020
 Lys Ile Arg Tyr Met Gly Ile Phe Leu Val Ile Glu Thr His Gly Met
 1025 1030 1035 1040
 Ala Val Ser Trp Asp Arg Lys Thr Ser Val Phe Ile Arg Leu His Gln
 1045 1050 1055
 Asp Tyr Lys Gly Arg Val Cys Gly Leu Cys Gly Asn Phe Asp Asp Asn
 1060 1065 1070
 Ala Ile Asn Asp Phe Ala Thr Arg Ser Arg Ser Val Val Gly Asp Ala
 1075 1080 1085
 Leu Glu Phe Gly Asn Ser Trp Lys Leu Ser Pro Ser Cys Pro Asp Ala
 1090 1095 1100
 Leu Ala Pro Lys Asp Pro Cys Thr Ala Asn Pro Phe Arg Lys Ser Trp
 1105 1110 1115 1120
 Ala Gln Lys Gln Cys Ser Ile Leu His Gly Pro Thr Phe Ala Ala Cys
 1125 1130 1135
 Arg Ser Gln Val Asp Ser Thr Lys Tyr Tyr Glu Ala Cys Val Asn Asp
 1140 1145 1150
 Ala Cys Ala Cys Asp Ser Gly Gly Asp Cys Glu Cys Phe Cys Thr Ala
 1155 1160 1165
 Val Ala Ala Tyr Ala Gln Ala Cys His Asp Ala Gly Leu Cys Val Ser
 1170 1175 1180
 Trp Arg Thr Pro Asp Thr Cys Pro Leu Phe Cys Asp Phe Tyr Asn Pro
 1185 1190 1195 1200
 His Gly Gly Cys Glu Trp His Tyr Gln Pro Cys Gly Ala Pro Cys Leu
 1205 1210 1215
 Lys Thr Cys Arg Asn Pro Ser Gly His Cys Leu Val Asp Leu Pro Gly
 1220 1225 1230
 Leu Glu Gly Cys Tyr Pro Lys Cys Pro Pro Ser Gln Pro Phe Phe Asn
 1235 1240 1245
 Glu Asp Gln Met Lys Cys Val Ala Gln Cys Gly Cys Tyr Asp Lys Asp
 1250 1255 1260
 Gly Asn Tyr Tyr Asp Val Gly Ala Arg Val Pro Thr Ala Glu Asn Cys
 1265 1270 1275 1280
 Gln Ser Cys Asn Cys Thr Pro Ser Gly Ile Gln Cys Ala His Ser Leu
 1285 1290 1295
 Glu Ala Cys Thr Cys Thr Tyr Glu Asp Arg Thr Tyr Ser Tyr Gln Asp
 1300 1305 1310
 Val Ile Tyr Asn Thr Thr Asp Gly Leu Gly Ala Cys Leu Ile Ala Ile
 1315 1320 1325
 Cys Gly Ser Asn Gly Thr Ile Ile Arg Lys Ala Val Ala Cys Pro Gly
 1330 1335 1340
 Thr Pro Ala Thr Thr Pro Phe Thr Thr Thr Ala Trp Val Pro His

1345

Ser Thr Thr Ser

1350

1355

1360

<210> 184

<211> 1296

<212> PRT

<213> Homo sapiens

<400> 184

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Met Ser Thr Ser Asp Ile Pro Ser Ser Pro Ser Ile Gln Asn Thr Glu
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Thr Ser Ser Leu Val Ser Met Thr Ser Ala Thr Ile Pro Ser Val Arg
      20      25      30
Pro Thr Phe Thr Ser Thr His Asn Thr Leu Thr Ser Ser Leu Leu Thr
      35      40      45
Thr Phe Pro Gly Thr Tyr Ser Phe Ser Ser Ser Met Ser Ala Ser Ser
      50      55      60
Asp Gly Thr Thr His Thr Glu Thr Ile Thr Ser Leu Pro Ala Ser Thr
 65      70      75      80
Ser Thr Leu His Thr Thr Ala Glu Ser Thr Thr Ala His Thr Thr Thr
      85      90      95
Thr Ser Phe Thr Thr Ser Thr Thr Met Glu Ser Pro Ser Ser Ser Val
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Ala Thr Thr Ser Thr Gly Gln Thr Thr Phe Ser Ser Ser Thr Ala Thr
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      130      135      140
Thr Leu Thr Thr Ala Met Thr Ser Thr Pro Pro Ile Thr Ser Ser Ile
 145      150      155      160
Thr Pro Thr Asn Thr Val Thr Ser Met Thr Thr Met Thr Ser Trp Pro
      165      170      175
Thr Ala Thr Asn Thr Leu Ser Ser Leu Thr Thr Asn Ile Leu Ser Ser
      180      185      190
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 210      215      220
Ser Thr Pro Thr Ser Glu Thr Thr Tyr Pro Ile Ser Ser Thr Ser Thr
 225      230      235      240
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      245      250      255
Thr Ser Ser Ser Ala Thr Ser Leu Pro Leu Thr Ser Pro Leu Val Ser
      260      265      270
Thr Thr Glu Thr Ala Lys Thr Pro Thr Thr Ile Leu Val Thr Thr Thr
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Thr Lys Thr Thr Ser His Ser Thr Thr Ser Phe Thr Ser Ser Thr Val
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Tyr Ser Thr Ala Ser Thr His Thr Thr Ala Ile Thr Ser Val Pro Thr
 305      310      315      320
Thr Leu Gly Thr Met Val Thr Ser Thr Ser Arg Ile Pro Ser Thr Val
      325      330      335
Ser Thr Ser Ile Pro Thr Ser Gln Pro Lys Thr Val Asn Ser Ser Ser
      340      345      350
Gly Gly Ile Thr Gly Ser Leu Pro Met Met Thr Asp Leu Thr Ser Gly
      355      360      365
Tyr Thr Val Ser Ser Met Ser Ala Ile Pro Thr Thr Val Ile Pro Thr
 370      375      380

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 420 425 430
 Ser Ser Ser Met Ser Glu Ser Ser Ala Gly Thr Thr His Thr Glu Ser
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 Ile Ser Ser Pro Pro Ala Thr Thr Ser Thr Leu His Thr Thr Ala Glu
 450 455 460
 Ser Thr Pro Ser Cys Thr Thr Thr Ser Phe Ile Thr Ser Thr Thr
 465 470 475 480
 Met Glu Pro Leu Ser Thr Ile Val Ala Thr Thr Gly Thr Val Lys Thr
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 Leu Thr Ser Ser Ile Leu Ser Ser Thr Leu Val Pro Ser Thr Asp Met
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				885					890					895															
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Ser	Ala	Ser	Ile	Thr	Pro	Val	Phe	Ser	Thr	Thr	Ile	His	Ser	Val	Pro														
				930				935						940															
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				965				970						975															
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				995				1000						1005															
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				1045				1050						1055															
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<211> 84

<212> PRT

<213> Homo sapiens

<400> 185

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Thr Thr Trp Asp Gln His Ala Pro Gly Asn Trp Ala Phe Lys Asp Gln
          20          25          30
Val Ala Ala Leu Ser Trp Val Gln Lys Asn Ile Glu Phe Phe Gly Gly
          35          40          45
Asp Pro Ser Ser Val Thr Ile Phe Asp Ser Val Ser His Gly Arg Arg
          50          55          60
Leu Ile Pro Gln Ser Arg His Gly Glu Trp Gly His His Pro Leu
 65          70          75          80
Pro Glu Gly Pro

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<210> 186

<211> 207

<212> PRT

<213> Homo sapiens

<400> 186

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Met Tyr Val Leu Arg Met Ser Val Cys Ala Val Cys Ala Cys Val Cys
 1          5          10          15
Cys Val Phe Val Cys Ala Val Phe Met Cys Ala Val His Ala Cys Val
          20          25          30
Leu Cys Ala Cys Val Cys Cys Val Leu Cys Ser Cys Val Cys Cys Val
          35          40          45
Cys Met Cys Cys Val His Val Cys Ala Val Phe Val Cys Val Leu Cys
          50          55          60
Val Leu Cys Ser Cys Val Leu Cys Ser Arg Val Cys Ala Val Cys Ala
 65          70          75          80
Cys Val Cys Cys Val Phe Val Cys Val Leu Cys Ala Ser Val Leu Cys
          85          90          95
Val His Val Cys Ala Cys Ala Val Arg Leu Cys Ala Val Cys Ser Cys
          100          105          110
Val Cys Cys Val Cys Val Cys Ala Val Arg Leu Cys Val Arg Val Arg
          115          120          125
Leu Arg Val Cys Cys Val Cys Met Cys Val Arg Val Cys Ala Val Arg
          130          135          140
Leu Cys Ala Val Cys Ala Cys Val Cys Val Cys Val Leu Cys Val Cys
          145          150          155          160
Val Cys Ala Val Cys Ser Ser Val Cys Cys Val Cys Cys Ala Phe Val
          165          170          175
Cys Val Leu Tyr Ala Arg Val Cys Ala Val Leu Val Cys Val Leu Cys
          180          185          190
Ser Cys Val Cys Cys Val Leu Cys Val Cys Ser Cys Gly Asp Ala
          195          200          205

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LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,
MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK,
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For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, polypeptide sequences encoded by these nucleic acids and uses thereof.

WO 02/044340 A3

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/47004

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07H 21/04; C12Q 1/68

US CL : 536/23.1, 24.3; 435/6

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1, 24.3; 435/6

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
GenCore Version 5.1.3, WEST 2.0**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 00/70050 A1 (GENENTECH, INC.) 23 November 2000 (23.11.2000) see entire patent, especially pages 9, 52-57, Figure 1.	1-9

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.*** Special categories of cited documents:**

A document defining the general state of the art which is not considered to be of particular relevance

E earlier application or patent published on or after the international filing date

L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

O document referring to an oral disclosure, use, exhibition or other means

P document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

Z document member of the same patent family

Date of the actual completion of the international search

19 March 2003 (19.03.2003)

Date of mailing of the international search report

11 APR 2003

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks

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Authorized officer

Gaby Benzon

Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/47004

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-9, 22-26, SEQ ID NO: 1

Remark on Protest

☐
☐

- The additional search fees were accompanied by the applicant's protest.
No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

The inventions listed as Groups 1-377 do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: The broadest recitation of the claimed product, namely a complementary sequence thereof of SEQ ID NO: 1 of claim 1 is known in the prior art. Hence, the "special" technical feature is not special and is not contribution over the prior art. For example, Baker et al. teach a complementary sequence thereof of SEQ ID NO:1 (WO 00/70059, publication date 23 November 2000, see SEQ ID NO: 1 and Figure 1). The sequence of Baker et al. meets the limitations of the claimed invention. Additionally, the sequences of SEQ ID NOS: 1-93 lack the same technical feature in that SEQ ID NO: 1 is not required or necessary for SEQ ID NO: 2 and visa versa. Similar reasons can be set forth for SEQ ID NOS: 3-93. Likewise the different sequences are both structurally and functionally distinct one from the other. Still further the polynucleotide composed of nucleotides, the polypeptide composed of amino acids, the composition composed of protein and carrier and the antibody composed of peptides are structurally and functionally distinct from each other. Still further, the different methods are distinct in that they require different starting materials, require different reagents and different methodologies that results in different effects. This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Groups 1-93, claim(s) 1-9, 22-26, in part, drawn to an isolated polynucleotide, vector and host cell selected from the group consisting of SEQ ID NOS: 1-93 and complementary sequences thereof, respectively. For example if the Group 1 is elected, the claims 1-9, 22-26 will be examined to the extent that they apply to SEQ ID NO: 1 whereas if the group 93 is elected, the claims 1-9, 22-26 will be examined to the extent that they apply to SEQ ID NO: 93.

Groups 94-186, claim(s) 10, 20, 21, in part, drawn to an isolated polypeptide encoded by any of the polynucleotide comprising the nucleic acid sequence selected from the group consisting of SEQ ID NO: 1-93, respectively. For example, if the group 94 is elected, the claims 10, 20, 21 will be examined to the extent that they apply to the polypeptide encoded by the polynucleotide of SEQ ID NO: 1 whereas if the group 186 is elected, the claims 10, 20 and 21 will be examined to the extent that they apply to the polypeptide encoded by the polynucleotide of SEQ ID NO: 93.

Groups 187-279, claim(s) 11, in part, drawn to a composition comprising the polypeptide encoded by any of the polynucleotide comprising the nucleic acid sequence selected from the group consisting of SEQ ID NO: 1-93, respectively. For example, if the group 187 is elected, the claims 11 will be examined to the extent that it applies to polypeptide encoded by the polynucleotide of SEQ ID NO: 1 whereas if the group 279 is elected, the claims 11 will be examined to the extent that it applies to the polypeptide encoded by the polynucleotide of SEQ ID NO: 93.

Group 280, claim(s) 12, drawn to an antibody.

Group 281, claim(s) 13-15, drawn to a method of detecting a polynucleotide.

Group 282, claim(s) 16, drawn to a method of detecting a polypeptide.

Group 283, claim(s) 17-18, drawn to a method of identifying a compound.

Group 284-376, claim(s) 19, in part, drawn to a method of producing a polypeptide comprising culturing a polynucleotide sequence selected from SEQ ID NO: 1-93 or complementary sequences thereof, respectively. For example if the group 284 is elected, the claim 19 will be examined to the extent that it applies to the polynucleotide sequence of SEQ ID NO: 1 whereas if the group 376 is elected, the claim 19 will be examined to the extent that it applies to the polynucleotide sequence of SEQ ID NO: 93.

Group 377, claim(s) 27-28, drawn to a method of treating.